## SiIC-Biotech/ChemLib



From: Sent: To: Subject:

Holleran, Anne

Friday, August 31, 2001 2:43 PM

STIC-Biotech/ChemLib

sequence search for 09/512,363

Please search the following sequences for 09/512,363:

commercial database and interference search for the following sequences: 1.

SEQ ID NO: 2(aa)

- 2. commercial database and interference search of SEQ ID NO: 2(aa) against nucleotide databases
- 3. oligomer search, commercial and interference databases, for SEQ ID NO: 2(aa)
- fragment search for SEQ ID NO: 2(aa): 4.

/amino acids -25 - 137 (if aa -25 is numbered as "1", then 1-162) " , then 26-162) ∠amino acids 1-137 then 26-139) amino acids 1-114 amino acids -25-139 , then 1-164) amino acids 21-139 then 46-164) then 33-154) amino acids 8-129 amino acids 8-48 then 33-73) amino acids 49-88 then 74-113) amino acids 89-129 then 114-154)

## Thanks

Anne Holleran AU: 1642 308-8892 Tel: Room: 8E03

Point of Contact: **Toby Port** Technical Info. Specialist CM1 1E01 TEL: 308-3534

<sup>\*</sup> note for fragment search: the application lists the fragments using the numbering of the specification which includes negative numbers. I have listed the fragments using the fragment numbering as listed in the claims and also the fragment numbers that would correspond if the first aa is numbered "1" and not numbered "-25".

inflammation; antiinflammatory; NF-KB activation;

autoimmune disease; therapy

Homo sapiens

Peptide Protein /note= "N-glycosylated" 162..180 /note= "transmembrane domain"

26..241 // peptide" // note= "mature protein" 146 /note= "signal peptide"

Modified-site

Domain

WO9940196-A1

Location/Qualifiers

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development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the sgulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or
                                                             Human 312C2 T cell. protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; heamatopoietic cells; lymphoid cell;
autofimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated 312C2 T cell gene - used to develop products for treating. e.g. cancers, auto-immune disorders, transplantation rejection and
                            Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                           /product- "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Pages 59-60; 71pp; English.
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Zlotník A;
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96US-0689943
28-JUL-1998 (flrst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Randall TD,
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N-PSDB; AAV19153.
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16-AUG-1996;
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100.0%; Score 246; DB 19; Length 241; 100.0%; Pred. No. 2.7e-24; Live 0; Mismatches 0; Indels 0
                                                                          7 1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                              Conservative
             Best Local Similarity
Matches 41; Conser
   Query Match
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Ş.
                AAY06605 standard; Protein; 241
                                AAY06605
RESULT
AAY06605
ID AAY0
XX
AC AAY0
XX
DT 26-0
XX
DE Humb
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26-OCT-1999 (first entry)

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RESULT 9
AAB27651
ID AAB27651 standard; Protein; 241 AA.
                                                  PRO364; tumour necrosis factor receptor; human; apoptosis;
Human TNF receptor homologue PRO364.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin Fc region are also claimed. PR0364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PR0364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PR0364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents human PRO364, a novel member of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are useful for modulating apoptosis, NF-KB activation and proinfiammatory or autoimmune responses in mammalian cells (claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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; Pred. No. 2.7e-24;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 41; Conservative 0
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Tumour necrosis factor receptor homologue – useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses

Marsters SA;

Gurney AL,

Goddard A,

Ashkenazi AJ, Godd Pitti RM, Wood WI;

WPI; 1999-494296/41. N-PSDB; AAX87670.

(GETH ) GENENTECH INC

99WO-US02642. 98US-0024087.

09-FEB-1999; 09-FEB-1998;

12-AUG-1999

inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.

/note= "transmembrane domain"

WO9940196-A1

99WO-US02642.

09-FEB-1999; 09-FEB-1998;

12-AUG-1999

'note= "N-glycosylated"

Modifled-site

..180

Domain

26..241 /note= "mature protein" /note= "signal peptide'

Location/Qualifiers

Homo sapiens

Peptide Protein

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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous onditions or degenerative conditions. They can be used in the egulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                  Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                 Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                                                    "human 312C2 protein"
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1..726
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96US-0689943
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/product=
(first entry)
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                                                                                                                         autoimmune disorders.
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N-PSDB; AAV19153.
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16-AUG-1996;
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28-JUL-1998
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Gaps
                                                                    The present sequence represents human PR0364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see ANX87610). Methods for the recombinant production of PR0364 polypeptides, e.g. in CHO.

Escherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respoises 157-167 of PR0364. PR0364 polypeptides proinfilmmatory or autoimmune responses in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                           (claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin For region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
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Mismatches 0;
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Claim 17; Fig 2A; 104pp; English.
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Best Local Similarity 100.0%; Pr
Matches 40; Conservative 0;
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Gaps

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Indels

20 ò

AAY06605 standard; Protein; 241 AA.

1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40

Length 241;

100.0%; Score 252; DB 19; 100.0%; Pred. No. 4.2e-20;

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 40; Conserv

Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses

Marsters SA;

Gurney AL,

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Goddard

Ashkenazi AJ,

Wood WI;

Pitti RM,

WPI; 1999-494296/41. N-PSDB; AAX87670.

(GETH ) GENENTECH INC

1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40 AAB27651 ID AAB2 RESULT g õ

AAB27651 standard; Protein; 241 AA

PRO364; tumour necrosis factor receptor; human; apoptosis;

Human TNF receptor homologue PRO364.

26-OCT-1999 (first entry)

AAY06605

RESULT 6
AAY06605
ID AAY06
XX
AC AAY01
XX
DT 26-OX
XX
DE HUMBI

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Gurney AL, Marsters SA;

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Tunnour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
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                                                                                                                                                                                                                                                                                                        Claim 17; Fig 2A; 104pp; English.
                                           99WO-US02642
                                                                          98US-0024087
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                                                                                                                                                                                      WPI; 1999-494296/41.
N-PSDB; AAX87670.
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Best Local Similarity
Matches 41; Conserv
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Pitti RM, Wood WI;
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PRO840; PRO877;
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                                            09-FEB-1999;
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           12-AUG-1999
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                                                                                                                                                                                                                                                       Isolated 312C2 T cell gene - used to develop products for treating, p.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
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100.0%; Pred. No. 6.4e-20;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
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162..180
/note= "transmembrane domain"
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/note- "signal peptide"
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                                                                97WO-US13931
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96US-0689943
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Best Local Similarity 100.
Matches 41; Conservative
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N-PSDB; AAV19153.
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   WO9806842-A1
                                                               14-AUG-1997;
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16-AUG-1996;
                                                                                                                                                                                 Gorman DM,
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tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO, Escherichia coll or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-x, 26-241 (i.e. the mature protein) and 26-x of the present sequence, where x is any one of amino acid respaise 157-167 of PRO364. PRO364 polypeptides
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PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;
PRO878; PRO879; PRO882; PRO885; PRO887;
                                                                                                                                                                       are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells (claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin Er region are also claimed. PRO364 can be used assays to identify other proteins or molecules involved in bind
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Pred. No. 6.4e-20;
Mismatches 0;
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Peptide
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WO9940196-A1

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Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-Inflammatory; antipsoriatic; anti-HIV; antiasthmatic; anaemia; dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.
                                                   Homo saptens
                                                                                                                                                                                                                                                                         21-JUL-1999;
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Baughn MR; Patterson C, "Potential phosphorylation site" "Potential phosphorylation site" "Potential phosphorylation "Potential phosphorylation "Potential phosphorylation 57.175 label Signature sequence /label = Signature\_sequence 'label- Signature\_sequence .- Signature\_sequence Signature\_sequence 165.,186 /label- Signature\_sequence "N-glycosylated Location/Qualifiers "Potential 99WO-US16637 98US-0093827 /label= s4 ..129 /note= ' 140 labelnote-/note= note. notenotenote-INCY-) INCYTE PHARM WO200005374-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Mod1fled-site Modified-site

Corley NC, Lal P, Hillman JL, ang YT,

2000-182699/16. N-PSDB; AAZ49948 Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease

Claim 1; Pages 64-65; 67pp; English.

The present sequence is a molecule associated with cell prollferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA -library. This sequence is expressed in cardiovascular and haematopoietic/lmmune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatoticopic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic, immunosuppressive, osteopathic, antiarthritic, uropathic, antiucer, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and anaemia

Ž 235 Seguence

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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement 5 312C2 stimulates proliferation of T cell Clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells
                           Gaps
                                                                                                       PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                            Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
autoimmune disorders.
                                                 1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                   Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                            ö
  Length 235;
                           Indels
                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of the human 312C2 T cell protein.
 Score 753; DB 21;
Pred. No. 2.8e-55;
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/product- "human 312C2 protein"
                        0; Mismatches
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96US-0689943.
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N-PSDB; AAV19153.
            Best Local Similarity
Matches 122; Conserv
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cv ·148
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recombinant production of PR0364 polypeptides, e.g. in CHO, Bscherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respdies 157-167 of PR0364. PR0364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells (claimed). Chimeric molecules comprising a PR0364 polypeptide (issed to a heterologous sequence such as epitope tag or immunoglobulin Fc region are also claimed. PR0364 polypeptide immunoglobulin Fc region are also claimed. PR0364 polypeptide interactions. This is useful for identifying inhibitors or aponters of receptor/ligand binding. The PR0364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PR0364 antibodies are useful in diagnostic articles, purification methods and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                       61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardiovascular; endothelial; anglogenic disorder; PR0179; PR0238; PR0364; PR0844; PR0846; PR01760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885; PR0887;
                                                                                                                                                                                                                                                                               100.0%; Score 753; DB 20;
100.0%; Pred. No. 2.9e-55;
ive 0; Mismatches 0;
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/label- "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB27651 standard; Protein; 241 AA.
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99US-0123957.
99WO-US12252.
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99US-0145698.
99WO-US20111.
99WO-US21090.
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Matches 122; Conservative
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12-MAR-1999;
02-JUN-1999;
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26-JUL-1999;
01-SEP-1999;
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30-NOV-1999
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Peptide
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                                                                                                                    1 GCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human PRO364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the
 which affect immunological responses, e.g. autoimmune disorders
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                                                                  Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NP-KB activation; autoimmune disease; therapy.
                                                                                           Indels
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                                                                Ouery Match 100.0%; Score 753; DB 19; Best Local Similarity 100.0%; Pred. No. 2.9e-55; Matches 122; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "transmembrane domain"
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162..180
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/note= "r
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N-PSDB; AAX87670.
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                            241 AA;
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                            Sequence
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Gaps

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Length 241; Indels 100 fsfgfgcidcasgtfsggheghckpwtdctqfgfltvfpgnkthnavcvpgsppaeplg 158

Standard; Protein; 241

AAW37839 AAW37839;

RESULT AAW37839

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he present sequence is a molecule associated with cell rollferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOTO6 coll illustriance. MACP-5 from Incyte clone 2809903 isolated from TLYMNOTO6 coll illustriance. MACP-5 shows antiarteriosclerotic, anti-HIV, hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antiinfrominetic, antiannosuppressalve, osteopathic, antiarthritic, uropathic, intiulcer, and ophthalmological activities. The present sequence is useful in the alignosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arterlosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders
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                                                                                                                                                               note- "Potential phosphorylation site"
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    /label = Signature_sequence
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N-PSDB; AAZ49948.
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Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell;

autoimmune disorders.

Homo sapiens.

/\*tag= a /product= "human 312C2 protein"

WO9806842-A1

19-FEB-1998

97WO-US13931 960S-0027901 960S-0689943

14-AUG-1997; 07-OCT-1996; 16-AUG-1996; Zlotník A;

Gorman DM, Randall TD, (SCHE ) SCHERING CORP.

WPI; 1998-159534/14. N-PSDB; AAV19153.

Location/Qualifiers

Amino acid sequence of the human 312C2 T cell protein.

(first entry)

28-JUL-1998

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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T treatment of conditions associated with abnormal physiology or treatment, of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         °,
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Pred. No. 5.2e-54;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Pages 59-60; 71pp; English.
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Matches 119; Conservative
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Length 235; Indels

Query Match 100.0%; Score 737; DB 21; Best Local Similarity 100.0%; Pred. No. 5.1e-54; Matches 119; Conservative 0; Mismatches 0;

235 AA;

Seguence

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FSFGFOCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVFGSFPAEPLG 119

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receptor-like protein (TRII receptor). The invention relates to TRII and two splice variants TRIISV1 and TRIISV2. The nucleotide sequences were determined by sequencing cloned coDNAs AAZ37765-23776. The TRII receptor and its splice variants show homology to the murine glucocorticoid induced tumnour necrosis factor receptor family-related gene (GITR).

TRIISVI and TRIISV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, blood coagulation disorders, blood cagulation cagula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, parkinson's disease, Huntington's disease, amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sclerosis, and Shy-Drager syndrome). The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                            the amino acid sequence of the human tumour necrosis factor
                                                                                                                                                                                                        tumour necrosis factor receptor-like polypeptides used to, e.g.
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                                                                                                                                                                                                                                                                                                                  Claim 14; Fig 1; 167pp; English
                                                                                                                                                                                                                                                 treat Digeorge syndrome -
                                                                                                      WPI; 2000-061922/05
                                                                                                                                          N-PSDB; AAZ37762
                                Ruben SM;
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234 AA; Seguence

Gaps ö Length 234; 0; Indels DB 21; Score 979; DB 21; Pred. No. 3.9e-70; Mismatches 0; ry Match 100.0%; S. best Local Similarity 100.0%; P. Matches 164; Conservative 0;

MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD

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YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTF 120 61 õ 8

SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164 121

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Amino acid sequence of the human 312C2 T cell protein. AAW37839 standard; Protein; 241 (first entry) AAW37839 AAW37839 RESULT BXBXBXB

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protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell chones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autbimmune disorders. Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autotimmune disorders. Isolated 312C2 T cell gene – used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders This is the amino acid sequence encoding the human 312C2 T cell Length 241; Indels SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164 100.0%; Score 979; DB 19; ő /product- "human 312C2 protein" 4e-70; Query Match 100.0%; Score 979; D Best Local Similarity 100.0%; Pred. No. 4e-Matches 164; Conservative 0; Mismatches Claim 2; Pages 59-60; 71pp; English. 'AAY06605 standard; Protein; 241 AA Location/Qualiflers Zlotník A; 97WO-US13931 96US-0027901 96US-0689943 Randall TD, /\*tag= (SCHE ) SCHERING CORP. WPI; 1998-159534/14. N-PSDB; AAV19153. 241 AA; Homo sapiens WO9806842-A1 14-AUG-1997; 07-0CT-1996; 16-AUG-1996; 19-FEB-1998 Gorman DM, AAY06605; Sequence 121 AAY06605 Key a XXX ð 셤 ò ò ; ;

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ö 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120 Gaps 9 9 1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 

80 cttcrhhpcppgggvgsggkfsfgfqcidcasgtfsggheghckpwtdctgfgf 133

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AAW37839 standard; Protein; 241

AAW37839

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Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autotimnue disorders.

/\*tag= a /product= "human 312C2 protein"

WO9806842-A1

19-FEB-1998

97WO-US13931 96US-0027901 96US-0689943

14-AUG-1997; 07-OCT-1996; 16-AUG-1996;

Location/Qualifiers 1..726

Homo sapiens

Amino acid sequence of the human 312C2 T cell protein.

28-JUL-1998 (first entry)

AAW37839;

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The present sequence is a molecule associated with cell notification, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 CDNA library. This sequence is expressed in cardiovascular and haematopoletic/lmmune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatotropic, antinflammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antihyroid, thyromimetic, immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease
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                                                                                                                                                             note- "Potential phosphorylation site"
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/label- Si
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protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
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Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders

Zlotník A;

Randall TD,

Gorman DM,

WPI; 1998-159534/14. N-PSDB; AAV19153.

(SCHE ) SCHERING CORP

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Gaps

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Length 235; Indels

Score 711; DB 21; Pred. No. 2.9e-50;

100.0%; 100.0%;

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 114; Conserv

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QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60 20 grptggppggpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 79

CTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114

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Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-inflammatory; antipsortatic; anti-HV; antiashmatic; anemaia; dermatological; antidabetic; nephrotropic; antithyroid; thyromimetic; hmmunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.
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WO200005374-A2

03-FEB-2000

21-JUL-1999;

98US-0093827. 22-JUL-1998;

INCY-) INCYTE PHARM INC.

Patterson C, Corley NC, fang YT, Lal P, Hillman JL, WPI; 2000-182699/16. N-PSDB; AAZ49948.

Baughn MR;

Polypeptides and polynuclectides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease

Claim 1; Pages 64-65; 67pp; English.

The present sequence is a molecule associated with cell proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMNOT06 CDNA library. This sequence is expressed in cardiovascular and heamatopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, dermatological, antidialetic, antipsoriatic, cytostatic, antiasthmatic, immunosuppressive, osteopethic, antidarthritic, uropathic, antiulcer, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, antiarcosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and

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CTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                   80 cttcrhhpcppgggvgsggkfsfgfqcidcasgtfsggheghckpwtdctqfgfltvffg 139
                                      Gaps
                                               1 ORPIGGPGCGPGRILLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCWCVQPEFHCGDPC 60
                                                                              79
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                Length 235;
                                   Indels
           Score 841; DB 21;
Pred. No. 1.8e-60;
                                 Mismatches
100.0%; Scc.
100.0%; Pre
0;
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Best Local Similarity 100.
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AAW37839 standard; Protein; 241 AA (first entry) 28-JUL-1998 AAW37839, AAW37839

Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen.specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell; Amino acid sequence of the human 312C2 T cell protein.

autoimmune disorders. Homo sapiens

"human 312C2 protein" Location/Qualifiers /\*tag= a /product= 1..726 /\*tag= Key

WO9806842-A1

97WO-US13931. 14-AUG-1997; 19-FEB-1998.

96US-0027901. 96US-0689943. 07-OCT-1996; 16-AUG-1996;

(SCHE ) SCHERING CORP.

Zlotnik A; 1998-159534/14

Randall TD,

Gorman DM,

WPI; 1998-159534/ N-PSDB; AAV19153

e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders Isolated 312C2 T cell gene

Claim 2; Pages 59-60; 71pp; English.

This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen specific proliferation and cytchine production by T cells, and potentiates T proliferation or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or treatment, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells 

> 235 AA; Sequence

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WO200053757-A2
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                                                                                                                  61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
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                                                          Gaps
                                                                                   1 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
which affect immunological responses, e.g. autoimmune disorders
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                                         Length 241;
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                                                         Indels
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                                                                                                                                                                                                                                                                            Inflammation; antiinflammatory; NF-KB activation;
                                        100.0%; Score 841; DB 19;
100.0%; Pred. No. 1.9e-60;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                      'note- "signal peptide"
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162..180
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                                                                                                                                                                                                                                                     Human TNF receptor homologue PRO364.
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                                          Query Match 100.
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N-PSDB; AAX87670.
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recombinant production of PRO364 polypeptides, e.g. in CHO,
Escherichia coli or yeast host cells, are provided. Claimed
polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the
mature protein) and 26-X of the present sequence, where X is any
cone of amino acid respoides 157-167 of PRO364. PRO364 polypeptides
are useful for modulating apoptosis, NF-KB activation and
proinfiammatory or autoimmune responses in mammalian cells
(claimed). Chimeric molecules comprising a PRO364 polypeptide
tused to a heterologous sequence such as epitope tag or
immunoglobulin Fc region are also claimed. PRO364 polypeptide
interactions. This is useful for identifying inhibitors or
agonists of receptor/ligand binding. The PRO364 polypeptides may
also be combined with an agent that is cyctoxic, chemicherapeutic
or a growth inhibitor. PRO364 antibodies are useful in diagnostic
inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CITCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
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100.0%; Pred. No. 1.9e-60;
iive 0; Mismatches 0;
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/label= "Signal peptide"
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99WO-US12252.
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Best Local Similarity 100.
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
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This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRII receptor). The invention relates to TRII and teceptor-like protein (TRII receptor). The invention relates to TRII and two variants TRIISVI and TRIISV2. The nucleotide sequences were determined by sequencing cloned COMAS AA237765-237766. The TRII receptor family related gene (GITR).

Induced Lumour necrosis factor receptor family related gene (GITR).

TRII, TRIISVI and TRIISV2 polypeptides may be involved in the requiation.

CC fall-type specific receptor-mediated call growth, differentiation, discontraction of the used for treating a disease state associated with abbrrant cell survival. They can be used for treating immune deficiency disorders, blood survival. They can be used for treating immune deficiency disorders, blood placeds syndrome, HIV infection, severe combined immunodeficiency from a second for treating immune deficiency disorders, blood placeds syndrome, HIV infection, severe combined immunodeficiency from a survival. They can be used for treating immune deficiency disorders, blood placeds used to treat heart attacks, strokes, Addison's disease, also be used to treat heart attacks, strokes, Addison's disease, also be used to treat heart attacks, strokes, Addison's disease, ansultiple solerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillann-Barre syndrome, insulin dependent of the placed of an antiquent molecule, organ rejection or graft versus host disease, inflammatory oconditions, ischaemia reperfusion of disease, inflammatory or organ rejection or graft versus host disease, inflammatory conditions, ischaemia and central nervous system disease, can be used to repair, reperfusion injury, postpheral nerve any protect tissue demaged by congenital callers. And short and subjects or protect tissue demaged by congenital nerve as system disease, parkinson's disease, matching or any protect surgery, fibrosis, reperfusion injury, partipheral nerve injures and central nervous syst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sclerosis, and Shy-Drager syndrome). The products can also be used for
                                                                                                                                                             tumour necrosis factor receptor-like polypeptides used to, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and prognosis
                                                                                                                                                                                                                                               Claim 14; Fig 1; 167pp; English
                                                                                                                                                                                         treat Digeorge syndrome -
                                                                            WPI; 2000-061922/05.
N-PSDB; AAZ37762.
                         Ruben SM;
                         IJ,
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234 AA; Seguence

Gaps ö Length 234; Indels Score 969; DB 21; Pred. No. 1.3e-69; ; Mismatches 0; ry Match 100.0%; Sc. Local Similarity 100.0%; Pr. Cches 162; Conservative 0;

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9 1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 

ò

1 maqhgamgafralcglallcals1ggrptggppgcgpgrlllgtgtdarccrvhttrccrd 60 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 윱 õ

õ 셤 ò g ò 염

> 61 ypgeccsewdcmcvqpefhcgdpccttcrhhpcppgggyqsqggkfsfgfqcidcasgtf 120 121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162 a ö

121

AAW37839 standard; Protein; 241 AA AAW37839; RESULT AAW37839 SX SX EX S

(first entry) 28-JUL-1998

Amino acid sequence of the human 312C2 T cell protein.

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protein. The 312C proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the
              Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; heamatopoletic cells; lymphoid cell; autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulation or development of haematopoietic cells, e.g. lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence encoding the human 312C2 T
                                                                                                                                                                          /product= "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Pages 59-60; 71pp; English.
                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                    Zlotnik A;
                                                                                                                                                                                                                                                                      97WO-US13931
                                                                                                                                                                                                                                                                                                                     96US-0689943
                                                                                                                                                                                                                                                                                                                                                                                 Randall TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other T cell disorders
                                                                                                                                                                                                                                                                                                                                                    (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-159534/14.
N-PSDB; AAV19153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which affect
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                      14-AUG-1997;
                                                                                                                                                                                                                                                                                                                     16-AUG-1996;
                                                                                                                                                                                                                                                                                                     07-OCT-1996;
                                                                                                                                                                                                                                       19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                   Gorman DM,
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61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120 Gaps 1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD ö Length 241; Indels SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162 100.0%; Score 969; DB 19; 100.0%; Pred. No. 1.3e-69; tive 0; Mismatches 0; Matches 162; Conservative Best Local Similarity Query Match 121

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AAY06605 standard; Protein; 241 AA. RESULT AAY06605 **BXXX**  2, Appl , Appli , Appli , Appli

Appli

2, Appli 5395760

Perfect score:

Run on:

Sequence:

Scoring table:

eq:

Database :

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Sequence 4, Appli
Sequence 23, Appli
                              Sequence 6, A
Sequence 49,
Sequence 11,
Sequence 6, A
Sequence 12,
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Sequence 7,
Sequence 2,
Patent No. 5
                                                                                                                                                                                        Sequence 2,
Sequence 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
TITLE OF INVENTION: RANGALIAN CELL SURFACE ANTIGENS; RELATED TITLE OF INVENTION: REAGENTS
CORRESPONDENCE ABENESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
COUTRY: California
COUNTRY: USA
ZIP: 94304-104
ZIP: 94304-104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CALING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: CALING EGVIN P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REFERENCE/COKET NUMBER: 34,090
REFERENCE/COKET NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
         US-08-996-139-6
US-08-995-659-6
US-08-974-022-49
US-08-974-022-6
US-08-995-659-2
US-08-995-659-2
US-08-995-659-2
US-08-995-139-15
US-08-995-139-15
US-08-995-659-15
US-08-995-659-15
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901 California Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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131
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; Search time 65.86 Seconds
(without alignments)
50.647 Million cell updates/sec
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                                                                                                                                                                                                                             1 MAQHGAMGAFRALCGLALLC......FPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcvGCOMB.pep:*
/cgn2_6/ptodata/2/laa/pcvGCOMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-911-423-2

US-09-188-930-191

US-08-097-827-7

US-08-097-827-1

US-08-097-827-11

US-08-097-827-11
                                                                                                                                                                                                                                                                                                                                                  number of hits satisfying chosen parameters:
                                                                                                                     September 4, 2001, 15:57:34;
                                                                                                                                                                                                                                                                                                                197339 seqs, 20590346 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                        US-09-512-363-2_COPY_1_162
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match 1
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605 255 166.5 166.5 166.5 166.5 160.

Result

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COUNTRY:
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                                                                                                                                   61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVGSGKFSFGFGCIDCASGTF 120
                                                                                                                   61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                        Gaps
                                                 1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                  MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 937; DB 3; Length 228;
Pred. No. 3e-74;
                   Indels
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APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                         121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
     5.3e-77;
                   Mismatches
     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         Acquence 6, Application US/08911423
nt No. 6111090
GERAL INFORMATION:
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100.0%; Pre
0;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gorman, Daniel M
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: RAMMALII
TITLE OF INVENTION: REGGENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 amino acids
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palo Alto
California
Best Local Similarity
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US-08-911-423-6
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                   162;
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                           CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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O
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.7%; Score 937; DB 3; 100.0%; Pred. No. 4e-74;
                                                                                                             HCKPWIDCIOFGFLIVFPGNKIHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.08; Pred. No. 4e-
Matches 156; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             ; Sequence 8, Application US/08911423
; Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS ADDRESSE: DNAX Rese
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304-1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162

127

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7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66 

Mismatches

Matches 156; Conservative

Best Local Similarity

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CITCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                  Sequence 8, Application US/08911423
Patent No. 6111090
                                                                                                                      121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                              US-08-911-423-8
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                                                                                                                                                              61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                  Gaps
                                                                          1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                              20 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
               Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 241;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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               Score 841; DB 3;
Pred. No. 3.2e-66;
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Pred. No. 3.3e-66;
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
GIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/027,901 FILING DATE: 07-0CT-1996 ATTORNEY/AGENT INFORMATION: NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DX0612K
                                                                                                                                                                                                                                                                                                                         pnce 4, Application US/08911423 nt No. 6111090
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Best Local Similarity 100.0%; P
Matches 137; Conservative 0;
                                                                                                                                                                                                                                          140 NKTHNAVCVPGSPPAEP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
          Ouery Match
Best Local Similarity 100.
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650-496-1200
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; MOLECULE TYPE: protein
US-08-911-423-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO
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California
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Best Local Similarity
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APPLICANT: Gorman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                       9-911-423-4
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901 California Avenue

E: Floppy disk IBM PC compatible

94304-1104 USA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 841; DB 3; Best Local Similarity 100.0%; Pred. No. 4.2e-66; Matches 137; Conservative 0; Mismatches 0;
PRIOR APPLICATION 5730
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                    DX0612K
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                           linear
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TOPOLOGY: lir
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Indels

Mismatches

1 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60 

Length 228;

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1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: 2locnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN STILL SOFTWARE SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-4UG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-4UG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,409
FILING DATE: 07-0021-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 711; DB 3;
100.0%; Pred. No. 2.8e-54;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DNAX Research Institute
STREET: 901 Callifornia Avenue
CITY: Palo Alto
STATE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          Sequence 8, Application US/08911423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1104
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-911-423-8
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                                                        Gaps
                                                                                              1 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                        20 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                             61 CTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                    Indels . 0;
                                                                                                                                                                                        CTICRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWIDCTQFGF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Gorman, Daniel M.
PPLICANT: Randall, Troy D.
PPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
    Score 711; DB 3;
Pred. No. 2.2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0%; Score 711; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 114; Conservative 0; Mismatches 0;
Query Match 100.0%; Score 711; DB Best Local Similarity 100.0%; Pred. No. 2.2e-Matches 114; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/911,423
CLASSIFICATION NUMBER: US/08/911,423
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AGC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: O7-0CT-1996
ATORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTAATION NUMBER: 34,090
REGISTAATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 901 Califo
CITY: Palo Alto
STATE: California
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Gaps

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Length 311; Indels

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RESULT 1
US-08-911-423-4
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135.5
135.5
131
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129.5
129.5
129.5
121
121
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121
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22266666666666444444
8000126450780012645
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Sequence 7, Appli
Sequence 7, Appli
Sequence 11, Appl
Sequence 11, Appl
                                                                  ; Search time 65.86 Seconds
(without alignments)
51.273 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                         US-09-512-363-2_COPY_1_164
979
1 MADHGAMGAFRALCGLALLC......GNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6,
Sequence 8,
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Sequence 2,
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Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
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.: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/ReCOMB.pep:*
.: /cgn2_6/ptodata/2/laa/ReCOMB.pep:*
.: /cgn2_6/ptodata/2/laa/ReCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-911-423-2
US-09-188-930-191
US-08-097-827-7
                                                                                                                                                                                                     I number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-494-574-7
US-08-097-827-11
US-08-494-574-11
US-08-147-784-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-195-967-2
US-08-236-918A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-236-918A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-996-139-4
                                                                                                                                                                                  197339 seqs, 20590346 residues
                                                                    4, 2001, 15:57:36
                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match ]
                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
166.5
166.5
166.5
166.5
160.5
160.5
150.5
158.5
158.5
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139.5
139.5
139.5
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APPLICANT: Gorman, Daniel M.

APPLICANT: Gorman, Daniel M.

APPLICANT: Randall, Troy D.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: REAGENTS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAK Research Institute

STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-40G-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION WHERE: US 60/023,419
FILING DATE: 16-40G-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-00T-1996
APPLICATION NUMBER: US 60/027,901
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-00T-1996
ATTORNEY/AGENT INFORMATION:
NAME: CALING EGATION P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
US-08-995-659-4
US-08-996-139-6
US-08-974-022-6
US-08-974-022-6
US-09-042-785A-12
US-09-042-785A-12
US-09-042-785A-12
US-08-996-139-2
US-08-996-138-2
US-09-042-785A-23
US-08-996-139-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 241 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein

US-08-911-423-4
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Length 241;

DB 3;

100.0%; Score 979;

RESULT

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61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGHEG 120
                      67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Felease #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911.423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 947; DB 3; 1
Pred. No. 4.3e-75;
); Mismatches 0;
                                                                                                                127 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                  STREET: 901 California Avenue CITY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-AUG-1997
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                       APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match . 96.7%;
Best Local Similarity 100.0%;
Matches 158; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,(
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650-496-1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-911-423-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                               121
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                                                                                                                                               61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSGGKFSFGFQCIDCASGTF 120
                                                                                                                           61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                      0; Gaps
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                                                     1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: REAGENTS
NUMBER OF SECUNCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 228;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.7%; Score 947; DB 3; Length 22. 100.0%; Pred. No. 3.2e-75; Live 0; Mismatches 0; Indels
                                                                                                                                                                                               121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                    121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
Best Local Similarity 100.0%; Pred. No. 5.7e-78; Matches 164; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
IOR ADDITOR: 536
                                                                                                                                                                                                                                                                                                       8-911-423-6
ence 6, Application US/08911423
nt No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-911-423-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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Gaps

127 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164

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Sequence 8, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TILLE OF INVENTION: RAMBALIAN CELL SURFACE ANTIGENS; RELATED
TILLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-A0C-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-007-1996
ATTORNEY AGENT INFORMATION
NAME: Ching, Edwin P
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                  DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                   901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SENGIH: 311 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                           Gaps
                                                                              1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60
                                                                                                                                                               61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                      100 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 158
                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
ITTLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
              Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FALALY
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
      Score 737; DB 3;
Pred. No. 1.2e-58;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 737; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e-58;
Matches 119; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DX0612K 'ELECOMMUNICATION INFORMATION: TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,090
Ouery Match
Best Local Similarity 100.0%;
Matches 119; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-911-423-4
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US-08-911-423-4
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1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60
                                                                                                    61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                    100 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 158
              Length 311;
Query Match (100.0%; Score 737; DB 3; Best Local Similarity 100.0%; Pred. No. 1.5e-58; Matches 119; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                        Randall, Troy D.
Zlotnik, Albert
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
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1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60

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PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120 93 PCPPGGGVGSGGKFSFGFGCIDCASGTFSGGHEGHCKPWTDCTGFGFLTVFPGNKTHNAV 152

CV 122 CV 154

153 121

MAMMALIAN CELL SURFACE ANTIGENS; RELATED

REAGENTS

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET:

TITLE OF INVENTION:

APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotnik, Albert

GENERAL INFORMATION:

E: DNAX Research Institute 901 California Avenue

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Sequence 8, Application US/08911423 Patent No. 6111090
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                                                                                                                                                       PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                  1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                          NERAL INFORMAN: Gorman, Danler ...
APPLICANT: Gorman, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: Albert, Albert, Albert, Albert, Albert, Albert, Albert, TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED TITLE OF INVENTION: REAGENTS
     DB 3; Length 228;
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                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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100.0%; Score 753; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.3e-60;
Matches 122; Conservative 0; Mismatches 0;
     Score 753; DB 3
Pred. No. 6e-60;
                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/027,901 FILING DATE: 07-0CT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          quence 4, Application US/08911423 pnt No. 6111090 NERAL INFORMATION:
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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amino acid
                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-AUG-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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STATE: California
               Similarity
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STREET: 90
Query Match
Best Local Simi
Matches 122;
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61 PCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
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                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 753; DB 3;
Pred. No. 7.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/023,419
FILIND DATE: 16-A0G-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILIND DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                             DX0612K
                                               ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 41sk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: 650-852-9196
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100.0%;
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Best Local Similarity 100.C
Matches 122; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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CITY: Palo Alto
STATE: California
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                                    USA
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                                    COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: 2.10cn111, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                            MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 73
                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
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Pred. No. 3.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-007-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                    DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
SIOR ADDITION: 536
                                                                                                                                                                                                                                                                   S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 6111090
                                                                                                                                                     901 California Avenue
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                                                                               REAGENTS
   Daniel M.
                         Troy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 241 amino acids
amino acid
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                              ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                          TITLE OF INVENTION: MA
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: E
CORRESPONDENCE ADDRESS:
                       Randall,
Zlotnik,
                                                                                                                                                                       CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 41; Conserv
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                                                                                                                                                                                                                                                                                            COMPUTER:
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                       APPLICANT:
APPLICANT:
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                                                                                                                                                       STREET:
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
MBER OF SEQUENCES: 8
CRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 232;
   Length 228;
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                                          Indels
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APPLICATION DATA:
APPLICATION UNMER: US/08/911,423
FILING DATE: US/08/911,423
FILING DATE: US/08/911,423
FILING DATE: US/08/911,423
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: US-07-07-1996
ATTORNEY/AGENT INFORMATION:
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                                                                               1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                   27 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 67
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100.0%; Pred. No. 3.6e-21;
tive 0; Mismatches 0;
   Score 255; DB 3;
Pred. No. 3.6e-21;
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 E: DNAX Research Institute
901 California Avenue
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US-08-911-423-4
Sequence 4, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
                                                                                                                                                                                                                Sequence 7, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
BLECOMMUNICATION INFORMATION:
FREEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
100.0%;
illarity 100.0%;
Conservative 0;
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STREET: 901 C.
CITY: Palo Alto
CITY: California
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     Query Match
Best Local Similarity
Matches 41; Conserv
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Matches 41; Conser
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

Query Match

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                 Gaps
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APPLICANT: Gorman, Daniel M.
APPLICANT: Gorman, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: RAGENTS
WHER OF SEQUENCES: 8
PRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 241;
      Length 228;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-Aug-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-Aug-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
ANDER ALL OF AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                          68 CVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCI 107
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  100.0%; Score 252; DB 3;
100.0%; Pred. No. 2.4e-20;
ive 0; Mismatches 0;
                                                                                   1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
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Pred. No. 2.5e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  Sequence 4, Application US/08911423 Patent No. 6111090
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Patent No. 6111090
GENBRAL INFORMATION:
APPLICANT: Gorman, Daniel M.
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TELEPHONE: 650-852-9196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
Query Match
Best Local Similarity 100.0
Matches 40; Conservative
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Best Local Similarity 100.
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-911-423-4
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California
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US-08-911-423-8
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Gaps
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 311;
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                                                                                                                                                                                                                 COUNTRY: CALLLY LILLY
COUNTRY: USA
ZIP: 94304-1104
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TAGEN: PC-DOS/MS-DOS
SOFTWARE: PAPELICATION DAR:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 10-AUG-1996
ATTONNEY ADDATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTONNEY AGASTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 252; DB 3;
Pred. No. 3.1e-20;
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APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURE
TITLE OF INVENTION: REGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STRY: Palo Alto
CITY: Palo Alto
STATE: California
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Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Some State Similarity 100.0%; P. Matches 40; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX(
TELECOMMUNICATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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California
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MAMMALIAN CELL SURFACE ANTIGENS; RELATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 246;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                               SSEE: DNAX Research Institute
F: 901 California Avenue
Palo Alto
: California
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901 California Avenue
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-08-911-423-2
Sequence 2. Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
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TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: MAMALIAN
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
STREET: 901 California Aven
                                                                             REAGENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 amino acids
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Conservative
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                         NUMBER OF SEQUENCES: ECORRESPONDENCE ADDRESS
                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 41; Conserva
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STATE: California
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                                                                                                                               ADDRESSEE:
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                                                  Gaps
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APPLICANT: Randall, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
ATTLE OF INVENTION: REAGENTS
MBER OF SEQUENCES: 8
ADDRESSEDONDE ADDRESS:
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          Length 228;
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                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-40G-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-40G-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
                                                                                                       108 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 148
                                                                           1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
ch 100.0%; Score 246; DB 3; 1 Similarity 100.0%; Pred. No. 1.2e-23; 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 246; DB 3;
Pred. No. 1.3e-23;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
LLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     Sequence 4, Application US/08911423 Patent No. 6111090
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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STREET: 901 C.
CITY: Palo Alto
Query Match
Best Local Similarity
Matches 41; Conserv
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US-08-911-423-8
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Gaps

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COUNTRY: USA ZIP: 94304-1104

Sequence 8, Application US/08911423 Patent No. 6111090 GENERAL INFORMATION:

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Gorman, Daniel M.

APPLICANT:

Length 311;

**09Y5U5**;

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STRAIN-BALB/C;
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Riccardi C.;
Migliorati G., Riccardi C.;
"Gene structure and chromosomal assignment of GITR, a mouse member of
the tumor necrosis factor/nerve growth factor receptor family.";
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U82534; AAB81231:1;
EMBL; AF109216; AAF14231:1;
MGD; MGI:894675; Infrsf18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 PGCGPGRLLLGTGTGARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 PGCGPGKVQNGSGNNTRCCSLYA------PGKEDCPKERCICVTPEYHCGDPQCKICKH 79
                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.; "A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.; "Identification of three novel mRNA splice variants of GITR."; Call Death Differ. 0:0-0(2000).

EMBL, AF229433; AR61567.1; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 05, Last sequence update)
GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
TNFRSF18 OR GITR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 AA; 24450 MW; 594932BA425A79CA CRC64;
                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5%; Score 373.5; DB 1753.7%; Pred. No. 1.8e-33; iive 19; Mismatches 24;
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                                                                                                                                                    Created)
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                                                                                                                                             (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
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Best Local Simi
Matches 58;
                                                                                                                                                01-0CT-2000
01-0CT-2000
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                                                                                     Q9JKR2
Q9JKR2;
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Q9JKR2
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                                                                                                                                                                                                                                                                                                                                                       TISSUE-BONE MARROW;
GUINEY A.L., MAISTERS S.A., Huang A., Pitti R.M., Mark M.,
GUINEY A.L., MAISTERS S.A., Huang A., Pitti R.M., Mark M.,
GODDANIN D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
GODDANIN D.T., Gray A.M., Baker K.P., Godowski P.J., Ashkenazi A.;
Indentification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
GUIT. Biol. 0:0-0(1999).
EMBL, AF125304; AAD22635.1;
InterPro; IPR001388;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Identification of a soluble human GITR splicing (hGITR-D).
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF241229; AAF63506.1; - C986652AC97AF2CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query.Match 96.1%; Score 683; DB 4; Length 255; Best Local Similarity 100.0%; Pred. No. 2.5e-67; Matches 109; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26000 MW; 90DC3B4AA7E82CBE CRC64;
                                                                  01-MAR-2001 (TrEMBLrel. 12, Last sequence update) GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
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008999 mus musculu

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Q63720 rattus norv Q63721 rattus norv

09s9f4 phytolacca 09ept5 mus musculu 018238 caenorhabdi 09xsz8 cercopithec 09gpm caenorhabdi 008727 rattus norv

29v383 drosophila

OM protein

Run on:

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Searched:

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MEDLINE-99156876; PubMed-10037686; Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Liu D., Wang S.X., Kwon B.S.; "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand."; J. Biol. Chem. 274:6656-6061(1999).
EMBL; AF17297; AAD19694.1; -...
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2010 (TrEMBLrel. 16, Last annotation update)
TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;
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                               Q18238
Q9X528
Q9GPM8
Q03727
Q02660
Q08712
Q35806
Q9UHP4
Q00300
Q003720
Q63720
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O75412
Q28019
Q94438
O57484
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O08999
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Receptor.
SEQUENCE 234 AA; 2511
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1587
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Q9jke0 rattus norv
Q9ddd2 gallus gall
Q95407 homo sapien
Q9xvx3 caenorhabdi
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022685 caenorhabdi
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_vertebrate:*
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                             STRIN-WISTAR: TISSUE-SMOOTH MUSCLE, AORTA;
MEDLINE-99330195; PubMed-10403401;
MEDLINE-99330195; PubMed-10403401;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle calls is mediated by nuclear factor kappaB and signal transducer and ress month transcription-1.";
FEBS Lett. 453:191-196(1999).
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                               RVHTTRCCRDYPGEE-----CCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQ 78
                                                                                                                                                                                                                                                                                                                                                                                           14 RCHQHRHCELNQGLQVKKEGTAVSDTVCTCKEGQ-HCASKECETCAQHRPCGPGFGVVQM 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .WD 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                           46; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBL; AJ293700; CAC20218.1;
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                     Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                     STRAIN-WISTAR; TISSUE-SMOOTH MUSCLE, AORTA;
Krzesz R., Hecker M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AFZ4131; AAF43717.1; -.
InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                       55BFF8327A0933B2 CRC64;
                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.7%; Score 119; DB 13; Best Local Similarity 26.7%; Pred. No. 1.6e-05; Matches 43; Conservative 7; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                     Score 122; DB 11;
Pred. No. 3.3e-06;
6; Mismatches 46;
107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ATETTOTVCQPCPVGFFSNGSSLFEKCHPWTSC 105
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                     Created)
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 PRT;
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                                                                                                                                                                                                                                                                                                       11819 MW;
                   01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16, CD40 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 33.3%;
Matches 31; Conservative
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                               107
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                                                                                                                                                                                                                                                                                                        107 AA;
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                           NCBI_TaxID-10116;
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SEQUENCE
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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Hunga A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.; "Genomic amplification of a decoy receptor for Fas ligand in lung and Nature 396:699-703(1998).
                                                KERHCTPHEICEDNAGLIVKRHGNATHNTVCQC-RAGMHCSDASCQTCVENBPCKQGFGF 131
----CMCVQPEFHCGDPCCTTC-RHHPCPPGQG- 74
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Bai C., Connolly B., Metker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Gallowy S.M., Liu Q., Austin C.P., Caskey C.T.;
"Overexpression of M68/DGR3 in human gastrointestinal tract tunors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TRG) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJS83P15.1.1)
DCR3 OR TR6 OR TNFRSF6B.
                                                                                                                                          75 VQSQGKFSFGFQCIDCASGTFS -- GGHEGHCKPWTDCTQFG 113
                                                                                                                                                                                                             132 VAAMAEARMISPCEPCAEGIFSNVSSKIEPCHFWISCEEKG 172
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                                                                                                                                                                                                                                                                                                                                                                                            300 AA
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE-99253915; PubMed-10318773;
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SEQUENCE FROM N.A.
MEDLINE=99087326; Pubmed=9872321;
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EMBL, AF217796; AAF35244.1;
EMBL, AF217794; AAF33686.1;
EMBL, AL121845; CAC03668.1;
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267 AA;
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Matches 38; Conserv
                                                              SEQUENCE FROM N.A.
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NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             27 PGCGPGKVQNGSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79
                                                                                                                                                                                                                                                                                                                                                                                           7 PGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                      GLUCOCORTICOID INDUCED THER FAMILY
                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                        DB 11; Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SO YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWINCSQFGF 127
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                                                                                                                                               RELATED PROTEIN,
50D8C275D9C56259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00181; EGF; 1.
SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;
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Last annotation update)
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InterPro; IPR000561; -.
                                                                                                                                                                                 25334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 15, TrEMBLrel. 15, TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
InterPro; IPR000561; -. SMART; SM0181; EGF; 1. Signal; Receptor.
                                                                                       19
228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                 228 AA;
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                70
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                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000
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                                                                                                                                                                                 SEQUENCE
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Q9JKR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9JKR3;
                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9JKR3
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                                                                                                                         CHAIN
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10 09,0KR3
10 09,0KR3
10 00,0KR3
10 01,0KR3
10 0
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100
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AC 005
DD 001
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         27 PGCGPGKVQNGSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQ-----PEFHCG 57
Nocential G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D., Migliorati G., Riccardi C.; Miglication of three novel mRNA splice variants of GITR."; Cell Death Differ. 0:0-0(2000).

EMBL; AF229434; AAF61568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 CQP-----GYGMVSRCNRSQDTICHPCEPGFYNEAVNYQACKPCTQCNRRSGSEPQQECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40 PRECURSOR (FRAGMENT).
Oytoclogus cuniculus.(Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 DPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                           Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.4%; Score 130.5; DB 6; Length 267; 32.8%; Pred. No. 8.3e-07; Live 7; Mismatches 50; Indels 21;
                                                                                                                                                                                                                                                         47.7%; Score 339.5; DB 11; Length 52.5%; Pred. No. 6e-30; cive 17; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isono T., Seto'A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003911; BAA20059.1; -.
HSSP, P19438; 1EXT.
InterPro; IPR001368; -.
Pfam; PF00020; TWRR_c6; 3.
PROSITE; PS00050; TWRR_NGFR_1; 2.
PROSITE; PS0050; TWRR_NGFR_2; 2.
SMART; SM00208; TNFR, 1.
                                                                                                                                                                                  14106 MW; F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A8B4CD3173C9500B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA
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Best Local Similarity 52.55
Matches 53; Conservative
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18
267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                     SMART; SM00181; EGF; 1
SEQUENCE 132 AA; 14
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9

Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

Rhabditidae; Peloderinae; Caenorhabditis. NCBI\_TaxID=6239;

01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

PROTEIN.

F01B7.8

Sims M.; submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.

MEDLINE-94150718; Pubmed-7906398;

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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Wilson R., Alnscoup R., Anderson K., Baynes C., Berks M.,
Wilson R., Alnscoup R., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Spreak J.; Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Best Local Similarity
Matches 30; Conserv
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9
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- 60
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                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. EMBL; AF018253; AAB86809.1; -. HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%; Score 108; DB 4; Length 616; 22.5%; Pred. No. 0.00049; tive 10; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 HTTRCCR-----DYPGEECCSEWDCMCVQPEFHCG-------DPC--
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N-LINKED (GLCNAC, . .) (PO
E3DE9A7A08196F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Signal; Repeat.
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CYTOPLASMIC (POTENTIAL).
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SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00208; TNFR; 1
Receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 32; Conserv
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NCBI_TaxID=9606;
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TRANSMEM
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SEQUENCE
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Matches
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Search completed: September 4, 2001, 16:14:31
Job time: 1218 sec
116 PCCCGCGC-----GCGCCGCGGG 133
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(TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)

164 AA

PRT;

PRELIMINARY;

022048 022048; 01-NOV-1996 01-NOV-1996

RESULT 15 Q22048 ID Q22048 AC Q22048; DT 01-NOV-DT 01-NOV-

158 YFSDAFSSTDKCRPWTNCTFLG 179

g

74 GCGGG----GGGCGCCCCR---PRCC-----CCCRRCCTCCRT--CCCTRCCTCCR-- 115

68 PCPPGQGVQSQGKFSFGFQCIDCASG 93

8 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 67

1; Mismatches

Conservative

15.0%; Score 107; DB 5; Length 164; 34.9%; Pred. No. 0.00021;

PS00269; DEFEMBLY,
PS0022; EGF\_1; UNKNOWN\_1.
PS01208; VWFC; UNKNOWN\_1.
16499 MW; C002D48D36C9FCED CRC64;

PROSITE; PS00198; 4FE45\_FERREDOXIN; UN PROSITE; PS00269; DEFENSIN; UNKNOWN\_1. PROSITE; PS0022; EGE\_1; UNKNOWN\_1. PROSITE; PS01208; VWFC\_1 UNKNOWN\_1. SEQUENCE 164 AA; 16499 MW; C002D46

EMBL; Z66499; CAA91301.1;

InterPro; IPR000561

InterPro; InterPro;

Wature 368:32-38(1994).

elegans.

UNKNOWN\_1

9

Gaps

26;

Indels

---GCGCCGCGGG 122

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105 PCCGCGC--
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                                                                                6HUM60
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Q9Y6Q6
                                      RESULT
Q9WUH9
qq
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                                       9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94150718; PubMed=7906398; Milson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Anderson K., Coper J., Cooper J., Cooles Denfield J., Burton J., Connell M., Copesy T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Fewello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Larreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin K., Wanterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                           52 CPPGTFV-----QRPCRRDSPTTCGPCPRHYTQFWNYLERCRYCNVLCGEREEEARAC 105
                                                                                                                      ---HHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG- 101
                                                                                                                                               106 HATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTOCOPCPPGTFSASSSSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCGGG----GGGCGCCCCR---PRCC------CCCRPKCCCTCCRTCCTRCCTCCR-- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                       Gaps
                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 67
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM--CVQPEFHCGD----PC
                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
           Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 112; DB 5; Length 152
Pred. No. 5.5e-05;
0; Mismatches 32; Indels
                                       54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcmurray A.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E254F0BE476D354 CRC64;
                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
           Score 117; DB 4;
Pred. No. 2.8e-05;
8; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00198; 4FE45_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS00764; ED00UCLEASE_III_1; 1.
SEQUENCE 152 AA: 15645 MW; 62254F0BE476D35
                                                                                                                                                                                                                                                                                                                                                                                            Rhabditidae, Peloderinae, Caenorhabditis
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.8%;
Best Local Similarity 34.9%;
Matches 30; Conservative (
                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
EMBL; 249886; CAA90055.1; -.
InterPro; IPR001561; -.
InterPro; IPR001007; -.
InterPro; IPR001450; -.
InterPro; IPR001502; -.
           16.5%;
ilarity 27.8%;
Conservative
                                                                                                                       61 CTT----CR-----
                                                                                                                                                                                                                                                                        PRELIMINARY;
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166 EQCQPHRNCTALG 178
                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                          102 -HCKPWTDCTQFG 113
        Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                        O9XVX3;
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                                                                                                                                                                                                                                               RESULT 12
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PROSITE; PRO0010; EGFBLOOD.
PROSITE; PRO0010; EGFBLOOD.
PROSITE; PRO0010; ASLAHUDROXIL; 43.
PROSITE; PRO1010; ASLAHUDROXIL; 43.
PROSITE; PRO10186; EGF_1; UNKNOWN_2.
PROSITE; PRO1187; EGF_2; 36.
PROSITE; PRO1187; EGF_CA; 43.
SMART; SM00179; EGF_CA; 43.
SMART; SM00179; EGF_LIKe domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 2906 AA; 313372 MM; 9EE64E727044EF58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676 CPPG---LAVGVDGRVCVDTHMRSTCYGEIKKGVCVRPFPG--AVTKYECCCANPDYGFG 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 DPCCTTCRHHPCPPGQGVQSQGKFSFGF-----QC-ID---CASG---TFSGGHE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 EPC-----QPCPAKNSAEFHGLCSGGVGITVDGRDINECALDPDICANGICENLRGSYR 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                   Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 CGPGRLLLGTGTGTDARCC-----RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG 57
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2906;
                                                                                                                                                                                                                                                                                              Yang Q., Ota K., Tian Y., Kumar A., Wada J., Kashihara N., Wallner E.I., Kanwar Y.S.; "Cloning of rat fibrillin-2 cDNA and its role in branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                morphogenesis of rat embryonic lung.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF135060; AAD34439.1; -.
                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 108.5; DB 11; 25.2%; Pred. No. 0.0016;
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2906 AA
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                                                Created)
PRT;
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                                              (TrEMBLrel. 12,
                                                                                                 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.2
Matches 31; Conservative
PRELIMINARY;
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                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; -. InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002212; -- Pfam; PF00008; EGF; 46 Pfam; PF00683; TB; 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                        FIBRILLIN-2.
                                                01-NOV-1999
                                                                       01-NOV-1999
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us-09-512-363-2\_copy\_26\_139.rspt

15;

Gaps

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123 GHEGHCKPWIDCIQFGFLIVFPGNKIHNAVC-----VPG--------156
                                                                                                                                                                                                                                                                                                --SPPAE-----PLGW-----LTVVLLAVAACVLLLTSAQ 184
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                                                                                                                                                                                             -CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 122
                                                                                                                                                                                                                     95 ICTC-RPGWYCALSKQEGCRLCAPLR--KCRPGFGVARPGTETSDVVCKPCAPGTFSNTT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CRVHTTRCCRDYPGEECCSEWD-- 71
                                                                                                                                                                  35 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR
                                                                                                                                                                                                                                                                       152 SSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP
                                                                                                                                                                                                                                                                                                                          208 TPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He Z. Y., Yang G.-Z., Zhang W.-J., Wu X.-F.,;
"Cloning and Expression of Osteoprotegerin from Homo sapiens.";
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
EMBL; AF194187; AAF20168.1; -.
HSSP; P25942; ICDF.
InterPro; IPR001888; -.
InterPro; IPR001888; -.
FinterPro; IPR001368; -.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                  Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                         Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 138; DB 4; Length 372; 21.8%; Pred. No. 4.7e-06; Live 18; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 HTTRCCRDYPG----EECCSEWDCMCV-----QPEFHCGDPC--CT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
                                                   FEBCBE329CC67FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                       ; Score 139.5; DB 4;
; Pred. No. 3.9e-06;
26; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                          ----QVKKKPLCLQREAKVPHLPADKARGTQGPEQQ 295
                                                                                                                                                                                                                                                                                                                                                   185 LGLHIWQLRKTQLLLE----VPPSTED-ARSCQFPEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                           34 CGPG---RLLLGTGTDARC-----
Prodom; PD000771; -; 1.
PROSITE; PS0652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SMART; SM00208; TNFR; 2.
SEQUENCE 439 AA; 46090 MW;
                                                                                         10.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSTEOPROTEGERIN (FRAGMENT).
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NON_TER 1 1
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                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-PLACENTA;
                                                                                                                  64;
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                                                                                                      Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPER 138
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEW---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91370690; PubMed-1966549;
MEDLINE-91370690; PubMed-1966549;
Demblic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
Brockhaus M., Lesslauer W.;
"Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences.";
Lyckline Z.121-237(1990).
EMBL; 863368; AAB19824.1; --
HSSP; P25942; LCDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHOLLC------DKCAPGTYL-----KQHCTVRRKTLCVPCPDHSYTDSWHTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                   LINKED (GLCNAC. .) (POTENTIAL).
LINKED (GLCNAC. .) (POTENTIAL).
-> P (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                      -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                        A (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                    NIH
                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                 10.4%; Score 139.5; DB 11; Length 401; 25.7%; Pred. No. 3.5e-06; Live 10; Mismatches 69; Indels 45;
                                                                                                                                                                                                                                                                                               D (IN STRAINS 129/OLA AND
                                                                                                                                                                                                                                                                                                                                                 -> R (IN STRAINS 129/OLA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 NTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                            CAA6102D3B312470 CRC64;
                                                                                                                                                                                                       N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
R -> P (IN STRAINS 129/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 09, Last sequence update)
01-NAN-1999 (TrEMBLrel. 16, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR.
                                                                                                                                                                                            N-LINKED (GLCNAC.
              OSTEOPROTEGERIN
                                                                                                                                         SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 AA
                         4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                 SIMILARITY
                                                                                        DEATH DOMAIN.
BY SIMILARITY
                                                                                                                                                                                                                                                                                   SWISS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
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161
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                                                                                                                                                                                                                                                                                                                          288
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Q16042
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Search completed: September 4, 2001, 16:14:30 Job time: 1217 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 CVYCSPVCKELQTVKQECNRTHNRVCECEEGRYLELEFC---LKHRSCPPGLGVLQAGTP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 C-----CSEWD-----CMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKF 106
                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRC--CRDY-----PGEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 GRQLLC------DKCAPGTYL----KQHCTVRRKTLCVPCPDYSYTDSWHTSDE 79
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(POTENTIAL).
(POTENTIAL).
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Indels
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W; FECGA31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.6%; Score 141.5; DB 11; 27.2%; Pred. No. 2.2e-06; Live 11; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEATH DOMAIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000488; -
InterPro; IPR001368; -
Pfam; PF00020; TNFR_c5; 4.
Probom; PF00071; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS00050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                           TISSUE-INTESTINE;
MEDLINE-97262071; Pubmed-9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46192 MW;
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401
201
63
106
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401 AA;
                                                                                                SEQUENCE FROM N.A.
                       INFRSF11B OR OPG
                                                                         NCBI_TaxID-10116
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SIGNAL
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SEQUENCE
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CHILDRICATION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
COF OSTEDCLAST DIFFERRWITATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CSTEDCLASTOGENESIS BY INTERINGE. MAY INHIBIT IN VITRO
CSTEDCLASTOGENESIS BY INTERINGE. MAY INHIBIT IN VITRO
CSTEDCLASTOGENESIS BY INTERINGENITORS.
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CSTROMAL CELLS AND OSTEDCTAST PROGENITORS.
CSTROMAL CELLS AND OSTEDCTED IN SPLEEN.
CSTROMAL CALVARIA AND
CST
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MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Simonet W.S., Lacey D.L., Dunstan C.R., Relley M., Shimmancto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Osteoprotegenin: a novel secreted protein involved in the regulation of bone density.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
Gene 215:339-343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
01-MR-2001 (TrEMBLRel. 16, Last annotation update)
03-EOPROPEGERIN PRECORSOR (OSTE
107 SFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
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                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB013900; BAA33388.1; JOINED
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PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-129/OLA, AND NIH SWISS;
MEDLINE-98382527; Pubmed-9714833;
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InterPro; IPR000488; -.
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                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                          INFRSF11B OR OPG.
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                                                                                                                                       RESULT 13
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66033
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Best Local Similarity 24.0 Matches 58; Conservative
 Nature 390:175-179(1997)
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                                                                                                                              SMART; SM00208; TNFR; 1.
Receptor; Glycoprotein; SIGNAL
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                                                                                                                                                                    EMBL; AF018253; AABE
HSSP; P25942; 1CDF.
MIM; 603499; -.
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126
127
154
175
105
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616 AA;
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234
234
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333
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1113
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01-JUL-1997
01-MAR-2001
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                 GFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVC-----VP 155
                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                      Gaps
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                 Bal C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V. Soderman A., Galloway S. M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                     56;
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Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.
Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                   Length 300;
                                                                                                                                                                                                                                                                                                     67; Indels
                                                                                                     the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                       300 AA; 32679 MW; F90AEE33718449AF CRC64;
                                                               Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000)
                                                                                                                                                                                                                                                                                  11.4%; Score 153; DB 4; 26.3%; Pred. No. 1.2e-07; tive 14; Mismatches 67.
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ProDom; PD000771; -; 1.
PROSITE; PS01186; BGF_2; UNKNOWN_1.
PROSITE; PS00055; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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         MEDLINE-20122600; PubMed-10655513;
                                                                                                                     AF134240; AAD29688.1; -- AF217796; AAF33284.1; -- AF217794; AAF33685.1; -- AF217794; AAF33686.1; -- AL121845; CAC03668.1; -- AL121845; CAC03668.1; --
                                                                                                   Submitted (NOV-2000) to the EMBL; AF104419; AAD03056.1;
                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                   P25942; 1CDF
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                                                                                            Matthews L.,
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SEQUENCE
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-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL) IN
-i- TISSUE SPECIFICITY: UBJOUTTOUS EXPRESSION WITH HIGH LEVELS IN
SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 CACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFSSTDKCRP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 WTDCTQFGFLTVFPGNKTHNAVC---VPG-SPPAEPLGWLT-VVLLAVAACVLLLTSAQL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION EMBL; AF018253; AAB86809.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RPLFALLLLCALL------ARLQVALQIAPPCTSEKHYEHLGRCCNKCEPGKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PGEECCSEWDCMCVQPEFHCG------DPC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------CTTCRHH-PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCR----VHTTRCCR-----DY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR ACTIVATOR OF NF-KAPPA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKED (GLCNAC. . .) (PORTION ENDER TANKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                               Transmembrane; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 150; DB 4; 24.0%; Pred. No. 4.6e-07; iive 22; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                    Interpro: IPR001368; -.
Pfam: PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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ΜΣ
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66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۵
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                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                          TISSUB-THYMUS;
Nocential G., Rochetti S., Bartoli A., Spinicelli S., Delfino
Nocential G., Riccardi C.;
Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL; AF220433; AAF6557.1; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
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EMBL, AF229434; ARE1568.1; -.
InterPro; IPR000561; -.
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8
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SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     594932BA425A79CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
46.1%; Score 618; DB 11;
Best Local Similarity 54.7%; Pred. No. 8.5e-55;
Matches 105; Conservative 31; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00181; EGF; 1.
SEQUENCE 222 AA; 24450 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 GLHIWQLRRQHM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLHIWQLRKTQL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                [1]
SEQUENCE FROM N.A.
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                                                                                                                                NCBI_TaxID=10090;
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                          FNFRSF18
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Q9JKR1;
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                                                                                                                                                        CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                                                                                                                                        DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                                                                                                                                                                                                                                                          GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185
                                                                                                                                                                                                                                                                                     66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 GHCKLWTNCSQFGFLTWFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
  Gaps
                                                                                                     53
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                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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  16;
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EMBL: AF229432; ARE61566.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             Score 625.5; DB 11; Length
Pred. No. 1.9e-55;
2; Mismatches 56; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SMO0181; EGF; 1.
SEQUENCE 294 AA; 32658 MW; FEOD4AE6A007BA9A CRC64;
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Last annotation update)
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Last annotation update)
58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AA
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32; Mismatches
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-OCT-2000 (
01-OCT-2000 (
01-MAR-2001 (
Matches 129;
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**09JKR3**; Q9JKR3

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Query Match
Best Local Similarity 25.55
Matches 73; Conservative
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                 Gallus gallus (Chicken).
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CD40-HOMOLOGUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                          SEQUENCE FROM N.A.
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                                                      NCBI_TaxID=9031;
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                                               Gallus
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                  61 YPG--EECCSEWDCM-CVQ-----PEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LTVVL-LAVAACVLLLTSAQLGLHI--- 189
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        CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE
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                                                                                                                                                               OX40 PRECURSOR (FRAGMENT).
Oyyctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 267;
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                                                                                                                                             Last sequence update)
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27.8%; Pred. No. 1.1e
tive 22; Mismatches
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Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SWART; SM00208; TNFR; 1.
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267 OX
28489 MW;
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(TrEMBLrel. 16, I
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Submitted (MAY-1997) to the
EMBL; AB003911; BAA20059.1;
HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 27.8 Matches 76; Conservative
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                                                         111 GHCRLWT 120
                                              126 GHCKPWT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKGLVVKVKGTNTSDVIC--ESSRRSSLSVLIPITAAVVTCL-----VGICIYCLVHT 220
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBL: AJ293700, CAC220218.1; -
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
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Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;

"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LiGHT-mediated apoptosis.";

J. Biol. Chem. 274:13733-13736(1999).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%; Score 182.5; DB 13; Length 25.5%; Pred. No. 1.1e-10; Live 20; Mismatches 94; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68E) (DJ583P15.1.1)
DCR3 OR TR6 OR INFRSF6B.
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0997W4 rattus sp.
061204 mus musculu
09xez8 cercopithec
09xvx3 caenorhabdi
035806 rattus norv
09er63 mus musculu

Perfect score: Sequence: Scoring table:

Minimum DB Maximum DB

Database

Searched:

OM protein

Run on:

088734 mus musculu 000508 homo sapien 09xsv8 bos taurus 088281 rattus norv

075412 homo sapien 075851 homo sapien

mus musculu

rattus norv

057484 gallus gall 002660 bos taurus 022685 caenorhabdi 094438 chironomus 022048 caenorhabdi 097172 rattus norv 068196 human cytom

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MEDLINE-99156876; PubMed-10037686; MEDLINE-99156876; PubMed-10037686; MEDLINE-99156876; PubMed-10037686; Mewon B., Yu K.Y., NJ J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Liu D., Wang S.X., Kwon B.S.; "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand."; Biol. Chem. 274:6056-6061(1999).

EMBL, ARIJ7297, AAAD19694.1; -...
InterPro; IPR001368; -...
SMART; SM00208; TNFR; 1.
Receptor.
SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
THE RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN
Homo sapiens (Human).
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100.0%; Pred. No. 8.9e-128;
ive 0; Mismatches 0;
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061204
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09ER63
09ER63
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000438
Q9JKE0
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Q88734
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Best Local Similarity 100.
Matches 234; Conservative
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232.602 Million cell updates/sec
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                                                                                                             4, 2001, 15:54:13; Search time 133.1 Seconds
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Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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sp_vertebrate:*
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sp_mammal:*
sp_mhc:*
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Copyright (c) 1993
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seq length: 20
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Length 234; Indels SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180 

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61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTF 120

Riccardi C.;

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Gaps

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61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Moraca R., Migliorati G., Riccardi C.;
Ma new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
TWERSTIB OR GITR.
TISSUE-THYMUS;
Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Ric
Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Ric
"Identification of a soluble human GITR splicing (hGITR-D)."
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF241229; AARF63506.1; -.
SEQUENCE . 255 AA; 26827 MW; C986652AC97AF2CC CRC64;
                                                                                                                                                                                                                                                                                                     Score 815; DB 4; Length 255; Pred. No. 1.2e-74; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                     Query Match 60.8%; Score 915; DB Best Local Similarity 75.1%; Pred. No. 1.2e Matches 142; Conservative 2; Mismatches
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54.9%;
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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TISSUB-BONE MARROW;
Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor family and its receptor. a human ortholog of mouse GITR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                               181 TSAQLGLHIMQLRKTQLLLEVPPSTEDARSCQFPEERGERSAEEKGRLGDLWV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 241;
                                       181 TSAQLGLHIWQLRKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLWV
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SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
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Last annotation update)
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EMBL; AF125304; AAD22635.1; -.
InterPro; IPR001368; -.
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SEQUENCE FROM N.A.
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01-NOV-1999
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STRAIN-BALB/C;
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Riccardi C.;
"Gene structure and chromosomal assignment of GITR, a mouse member of
                                                                                                                the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U82534; AAB81243.1; -
EMBL; ATL09216; AAF1431.1; -
MGD; MGI:894675; Tnfrsf18.
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
GLUCOCÓRTICOID INDUCED TNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 50D8C275D9C56259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 703; DB 11;
Pred. No. 2.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                         RELATED PROTEIN.
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Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D., Migliorati G., Riccardi C.; Miglication of three novel mRNA splice variants of GITR."; Cell Death Differ. 0:00(2000).

EMBL; AF22943; AAF61566.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                      Mus musculus (Mouse),
Starayota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C;
MOCHELIAIG, Bartcoll A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Bartcoll C.; Riccardi C.; Ric
                                                                                                                                                                                                                                                                Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.;
A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. GLUCOCORTICOID INDUCED THER FAMILY
GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR TNFRSF18 OR GITR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%; Score 192; DB 11; Length 228; 75.0%; Pred. No. 1.4e-19; ive 6; Mismatches 4; Indels
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50D8C275D9C56259 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16; Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 CAMGTFSAGRDGHCRLWTNCSQFGFLTWFPGNKTHNAVCI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
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Pred. No. 1.8e-19;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 AA
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                                                                                                                                                                                                                  STRAIN-C3H/HEN;
MEDLINE-97322352; PubMed-9177197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25334 MW;
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1 Similarity 75.0%;
30; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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SEQUENCE 294 AA: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 30; Conserv
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Matches 30; Conser
                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                             Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Goddard A.D., Ashkenazi A.; Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR."; Curr. Biol. 0:0-0(1999).

InterPro: IPR001369:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Migliorati G., Riccardi C.;
Midentification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL; AF229433; AAF61567.1; -.
InterPro: IPR000561; -.
                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 246; DB 4; Length 241; 100.0%; Pred. No. 3e-27; 1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00208; TNFR; 1.
SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24450.MW; 594932BA425A79CA CRC64;
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Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 192; DB 11;
Pred. No. 1.3e-19;
6; Mismatches 4;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-MAR-2001 (TrEMBLrel, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
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SEQUENCE 222 AA;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Matches 30; Conserv
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RESULT Q9Y5U5 ID Q9 AC Q9 DT 01

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Result Š

human cytom human cytom human cytom

Total number of

Searched:

Minimum Maximum Database

Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

human cytom

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PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
Glycoprotein; Repeat; Cytokine; Signal.
SIGNAL 1 21 OSTEOPROTEC
CHAIN 22 401 4 X TNFR-CY
REPEAT 23 201 4 X TNFR-CY
REPEAT 23 63 TNFR-CYS 1
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SWISS)
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(TrEMBLrel. 15, I
(TrEMBLrel. 16, I
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66.7%;
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Best Local Similarity
Matches 12; Conserv
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Matches 17; Conser
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01-MAR-2001
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SMART; SMO
SEQUENCE
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TNFRSF18.
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Q9JKR1
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STRAIN-BALB/C; TISSUE-KIDNEY;
STRAIN-BALB/C; TISSUE-KIDNEY;
SIMONOTH W. S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyên H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Suggs S., Boyle W.J.;
Suggs S., Boyle W.J.;
Campboll P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Cangolin: a novel secreted protein involved in the regulation
of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTECCLASTOGENESIS BY INVERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTECCLAST PROCENTYORS.
SUBUNIT: HOMODIMER (MAJOR PERM) AND MONOMER (MINOR FORM).
SUBCELLULAR LOCATION: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG, BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND PLACENTA. NOT DETECTED IN SPLEEN
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT AV 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY SIN DAY 17.
SIMILARITY: CONTAINS A LA-NGFR/THER-TYPE CYSTEINE-RICH REGION.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                             008712: 070202;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0STEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                           3
                           17; Indels
                                                                                                     2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
Pred. No. 0.00079;
6; Mismatches 17
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EMBL; AB013898; BAA58269.1; --
EMBL; AB013803; BAA33388.1; --
EMBL; AB013899; BAA33388.1; JOINED.
EMBL; AB013900; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
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recobon; P0000771; -; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
ilarity 39.0%;
Conservative
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InterPro; IPR000488; -.
InterPro; IPR001368; -.
                                                                                                                                                                                                                                              PRELIMINARY;
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P25942; 1CDF
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Sukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> P (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S -> A (IN STRAINS 129/OLA AND NIH SWISS).
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TISSUE-THYMUS,
MOCENTIAI G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
Adentification of three novel mRNA splice variants of GITR.";
Call Death Differ 0:0-0(2000).
EMBL; AF229434; AAF61568.1;
InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D (IN STRAINS 129/OLA AND NIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79; DB 11; Length 132;
Pred. No. 0.00094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
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4 X TURE-CYS.
TURE-CYS 1.
TURE-CYS 2.
TURE-CYS 3.
TURE-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
CHOCKED (GLCNAC. ..) (POLINED (GLCNAC
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Last sequence update)
Last annotation update)
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201
63
106
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365
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165
178
289
401 AA;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                          (OCIF).
TNFRSF11B OR OPG.
                                                                                                                                                     NCBI_TaxID=10116
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23
23
64
107
1144
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                  Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                     54.9%; Score 135; DB 4; Length 255; 100.0%; Pred. No. 2e-11; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96; DB 6; Length 267; Pred. No. 7.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isono T., Seto A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003911; BAA20059.1; -.
HSSP; P19438; LEXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 POTENTIAL.
267 0X40.
28489 MW; A8B4CD3173C9500B CRC64;
                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0X40 PRECURSOR (FRAGMENT).
                                                                                      (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
               103 CAMGTESAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCI 142
        2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                      255 AA
                                                                                                                                                                                                                                                                                                                                                       267 AA
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Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMARY; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                   114 DCASGTFSGGHEGHCKPWTDC 134
                                                                                                                                                                                                                                                                                        1 DCASGTFSGGHEGHCKPWTDC 21
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                       PRELIMINARY;
                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 AA;
                                                                                                                                                                                                                                                              Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE-THYMUS;
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                                                                                                                                                     NCBI_TaxID-9606;
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                                                                                              01-0CT-2000
01-0CT-2000
GITR-D.
                                                                                       -OCT-2000
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SIGNAL
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Q9NYJ9;
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Q9NYJ9
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A Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
A Davy E., Bliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Geg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Cappage S., W.J.;
Cappage S., Boyle W.J.;
Cappage S., W.J.;
Cappage S., Boyle W.J.;
Cappage S., W.J.;
Cappage S.,
                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAK LOCATION: EXTRACELLULAR.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U94330; AAB53707.1; -.
HSSP; P25942; ICDF.
                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLR-E). 16, Last annotation update)
05TEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .) (POTENTIAL) . . . (POTENTIAL) . . . (POTENTIAL)
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FEC6A31F1D4E573A CRC64;
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TWER-CYS 3.

TWER-CYS 3.

DEATH DOMAIN.

BY SIMILARITY.

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

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401 AA
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SIGNAL 1 21 BY SIMILARITY
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InterPro; IPR001368; -
Pfam; PF00020; TRFR_C6; 4.
ProDom; PD000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=INTESTINE;
MEDLINE=97262071; PubMed=9108485;
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-!- SUBCELLULAR LOCATION: EXTRACELLULAR (FILOR FORM) (BILD SIMILARITY).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR LOCATION: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROLD, SPINAL CORD AND LIVER. ALSO DETECTED IN THE PANCREAS OF PERIPHERAL BLOOD LYMPHOCYTES.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. EMBL, AB0002146; BAA25910.1; --
EMBL, AB000812; BAA32076.1; --
EMBL, AB008821; BAA33076.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simonet W.S., Lacey D.L., Dunsten C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimmamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoprotegerin/osteoclastogenesis-inflibitory factor.",
Eur. J. Blochem. 254:685-691(1998).
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N. Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.; "Identity of costeoclastogenesis inhibitory factor (OCIF) and osteoclastogenesis inhibitory factor (OCIF) and osteoclastogenesis in vitro."; Endocrinology 139:1329-1337(1998).
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel, 04, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
0STEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
HORNELED DR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K., "Cloning and characterization of the gene encoding human
                   Length 372;
                                                              18; Indels
                                                                                                                                         2 CASGIFSG--GHEGHCKPWIDCIQFGFLTVFPGNKTHNAVC 40
                   Score 77; DB 4;
Pred. No. 0.0052;
                                                                 6; Mismatches
                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PLACENTA;
MEDLINE-98351569; PubMed-9688283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-LUNG FIBROBLAST;
MEDLINE-98151033; PubMed-9492069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97262071; PubMed-9108485;
                   31.3%;
36.6%;
                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MR-2001 (TrEMBLrel. 16, 03TEOPPOTEGERIN PRECURSOR (C
                                           Best Local Similarity 36.6
Matches 15; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                   000300; 060236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-KIDNEY
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                   Query Match
                                                                                                                                                                                                                                                                              000300
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0000300

AC 0003000

AC 0003000

DT 01-JUL

DT 01-JUL

DT 01-JUL

DT 01-JUL

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RA HOMO S

COCTED

RA LUETHY

RA CAMPDE

RA CAMPDE

RA CAMPDE

RA CAMPDE

RA SALO Y

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"A homologue of the TNF receptor and its ligand enhance T-cell growth
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TRECEPTOR OF WE-KAPPA-B PRECURSOR (TWE-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and dendritic-cell function.";

Nature 390.175-179(1997).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AF019046; AB886810.1;
--- HSSP; P25942; ICDF.
MGD; MGI:1314891; Tnfrsfila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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MEDLINE-98032977; PubWed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 77; DB 4; Length 401;
Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> D (IN REF. 2 AND 3).
EB42FA51C9D7C71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 CPDGFFSNETSSKAPCRKHINCSVFGLLLTQKGNATHDNIC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                               DEATH DOMAIN.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                             OSTEOPROTEGERIN
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                                                                                                                                            BY SIMILARITY
                                                                                                                                                                               4 X TNFR-CYS.
                               Pfam; PF00020; TNFR_c6; 3.
Probom; PP000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                             TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                        Repeat; Cytokine; Signal
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InterPro; IPR000488; -
                                                                                                     SMART; SM00005; DEATH;
Glycoprotein; Repeat; (
                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
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CONFLICT
SEQUENCE
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                  InterPro
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REPEAT
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                                                                                                                                          SIGNAL
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2 CASGTFSGGHEG - HCKPWTDCTQFGFLTVFPGNKTHNAVC
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                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00042; CUB;
NON_TER 267 26
SEQUENCE 267 AA; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Betstein D., Ashkenazi A.; Geomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE-20122600; PubMed-10655513;
MEDLINE-20122600; PubMed-10655513;
Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
"Overaxpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104419; AAD03056.1; -.
EMBL; AF134240; AAD29688.1; -.
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                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJS83P15.1.1)
DCR3 OR TR6 OR TRFRSF6B.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000)
                                                                                                                                                                                                   300 AA.
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99087326; PubMed-9872321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF217796; AAF35241; --
EMBL, AF217794; AAF336851; --
EMBL, AF217794; AAF336861; --
EMBL, AL121845; CAC036681; --
                                                  103 CAMGTFSAGRDGHCRLWT 120
                     2 CASGTFSGGHEGHCKPWT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P25942; ICDF.
InterPro; IPR001561; -.
InterPro; IPR001368; -.
Pfam: PF00020; TNFR_G5; 4.
ProDom; PD000771; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 396:699-703(1998).
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Best Local Similarity 34.1
Matches 14; Conservative
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer
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SEQUENCE
                                                                                                                                            RESULT 11
095407
AC 095407
DT 01-MAX DT 095407
DT 01-MAX DT 01-MAX DT 01-MAX DT 01-MAX DT 00-MAMMA1.

RE DECOY OC ENKARY, OC ENKARY DT 01-MAX DOWN DT 01-MAX DT 01-MAX
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG (FRAGMENT).
Fish lymphocystis disease virus (FLDV).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Essbauer S., Ahne W.;
Essbauer S. Ahne W.;
"ORF of Lymphocystis disease virus of plaice - encoding for a TNFR-NGFR-homolog that has a CUB-domain.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF074011; AAC25600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.; "Cloning and Expression of Osteoprotegerin from Homo sapiens."; Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999) EMBL; AF134187; AAF20168.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.3%; Score 77; DB 14; Length 267; 54.5%; Pred. No. 0.0037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F02527A5CD01CCD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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InterPro; IPR001488; -.
InterPro; IPR001368; -.
Pfam: PF00020; TNFR_G6; 3.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, OSTEOPROTEGERIN (FRAGMENT).
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NON_TER 1 1
SEQUENCE 372 AA; 427
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N. LINKED (GLONG. ..) (POTENTIAL).
N-LINKED (GLONG. ..) (POTENTIAL).
WHEREN FROM CALCHONG. ..) (POTENTIAL).
                                                                                                                        RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL).
InterPro; IPR000561; -.
InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 3.
Probom; DD00771; -; 1.
PROSITE; PS00186; EGE_2; UNKNOWN_1.
PROSITE; PS00052; TNFR_NGFR_1; UNKNOWN_1.
SMART; SM00208; TNFR_NGFR_2; 1.
SMART; SM00208; TNFR; 1.
Receptor; Glycoprofin; Transmembrane; Signal; Repeat.
                                                                                                                                             CYTOPLASMIC (POTENTIAL).

4 X TNFR-CYS.

TNFR-CYS. 2.

TNFR-CYS. 2.

TNFR-CYS. 4.

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61
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87
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SEQUENCE
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2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40 ð

Query Match 30.5%; Score 75; DB 11; Length 625; Best Local Similarity 39.0%; Pred. No. 0.017; Matches 16; Conservative 2; Mismatches 21; Indels

1;

Gaps

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155 CLLGFFSDVFSSTDKCKPWTNCTLLGKLEAHQGTTESDVVC 195

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Search completed: September 4, 2001, 16:14:33 Job time: 1220 sec

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Gaps

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Indels

Length 132;

DDT READ BY SERVICE OF SERVICE OF

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TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Migliorati G., Riccardi C.;
Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL; AF229434; AAF61568.1;
InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Migliorati G., Riccardi C.;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoml;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL; AF229433; AAF61567.1; -.
InterPro; IPR000561; -.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOID INDUCED THER FAMILY RELATED PROTEIN PRECURSOR.
                                                                                                                                                                                                     SMART; SM00181; EGF; 1.
SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA; 24450 MW; 594932BA425A79CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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62 CVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCV 101
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Pred. No. 6.5e-15;
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                                                                                                                                                                                                                                                                       Score 168; DB 11;
Pred. No. 4.2e-15;
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ilarity 62.5%; Pred. No. 6.5e
Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                         6; Mismatches
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62.5%;
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Best Local Similarity 62.5
Matches 25; Conservative
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nes 25; Conserv
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                                                                  SEQUENCE FROM N.A
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01-MAR-2001
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                                                                                                                                                                               Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Goddwski P.J., Ashkenazi A.; "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                    Euteleostomi;
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Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Ricaldentification of a soluble human GITR splicing (hGITR-D)."
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241229; AAF63506.1; -. C986652AC97AF2CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 255;
                                                                 Homo sapiens (Human).
Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Euthele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Last annotation update) GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
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Last sequence update)
Last annotation update)
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Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 4.9e-26;
Matches 40; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                        Score 252; DB 4;
Pred. No. 4.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI
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EMBL; AF125304; AAD22635.1; -.
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16,
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Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                     TISSUE-BONE MARROW;
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01-OCT-2000 (
01-MAR-2001 (
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homo sapien

homo sapien.

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Q9w343 drosophila
Q9Z795 homo sapien
Q9Z795 homo sapien
Q14Z26 homo sapien
Q94ZX1 homo sapien
Q9qXX1 homo sapien
Q9qX1 homo sapien
Q9u37 drosophila
Q9v383 drosophila
Q9v383 drosophila
Q9yB8 drosophila
Q9yB8 qualus gall
Q9psh2 gallus gall
Q9psh2 mus musculu
Q9qy12 mus musculu
Q9qy12 mus sapien
                                                                O9wt14 mus musculu
075372 homo sapien
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Q9jkw7 mus musculu
Q63720 rattus norv
                 09r172 rattus
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MEDLINE=99156876; PubMed=10037686;

Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

Kwon B., Yu K.Y., Ni J., Yu G.L.,

Kwon B.S.;

"Identification of a novel activation-inducible protein of the tumor
necrosis factor receptor superfamily and its ligand.";

EMBL: AF117297; AAD19694.1;

InterPro; IRRO1368;

InterPro; ARRO1368;

InterPro; ARRO1368;

InterPro; ARRO1368;

MEDIA AR
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last sequence update)
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100.0%; Pred. No. 4.5e-26;
tive 0; Mismatches 0;
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                              Q9PSN7
Q14425
Q9W7L4
Q75372
Q9W343
Q9W343
Q9BZX1
Q9GXX1
Q9CX7
Q9CX7
Q9TU5
Q9TU5
Q9T331
Q9T331
Q9T331
Q9T331
Q9T332
Q9T342
Q9T331
Q9T331
Q9T331
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063720
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09Y5U5
ID Q9Y5U5
O9Y5U5
DT 01-NOV-1999 (TrEMBLrel. 12,
DT 01-NOV-1999 (TrEMBLrel. 12,
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Local Similarity
nes 40; Conserv
                                00000000000000000
58.5
58.5
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57.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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EMBL; AF275364; AAG28046.1; JOINED EMBL; AF275365; AAG28046.1; JOINED.
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                                                                      Receptor.
SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-C3H/101, 129/SVJ, 129/SVEVTAC; STRAIN-C3H/101, 129/SVJ, 129/SVEVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Yu Y., Moshier J.A., Majumdar A.P.N.;
"Cloning of a novel EGFR-related peptide: A putative negative
                                                                                                                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

25.4%; Score 64; DB 11; Length 473;
Best Local Similarity 34.2%; Pred. No. 0.86;
Matches 13; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulator of EGFR.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF187818; AAG17037.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF275366; AAG28046.1; -.
                                                                55BFF8327A0933B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 AA; 52903 MW; 4E0D7C3074F28973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EPIDERWAL GROWTH FACTOR RECEPTOR ISOFORM 2.
                                                                                                                                                              26.4%; Score 66.5; DB 11;
54.5%; Pred. No. 0.11;
tive 1; Mismatches 8;
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                                                                                                                                                                                                                                                                                              7 HCGDPCCTTC-RHHPCPPGQGV 27
                                                                                                                                                                                                                                                                                                                                    || | | || :| || || || || || || || || HCASKECETCAQHRPCGPGFGV 69
                           107
11819 MW;
                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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   107
107 AA;
                                                                                                                                                                                             Best Local Similarity
Matches 12; Conserv
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SEQUENCE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C3H/J01, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
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                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Alternative Transcripts from the Human and Mouse EGFR Genes Encode Carboxy-Terminal Truncated Receptors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR (EPIDERMAL GROWTH FACTOR RECEPTOR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/63; TISSUE-LIVER;
STRAIN-C57BL, 63; TISSUE-LIVER;
SElter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
Maihle N.J.;
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                                                                                           Length 643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF124513; AAD44149.1; -.
71477 MW; DEF22002C84911B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6B34063B1BC928CB CRC64;
                                                                                     25.4%; Score 64; DB 11; 34.2%; Pred. No. 1.1; iive 5; Mismatches 20;
                                                                                                                                                                                                                                                 255 QDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292
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                                                                                                                                                                                                                                                                                                                                                                                                                          655 AA
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                                                                                        Query Match 25.4
Best Local Similarity 34.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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643 AA;
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InterPro; IRR000561; -.
InterPro; IRR001881; -.
Pfam; PF00008; EGF; 25;
PROSITE; PS000010; ASX_HYDROXIL; 5,
PROSITE; PS010022; EGF_1; UNKNOWN_23.
PROSITE; PS01186; EGF_2; 23.
PROSITE; PS01187; EGF_1, 5.
SMART; SM00001; EGF_1ke; 5.
SMART; SM00001; EGF_1ke; 1.
Calcium-binding; EGF-1ike; domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 1574 AA; 165445 MW; 2B48533D8F77F6E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09JKEO;
01-0CT-2000 (TTEMBLrel. 15, Created)
01-0CT-2000 (TTEMBLrel. 16, Last sequence update)
01-MAR-2001 (TTEMBLREL. 16, Last annotation update)
CD40 PROTEIN (FRAGMENT)
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-WISTRAR; TISSUE-SMOOTH MUSCLE, AORTA;
MEDLINE-99330195; PubMed=10403401;
MEDLINE-99330195; PubMed=10403401;
Microsaz R., Wagner A.H., Cattaruzza M., Hecker M.;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer and activation of transcription-1.";
FEBS Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                  "Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
EMBL; AB011532; BAA32462.1; -.
HSSP; P00736; lAPQ.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF241231; AF4431717.1; ...
InterPro; IPR001368; ...
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVQPEFHCGDPCCTT----CRHHPCPPGQGVQSQGK 32
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                  1574 AA
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STRAIN-WISTAR; TISSUE-SMOOTH MUSCLE, AORTA;
                                                         Created)
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STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
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                                                       08,
08,
16,
                  PRELIMINARY;
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01-NOV-1998 (
01-MAR-2001 (
MEGF6.
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088281
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"Gene structure and chromosomal assignment of GITR, a mouse member of the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 08254; AAB81243.1; -
EMBL; AF109216; AAF14231.1; -
EMBL; MGJ WGI: 894675; Thfrsf18.
InterPro; IPR000561; -
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
SIGNAL 199 POTENTIAL.
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Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D., Magliorati G., Riccardi C.;

"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL, AF229432; AAF61566.1; -.
Interpor. IPR000561; -.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                  STRAIN=C3H/HEN;

Mochattini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,

Moraca R., Migliorati G., Riccardi C.;

Moraca R., Migliorati G., Rattoli Factor

Force Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN. 50D8C275D9C56259 CRC64;
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Last annotation update)
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Pred. No. 6.7e-15;
6; Mismatches 9;
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Pred. No. 8.3e-15;
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Best Local Similarity 62.5%;
Matches 25; Conservative
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228
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Score 63; DB 5; Length 62; Pred. No. 0.21; 4; Mismatches 18; Indels

25.0%; 36.2%;

62 6794 MW; 154CE25A375E0B2C CRC64;

14 CTGCEMKCGDPENTPCPLMCRRPSCECSPGRGMRRTNDGKCIPASQC 60

1 CVQPEFHCGD----PCCTTCRHH--PCPPGQGVQ--SQGKFSFGFQC

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Search completed: September 4, 2001, 16:14:33
Job time: 1220 sec
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Matches 17; Conservative
Pfam; PF01826; TIL; 1.
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SEQUENCE 62 AA; 6799
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                                                                                                                                                                                                                                                                                                                                                              Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98297373; PubMed-9635450;
Lu C.C., Mquyen T., Morris S., Hill D., Sakanari J.A.;
Lu C.C., Mquyen T., Morris S., Hill D., Sakanari J.A.;
Anlsakis simplex: mutational bursts in the reactive site centers of serine proctease inhibitors from an ascarid nematode.";
Exp. Parasitol. 89:257-261(1998).
Exp. Parasitol. 89:257-261(1998).
HSSP: P07851; 18A1.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                             "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
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1.9;
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                                                                                                                                                                                                                                                                                                       Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                         01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR ISOFORM 1.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
CHYMOTRYPSIN/ELASTASE INHIBITOR-1 (FRAGMENT).
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Pred. No. 1.9;
5; Mismatches
PRT; 1210 AA.
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                             Created)
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                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
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EMBL; AF275364; AAG28045.1;
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Best Local Similarity 34.2%;
Matches 13; Conservative
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 PRELIMINARY;
                                                                                                  Mus musculus (Mouse)
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SEQUENCE
Q9EP98
Q9EP98;
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077419
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Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
"Herpes simplex virus-1 entry into cells mediated by a novel member of the TRF/NGF receptor family.";
Cell 87:427-436(1996).
EMBL: 070321; AAB58354.1; -...
HSSP: P25942; ICDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.75;
3; Mismatches 22; Indels
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Last annotation update)
                                                                                                            283 AA
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Pfam; PF00020; TNFR_C6; 3.
Probon; PD000771; -. 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SMART
                                                                                                                                                                                                                  Created)
                                                                                                            PRT;
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25.5%;
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                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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01-JUL-1997
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RESULT
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Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                         Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL; AF229434; AAF61568.1;
InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Ricardi C.;
"Identification of three novel mRNA splice variants of GITR."; Cell Death Differ. 0.0-0(2000).
EMBL: AF229433; AAF61567.1; -.
InterPro: IPR000561;
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                          Score 87.5; DB 11; Length 132;
Pred. No. 0.00023;
9; Mismatches 10; Indels 7.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCCORTICOID INDUCED THER FAMILY RELATED PROTEIN PRECURSOR.
THERSFI8 OR GITR.
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                                                                                                                                                                                                                           132 AA; 14106 MW; F586A5404B1DFEDE CRC64;
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Last annotation update)
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36.6%;
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Matches 15; Conser
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                                                                              TISSUE-THYMUS;
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Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,

Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,

Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;

"Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
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Last annotation update)
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100.0%; Pred. No. 1.7e-26;
1ve 0; Mismatches 0;
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EMBL; AF125304; AAD22635.1; -.
InterPro; IPR001368; -.
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Best Local Similarity 100.
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Matches 41; Conservative
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TISSUE-THYMUS;
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RESULT 10 090 V 39 10 099 AC 099 AC 099 BDT 011 BDT

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09qx30 mus musculu 073791 brachydanio

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musculu

Ogvvp5 drosophila Og99f4 phytolacca O96100 asterina pe Q9u8p9 asterina pe Q91190 entamoeba d O99qr0 drosophila

Minimum DB Maximum DB

Database

Searched:

Seguence:

Run on:

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SEQUENCE FROM N.A.
MEDLINE=99156876; PubMed=10037686;
Kwon B., Yu K.Y., N.J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,
Liu D., Wang S.X., Kwon B.S.;
"Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";
J. Biol. Chem. 274:6656-6061(1999).
EMB. AR17297; AA119694.1;
—InterPro: IPR001368;
                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TNF RECEPTOR SUPERRAMILY ACTIVATION-INDUCIBLE PROTEIN.
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 255; DB 4; Length 234; 100.0%; Pred. No. 1.7e-26;
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Last sequence update)
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               Q9JJH6
Q9SZR8
Q9QX30
O73791
Q18238
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Q9XFF4
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Q9SBW5
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Q07628
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Q9SBW9
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Q9S9F4
Q9U8P9
Q9UBP9
Q9NL90
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Q69581
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Q9Y5U5;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
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Receptor.
SEQUENCE 234 AA; 2511
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                                                                                                         1 GCGPGRLLLGTGTDARCCRV......TTRCCRDYPGEECCSEWDCM 41
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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WEDLINE-20347167; PubMed-10764796;

WEDLINE-20347167; PubMed-10764796;

Kojima T., Morkkawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,

Senba E., Kitamura T.;

"TROY, a newly identified member of the tumor necrosis factor receptor

superfamily, exhibits a homology with Edar and is expressed in

embryonic skin and hair follicies.";

J. BAOL Chem. 275:20742-20747(2000).

EMBL; ABO40434; BAB03269.1;

InterPro; IPR001368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                               Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                  14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        2 CGPGRLL----LGTGTDARC--CRVHTTRCCRDYPGEECCSEWDC 40
                                                                                                                                                                                                               2 CGPGRLL----LGTGTDARC--CRVHTTRCCRDYPGEECCSEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 CGPGMELSKECGFGYGEDAQCVTCRLH--RFKEDWGFQKCKPCLDC 95
                                                      BB7C9917132A4B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B5891CEA9ED45361 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 0.55;
5; Mismatches 14;
                                                                                                               4
                                                                                                         Score 65.5; DB Pred. No. 0.55; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00020; TNFR_CG; 2.
PROSITE; PS00622; TNFR_NGFR_1; UNKNOWN_2.
PROSITE; PS50050; TNFR_NGFR_2; 1.
SEQUENCE 423 AA; 46015 MW; B5891CEA9E
                                                                                                                                                                                                                                                                                                                         423
               PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
PROSITE; PS50050; TNFR_NGFR_2; 1.
SEQUENCE 423 AA; 46071 MW; BB7C991713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        788 AA
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39.1%;
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39.1%;
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Pfam; PF00020; TNFR_c6; 2
                                                                                                           Query Match
Best Local Similarity 39.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 39.1 es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9NS68;
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Q22631
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Wilson R., Andrewson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscoup R., Anderson K., Baynes C., Berks M.,
Bonfield J. Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Waterson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: Z68011; CAA32014.1; -.
InterPro: IPR001884; -.
InterPro: IPR002965; -.
InterPro: IPR003609; -.
Pfam: PF00090; tsp_1; 6.
PRINTS: PR01217; PRICHEMENSN.
SMART: SMO473; PAM. AP: 1.
SEQUENCE 788 AA: 88727 MW; BB0DD9F1D29BD961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CGPG-----RLLLG-TGTDARCCR---VHTTRCCRDYPGEECC--SEW
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01, Last sequence update)
13, Last annotation update)
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PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.3%; Score 64.5; D
39.6%; Pred. No. 1.3;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 AA
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EMBL; 266499; CAA91301.1;
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.3°
Best Local Similarity 39.6°
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01-MAY-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001007; -.
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A SUGUENCE TRUEN N.A.

RA STRAINECY. COLUMBIA,

RA ATAUJO R.V. S., OSDORNE B.I., Toriumi M., Yu G., Oji O., Shen Y.K.,

RA ATAUJO R.V. Au M., Buehher E., Conway A.B., Conway A.R., Dewar K.,

RA Ecker J.R., Kuntz D., Li Y., Shinn P., Sun H., Davis R.W.,

R. Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, ACOOOL32. AAB60738.1; -.

DR Mendel, 15355, Arath;1134;1535.

BR InterPro; IPRO00169; -.

BR InterPro; IPRO00668; -.

BR InterPro; IPRO00668; -.

BR InterPro; IPRO00668; -.

BR InterPro; IPRO0122; Peptidase_C1; 1.

BR PROSITE; PSO0070; ALDEHYDE_DEHYDR_CXS; UNKNOWN_1.

BR PROSITE; PSO0040; THIOL_PROTEASE_ASN; 1.

BR PROSITE; PSO0040; THIOL_PROTEASE_ASN; 1.

BR PROSITE; PSO00639; THIOL_PROTEASE_CXS; 1.

BR PROSITE; PSO00639; THIOL_PROTEASE_CXS; 1.
                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Embryophyta: Tracheophyta; Spermatophyta:
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20270246; Pubmed-10809768; BDY M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.; BDY M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.; TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45684 MW; 15BCB47F5430F922 CRC64;
                                                                                                                                              U1-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) SIMILARITY TO DIANTHUS CYSTEINE PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.9%; Score 66; DB 10; 35.3%; Pred. No. 0.47;
                                         416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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EMBL; AF167555; AAF71828.1; -.
InterPro; IPR001368; -.
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                Created)
                                                                                                        01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2001 (TrEMBLrel. 16,
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MOCENTIAI G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D., Migliorati G., Riccardi C., "Identification of three novel mRNA splice variants of GITR."; Cell Death Differ. 0:0-0(2000).
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"Gene structure and chromosomal assignment of GITR, a mouse membs the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U8253; AAB81243:1;
EMBL; MGDS, ARIA231:1;
MGD; MGI:894675; Thfrsf18.
SMART; SMO0181; EGF; 1.
                                 STRAIN=C3H/HEN;
MEDILINE-9732335; PubMed-9177197;
Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
Moraca R., Migliorati G., Riccardi C.;
A new member of the tumor necrosis factor/nerve growth factor
receptor family inhibits T cell receptor-induced apoptosis.";
Proc. Natl. Acad. SGI. U.S.A. 94:6216-6221(1997).
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Pred. No. 0.00046;
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InterPro; IPR000561; -.
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MEDLINE-20441562; PubMed=10987278; Yang Z., Imoto I., Fukuda Y., Pimkhaokham A., Shimada Y., Imamura M., Sugano Z., Inakamura Y., Inazawa J.; Pimkhaokham A., Shimada Y., Imamura M., Sugano S., Nakamura Y., Inazawa J.; Nathin an Amplicon at 9p23-24 Frequently Detected in Esophageal Cancer Cell Lines."; Cancer Res. 60:4735-4739(2000). EMBL: AB037901; Bab16102.1; SEQUENCE 1056 AA: 120023 MW; 8FC6A8BBC458F8F1 CRC64;
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                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2651BC55D5FCF9B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 PNAFLEEDGTSLLISCAKCCVRVHAS--CYGIPSHEICDGWLC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PGRLLLGTGTD----ARCC-RVHTTRCCRDYPGEECCSEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
KIAA0780 PROTEIN (FRAGMENT).
   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PGRLLLGTGTD-----ARCC-RVHTTRCCRDYPGEECCSEWDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123998 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for large proteins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB018323; BAA34500.1; -.
InterPro; IPR002999; -.
01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.3%;
Best Local Similarity 37.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00333; TUDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02373; jmjC; 1.
Pfam; PF02375; jmjN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003349; -
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                              GASC-1 PROTEIN.
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SEQUENCE
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                                                                                             GASC-1.
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094877
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Bightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Shownken R.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaugham K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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8
                                                                                                                                                  Length 164;
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Pred, No. 0.49;
                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
EGF_1; UNKNOWN_1.
VWFC; UNKNOWN_1.
; 16499 MW; C002D48D36C9FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01208; VWFC; UNKNOWN_1.
152 AA; 15645 MW; 6E254F0BE476D354 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                             12;
                                                                                                                                            tch 24.9%; Score 63.5; DB 5; al Similarity 38.9%; Pred. No. 0.45; 14; Conservative 1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00122; EGF_1; UNKNOWN_1.
PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
                                                                                                                                                                                                                                                                                                                                 74 GCGGG----GGGCGCCCCRPRCCCCCR----RCCT 100
                                                                                                                                                                                                                                                                         1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.7%; Sco. 40.0%; Pred. No. v. 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1056 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCGGG----GGGCGCCCCRPRCCCCCR----PKCC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9H3RO PRELIMINARY; PRT; Q9H3RO; 01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
EMBL; Z49886; CAA90055.1; -.
InterPro; IPR001007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13, COGAl.6 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001450; -. InterPro; IPR001502; -.
                                                           164 AA;
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                           Best Local Similarity
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PS00022;
PS01208;
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                        PROSITE; I
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PROSITE;
                                                                                                                                                  Query Match
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RESULT 13
09XVX3
AC 09XXX3
AC 09XXX3
DT 01-NOV

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Gaps

8

RESULT 14 Q9H3R0 ID Q9H3R0 AC Q9H3R0 DT 01-MAR

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Gaps

8;

Q9XVX3;

**09XVX3** 

Matches

DR SQ

q

C06A1.6

**09Y5U5** 

RESULT
109 YSUS
109 Y

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GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH
                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                              PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDC 102
                                                                                PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKFWTDC 134
                                                                                                                                                                                    AA.
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                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-THYMUS;
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141 CI 142
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Matches
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035714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riccardi C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 GCGPGRLLLGTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                            Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
Goddard A.D., Wood W.I., Baker K.P., Goddowski P.J., Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
Curr. Biol. 0:0-0(1999)
EMBL, ARISSA04, AAA22633.1; -.
SMART; SM00208; TNFR; 1.
SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7EB2CBE CRC64;
                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.3%; Score 642; DB 4; Length 25
100.0%; Pred. No. 4.5e-65;
Live 0; Mismatches · 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 753; DB 4; 100.0%; Pred. No. 1.2e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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TISSUE-THYMUS;
Nocentini G., Barto
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                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi; Muridae; Murinae; Mus
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EMBL; AF22943; AAF61567.1; -.
INTERPO: PR000561; -.
SMART; SM00181; EGF; 1.
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Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.;
A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis.";
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
TNFRSF18 OR GITR.
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                                                                                                                                                                                                                                                                                                                         95 HTRDTVCR---CRP--GTQPLNGYKHGVDCAPCPQGHFSEGNNRACRPWTNCTLAGKRTL 149
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                                                                                                                                                                                                                                                   40 CQP-----GYGMVSRCNRSQDTICHPCEPGFYNEAVNYQACKPCTQCNRRSGSEPQQECT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606;
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                                                                                                              20.3%; Score 152.5; DB 6; Length 267; 32.8%; Pred. No. 1.2e-09; ive 10; Mismatches 57; Indels 21.
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MEDLINE-99253915; PubMed=10318773;
Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
A newly identified member of tumor necrosis factor receptor superfemily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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                                            A8B4CD3173C9500B CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJS83P15.1.1).
DCR3 OR TR6 OR TNFRSF6B.
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EMBL; AF104419; AAD03056.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF134240; AAD29688.1;
                                                                                                                                     Best_Local Similarity 32.8
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 396:699-703(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         111 FPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                   150 OPASSISDAVC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                          267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=PANCREAS;
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SIGNAL
CHAIN
SEQUENCE
                                                                                                              Query Match
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A Luethy R., Nguyen H.Q., Mooden S., Relley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
A Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RY Suggs S., Boyle W.J.,
RY O'Steoprotegarin: a novel secreted protein involved in the regulation
RY Cell B9:309-313(1997).
Cell B9:309-313(1997).
Cell B9:309-313(1997).
Cell B9:309-313(1997).
Cell SYNHESIZED BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
Cell SUBUNIT: HOMODINER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
SIMILARITY).
Cell SUBUNITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
REBEL, U34330; AABS3707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM--CVQPEFHCGD-----PC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTT-----CR------HHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (FERBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
03TEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                  Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                  F90AEE33718449AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                           Score 145; DB 4;
Pred. No. 9.2e-09;
2; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 AA.
HSSP; P25942; ICDF.
InterPro; IPR00561; -.
InterPro; IPR001368; -.
Pfan; PF00020; TNFR_c6; 4.
ProDom; PD000771; -; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00625; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00020; TNFR_c6; 4.
ProDom; P0000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 -HCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 EQCOPHRNCTALGLALNVPGSSSHDTLC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-INTESTINE; MEDLINE-97262071; PubMed-9108485;
                                                                                                                                                                                                                                                                                                                                                                     19.3%; Scor
27.7%; Pred
ative 12; I
                                                                                                                                                                                                                                                                                  300 AA; 32679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000488; -. InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Gaps
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                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Sukaryota Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus:
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                              S., Delfino
                                                                                                                                                                                                                                                                                                                                                                           Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
cell Death Differ. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
44.2%; Score 332.5; DB 11; Length
Best Local Similarity 52.0%; Pred. No. 2.7e-30;
Matches 52; Conservative 17; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14106 MW; F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWT 100
                                                                                                                                                        132 AA
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                                                                                                                                                                                       Created)
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Pfam; PF00020; TNFR_C6; 3,
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                   (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 16, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isono T., Seto A.;
Submitted (MAY-1997) to the
EMBL, AB003911; BAA20059.1;
HKSP; P19438; IEXT.
InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF229434; AAF61568.1;
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OX40 PRECURSOR (FRAGMENT).
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00208; TNFR; 1
Signal.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00181; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AA;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                               TISSUE-THYMUS;
                                                                                                                                                                                   01-OCT-2000
01-OCT-2000
01-MAR-2001
                                              121 CV 122
                                                                           141 CI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM
SEQUENCE
                                                                                                                                                                                                                                                  TNFRSF18.
                                                                                                                                                                        Q9JKR1;
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                                                                                                                                                        Q9JKR1
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Q9JKR1
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                                                                                           member of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
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Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Migliorati G., Riccardi C.;
Migliorati G., Riccardi C.;
Cell Death Differ. 0:0-0(2000).
EMBL; AF229432; AAF61566.1; -.
Interpro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Westaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                        Nocentini G., Bartoli A., Ronchetti S., Glunchi L., Cupelli A., Migliorati G., Riccardi C.;
Migliorati G., Riccardi C.;
"Gene structure and chromosomal assignment of GITR, a mouse member the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, 082534; AAB81243.1; -.
EMBL, AR109216; AAF14231.1; -.
MGD; MGI:894675; Tnfrsf18.
InterPro; IPR000561; ..
SWART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                    POTENTIAL.
GLUCOCORTICOID INDUCED THER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.2%; Score 445.5; DB 11; Length 294; Best Local Similarity 57.4%; Pred. No. 8.8e-43; Matches 70; Conservative 21; Mismatches 24; Indels 7;
                                                                                                                                                                                                                                                                                                                              59.2%; Score 445.5; DB 11; Length 228; 57.4%; Pred. No. 7e-43; ive 21; Mismatches 24; Indels 7;
                                                                                                                                                                                                                                                                  RELATED PROTEIN.
50D8C275D9C56259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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 Sci. U.S.A.
                                                                                                                                                                                                                                                                                  25334 MW;
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                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 57.4
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                    19
228
                                                                                                                                                                                                                                                                                  228 AA;
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                                SEQUENCE FROM N.A.
                                                                                                                                                                                                             Signal, Receptor.
 Natl. Acad.
                                            STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
GITR-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 CI 142
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                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JKR3
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GDPCCTTC-----RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GHE 93
                                                                                                                                                                                                                                                                                                                                                                                                ----EFHC 49
                                                                                                                                                                                                                                                                                                                                                                                                                  44 CAPGTYL-----KQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TEMBLEEL: 16, Last annotation update)
OSTEDPROTECERIN (FRAGMENT).
Homo sapidate)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE-PLACENTA; TISSUE-PLACENTA; "TISSUE-PLACENTA; "Cloning and Expression of Osteoprotegerin from Homo sapiens."; Sheng Wu Hua Hauch Yu Sheng Wu Lua Hauch Yu Sheng Wu Lua Hauch Yu Sheng Wu Li Hsuch Pao 31:680-684(1999). HSSP; P25942; ICDF.
                                                                                                                                                                                                         LINKED (GLCNAC. . .) (POTENTIAL)
-> P (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                             S -> A (IN STRAINS 129/OLA AND NIH SWISS).
                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                         -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                            N -> D (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                     -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                       18.5%; Score 139; DB 11; Length 401; 26.4%; Pred. No. 5.6e-08;
                                                                                                                                                                                                                                                                                                                                                                            65; Indels
                                                                                                                                                                                                                                                                                                                                                                                               2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEW----DCMCVQP----
                                                                                                                                                                                                                                                                                                                         CAA6102D3B312470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                     N-LINKED (GLCNAC.
                               OSTEOPROTEGERIN.
                                                                                                   SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                            DEATH DOMAIN.
                                        4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372
SMART; SM00005; DEATH; 1.
Glycoprotein; Repeat; Cytokine; Signal.
                                                                                                                                                                                                         N-LINKED
R -> P (I)
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                                                                                                                                                                                                                                                                                                                          401 AA; 45923 MW;
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01-MAY-2000 (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 26.49 Local Similarity 26.49
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2011
1063
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InterPro; IPR001368;
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DISULFID
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REPEAT
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"Cloning and characterization of the gene encoding human osteoprotegerin/Osteocolastogenesis-inhibitory factor.";
Eur. J. Blochem. 254:685-691(1998)
- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-LUNG FIBROBLAST;
MEDLINE-98151033; Pubmed-9492069;
MEDLINE-98151033; Pubmed-9492069;
MEDLINE-98151033; Pubmed-9492069;
MEDLINE-98151031; Pubmed-9492069;
Sato Y., Goto M., Yamaquch K., Kuriyama M., Kanno T., Murakami A.,
Tsuda E., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSS 135
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TC----TC-----RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
0STEOPROFEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
TURFSF11B OR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                    Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                              HTTRCCRDYPG----BECCSEWDCMCV-----QPEFHCGDPC--CT---
                                                                                                                                                               372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
                                                                                                                                                                                                                                                             ; Score 133; DB 4;
; Pred. No. 2.5e-07;
14; Mismatches 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AA
Pfam; PF00020; TNFR_c6; 3.
PROSITE: P800652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE: PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 EGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoclastogenesis in vitro.";
Endocrinology 139:1329-1337(1998).
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MEDLINE-98351569; PubMed-9688283;
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                                                                                                                                                                                                                                                             17.78;
24.28;
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 89:309-319(1997).
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                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE
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73 KERHCTPHEICEDNAGLIVKRHGNATHNTVCQC-RAGMHCSDASCQTCVENEPCKQGFGF 131
                                                                                                                                                           Mus musculus
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                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                 2 CGPGRLLLGTGTDARCCRVHTTRC--CRDY------PGEEC-----CSEWD----- 39
                                                                                                                                                                                                                                                           CAPGIYL-----KQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSPVCKELQTVKQECN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CMCVQPEFHCGDPCCTTC-RHHPCPPGQG- 67
                                                                                                                                                                                                                                                                                 40 -----CMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--G
                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                           .) (POTENTIAL)
                                                                                                                                                                                                                                  38;
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Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBE: AJ293700; CAC220218.1; -
SEQUENCE 276 AA: 30009 MW; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                   Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 276;
                                                                                                                                                                                                                                  Indels
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; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                          FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLGTGT - - DARCCR - - - - VHTTRCC - RDYPGEECCSE - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.5%; Score 139; DB 13; 26.1%; Pred. No. 4.1e-08; ive 10; Mismatches 58;
                                                                                                                                                                                                                 18.6%; Score 140; DB 11; 28.0%; Pred. No. 4.3e-08;
                                                                                                                                                         N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
SMART; SM00005; DEATH; 1.

21 BY SIMILARITY.

21 OSTEOPROTEGERIN.
                                                 4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                         276 AA
                                                                                                                                         SIMILARITY. SIMILARITY.
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                                                                                                                  SIMILARITY
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                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                           SKAPCRKHTNCSSLGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                92 HEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                   BY
BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.35;
Best Local Similarity 26.1%;
Matches 46; Conservative
                                                                                                                                                                                          46192
                                                                                                                                                                                                                                 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN CD40-HOMOLOGUE.
                                                                                                                                                                                                                         Best Local Similarity
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DISULFID
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                                                  DOMAIN
REPEAT
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gene and its expression nembryogenesis.";

Gene 215:339-343(1998).

1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES

1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES

OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY

SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO

OSTEOCLAST OSTEOCLAST PROGRITORS.

STROMAL CELLS AND OSTEOCLAST PROGRITORS.

1- SUBGLIULAR LOCATION: EXTRACELLULAR.

1- SUBGLIULAR LOCATION: EXTRACELLULAR.

1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,

PLACENTA. NOT DETECTED IN SPIESEN.

1- DEVELOPMENTAL STAGES: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT

1- DEVELOPMENTAL STAGES: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT

1- DEVELOPMENTAL STAGES: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT

1- DEVELOPMENTAL STAGES: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT

1- DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Sugs S., Boyle W.J.;

"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E., Morinaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
68 VQSQGKFSFGFQCIDCASGTFS--GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                             VAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCEEKGLVVKVKGTNTSDVIC 187
                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0STEOPROFECERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda
Higashio K.;
                                                                                                                                                                                                                                                                              401 AA
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB013898; BAA28269.1; --
EMBL, AB013903; BAA33388.1; --
EMBL, AB013999; BAA33388.1; --
EMBL, AB013900; BAA33388.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB013901; BAA33388.1; JOINED EMBL; AB013902; BAA33388.1; JOINED HSSP; P25942; 1CDF.
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ProDom; PE000771; -; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00052; TNFR_NGFR_1; 1.
PROSITE; PS00050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/C; TISSUE=KIDNEY; MEDLINE=97262071; Pubmed=9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9714833;
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STRAIN=129/OLA, AND NIH SWISS;
MEDLINE=98382527; PubMed=97148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:109587; Tnfrsf11b
InterPro; IPR000488; -.
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                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFRSF11B OR OPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of bone density.
                                                                                                                                                                                                                                                                                                                       008712; 070202;
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9
                                                        -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
A NUMBER OF OTHER HEMATOPOLISTIC AND IMMURE ORGANS. NOT DETECTED IN
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL, AB008821; BAA32076.1; -.
EMBL, AB008822; BAA32076.1; -.
EMBL, AB008821; BAA32076.1; -.
EMBL, AB008821; LOFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSS 156
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : || : || : |- HOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TC----TC-------RHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSG--GH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 HTTRCCRDYPG----EECCSEWDCMCV-----QPEFHCGDPC--CT------
                                    HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.7%; Score 133; DB 4; Length 401; 24.2%; Pred. No. 2.7e-07; Live 14; Mismatches 51; Indels
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EB42FA51C9D7C71E CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                       MIM; 6U2043;
InterPro; IPR001488; -.
InterPro; IPR001368; -.
Ptan; PF00020; TNFR_C6; 3.
ProDom; PD000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS00650; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
Glycoprotein; Repeat; Cytokine; Signal.
1 Glycoprotein; Repeat; Cytokine; Signal.
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                        STROMAL CELLS AND OSTEOCLAST PROGENITORS
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TNFR-CYS 3.
TNFR-CYS 4.
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Matches 36; Conservative
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01-NOV-1998 (
01-MAR-2001 (
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Last sequence update)
Last annotation update)

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(TrEMBLrel. 08, (TrEMBLrel. 08, 1)

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SEQUENCE FROM N.A.
Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
Vincenz C., Aggarwal B.B., Dixit V.M.;
"Identification and functional characterization of DR6, a novel death
domain-containing TNF receptor.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 MCVQPEFHCGDPCCTTCRHHPCPPGGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKP 98
TNFR-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNFR-RELATED DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 655;
                                                 Homo sapiens (Human).
Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.1%; Score 128.5; DB 4; Length Best Local Similarity 27.3%; Pred. No. 1.3e-06; Matches 39; Conservative 12; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                      Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF088868; AAC34583.1; -. EMBL, AL096801; CAB75692.1; -. HSSP: P07174; INCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             655 AA; 71844 MW; 48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GIGIDARCCRVHITRCCRDYPG------EEC--CSE---W-
                                                                                                                                                                                                                                                                                                                                                                                                                  Prodom; PD00071; ..., 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50052; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
SMART; SM00005; DEATH; 1.
Receptor.
SEQUENCE 655 AA; 71844 MW; 48939391C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 WTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00020; TNFR_c6; 4. Pfam; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000488; -. InterPro; IPR001368; -.
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                               DR6 OR DJ181J13.1
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94 FLTVFPGNKTHNAVCVPGSPPAEP 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 DARCCRYHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                    Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Goddard P.J., Ashkenazi A.; "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR."; Curr. Biol. 0:0-0(11999).

EMBL, AF125304; AAD22635.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Riccardi "Identification of a soluble human GITR splicing (hGITR-D)."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF241229; AAF65506.1; - SEQUENCE 255 AA; 26827 WW; C986652AC97AF2CC CRC64;
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 6.2e-56;
2; Mismatches 9; Indels
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                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
241 AA
                                                                                                    01-MAR-2001 (TremBLrel. 16, Last annotation GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN
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Local Similarity 67.4%;
nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15,
                                                                         (TrEMBLrel. 12,
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Best Local Similarity 100.
Matches 119; Conservative
PRELIMINARY;
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                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                               01-NOV-1999
01-NOV-1999
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STRAIN-BALB/C; Norther S., Giunchi L., Cupelli A., Mocentini G., Bartoli A., Riccardi C., Gene Structure and chromosomal assignment of GITR, a mouse member of the tumor necrosis factor/nerve growth factor receptor family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ 66
                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D., Migliorati G., Riccardi C.; Midentification of three novel MRNA splice variants of GITR."; cell Death Differ. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NGBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE—993255; PubMed—9177197; Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Mocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.; Riccardi C.; Riccardi C.; Riccardi C.; Riccardi C.; Faceptor family inhibits T cell receptor induced apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 CIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 222;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
TNFRSF18 OR GITR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 425.5; DB 11; Length
Pred. No. 1.2e-39;
" Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 AA; 24450 MW; 594932BA425A79CA CRC64;
                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                   222 AA
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                                                                                                                     PRT;
166 WET-----CGCEPGRPPGPP 180
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61.18;
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InterPro; IPR000561; -.
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01-MAR-2001
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01-JAN-1998
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0999f4 phytofacca
035806 rattus norv
008999 mus musculu
057117 cowpox viru
068396 human cytom
09pz67 human cytom
09px59 human cytom
09px89 bos taurus
09r172 rattus norv
09r172 rattus norv
09r172 rattus norv
09pzr8 human cytom
09pzr8 human cytom
09px6 human cytom
09px76 drosophila
099x81 caenorhabdi
099y12 mus musculu
099y12 mus musculu
099y12 mus musculu
099y12 mus musculu
                                           Q9qvw4 rattus sp.
O88281 rattus norv
Q9v383 drosophila
Q9vai2 drosophila
                      016042 homo sapien
                                  Q9pus0 salvelinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99156876; PubWed=10037686;
Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,
Kwon B., Yu K.Y., Wang S.X., Kwon B.S.;
"Identification of a novel activation-inducible protein of the tumor
necrosis factor receptor superfamily and its ligand.";
J. Biol. Chem. 274:6056-6061(1999).
EMBL: AF117297; AAD19694.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG
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01-WAR-2001 (TrEMBLE). 16, Last annotation update)
TWF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;
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095851;
01-MAY-1999 (TrEMBLrel. 10, Created)
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09PXQ7
09PXS9
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                     Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PANCREAS;
MEDLINE-20122600; PubMed-10655513;
MEDLINE-20122600; PubMed-10655513;
Bal C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
"Overexpression of M68/DGR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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EMBL, AF134240; AAD2968.1; --
EMBL, AF217793; AAF3368.1; --
EMBL, AF217793; AAF3366.1; --
EMBL, AF217794; AAF3366.1; --
EMBL, AF217794; AAF3368.1; --
INTERPROSE PESSA 2; LODF.
InterPro; IPR000561; --
InterPro; IPR000561; --
InterPro; IPR001368; --
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68E) (M68E) (DJ583P15.1.1.)
DCR3 OR TR6 OR TWFRSF6B.
                                                                      139 INCTLAGKRILQPASSISDAVCEDRSSLATQPWETPSAP 177
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                          87 TDCTQFGFLTVFPGNKTHNAVC-----VPGSPPAEP
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ProDom: PD00071; -; 1.
PROSITE: PS01186; EGE_2; UNKNOWN_1.
PROSITE: PS00652; TWFR_NGFR_1; UNKNOWN_1.
PROSITE: PS50050; TWFR_NGFR_2; 2.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
02TEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
TNERSF11B OR OPG OR OCIF.
Homo sapiens (Human).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEF-HCGDPCCTTCRHHPCPPGQGVQSQG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He Z. Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and Expression of Osteoprotegerin from Homo sapiens.";
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
EMBL; AFI14187; AAF20168.1; -.
HSSP; P2594.2; LODF.
InterPro; IPRO00488; -.
InterPro; IPRO00188; -.
FinterPro; IPRO01368; -.
Pfam: PF00020; TNFR_NGFR_1; UNKNOWN_1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 23.89
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                     109 -- VPGSPPAE 116
                                                                                                                                                                                                                                                       203 TRVPGAEECE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
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; 9

> ς. ..

> Gaps

32;

19.7%; Score 145; DB 4; Length 300; 30.0%; Pred. No. 1.8e-08; Live 9; Mismatches 50; Indels

Query Match 19.7 Best Local Similarity 30.0 Matches 39; Conservative Ξ,

Gaps

D.,

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| | : | | | | | | | | | 120 CNRRSGSEPQQECTHTRDIVCRCRPGTQPLNGYKHGVDCAPCPQGHFSEGNNRACRPW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 HTTRCCRDY - PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 CVGDTYPGGDRC----CLECQPGYGMVSRCNRSQDTIC--HPCEPGFYNEAVNYQACKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0X40 PRECURSOR (FRAGMENT).
0Xyctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                             TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
cell Death Differ. 0:0-0(2000).
EMBL; AF229434; AAF61568.1; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                    Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.0%; Score 147.5; DB 6; Length 267; 25.8%; Pred. No. 8.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 CCRD-YPGEECCSEWDCMCVQPEF----HCGDPCCTTCRHHPCPPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isono T., Seto A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AB003911, BAA20059.1;
HSSP, P19438, LEXT.
InterPro; IPR001368; -.
Pfam, PF00020; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS0050; TNFR_NGFR_2; 2.
SMART; SM00208; TNFR, NGFR_2; 2.
                                                                                                                                                                                                                                                                                                         F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A8B4CD3173C9500B CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.1%; Score 295.5; DB 11; Best Local Similarity 58.0%; Pred. No. 1.9e-25; Matches 47; Conservative 12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AA; 14106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 67 CIDCASGTFSGGHEGHCKPWT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.0
Best Local Similarity 25.8
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                               SMART; SM00181; EGF;
SEQUENCE 132 AA: 1
                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 AA;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CHBB: HM;
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SIGNAL
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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                               8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ 66
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω.
                                                                                                                                                 POTENTIAL.
GLUCOCORTICOID INDUCED TNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of three novel mRNA splice variants of GITR."; cell Death Differ. 0:0-0(2000).

EMBL; AF229432; AAF61566.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 CIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.7%; Score 425.5; DB 11; Length 228; 61.1%; Pred. No. 1.2e-39; ive 16; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.7%; Score 425.5; DB 11; Length ilarity 61.1%; Pred. No. 1.5e-39; Conservative 16; Mismatches 27; Indels
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U82534; AAB81243.1; -.
BMBL; AR109216; AAR14231.1; -..
MGD; MGI:894675; Tufrsf18.
InterPro; IPR000561; -.
SAMRT; SM00181; EGF; 1.
SIGNAL.
1 19 POTENTIAL.
                                                                                                                                                                                      RELATED PROTEIN.
50D8C275D9C56259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                          25334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JKR1;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                 Best Local Similarity 61.1%
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00181; EGF;
                                                                                                                                                                                                          228 AA;
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                 20
                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                             45 -----RHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLT 96
                                                                                                                                                                                                                                   LINKED (GLCNAC...) (POTENTIAL)
-LINKED (GLCNAC...) (POTENTIAL)
-LINKED (GLCNAC...) (POTENTIAL)
-> P (IN STRAINS 129/OLA AND NIH)
                                                                                                                                                                                                                                                                        N -> D (IN STRAINS 129/OLA AND NIH SWISS).
S -> A (IN STRAINS 129/OLA AND NIH SWISS).
                                                                                                                                                                                                                                                         SWISS).
I -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                   AND NIH
                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                               Score 131; DB 11; Length 401;
Pred. No. 8.3e-07;
9; Mismatches 60; Indels 20
                                                                                                                                                                                                                                                                                                                                                       5 CRVHTTRCCRDYPGEECCSEW----DCMCVQP-----EFHCGDPCCTTC
                                                                                                                                                                                                                                                                                                   -> R (IN STRAINS 129/OLA
                                                                                                                                                                                                                                                                                                              CAA6102D3B312470 CRC64;
                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                             OSTEOPROTEGERIN.
                                                                                                                                                                             DEATH DOMAIN.
BY SIMILARITY
                                                                                                Probom; PD000771; -; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
PROSITE; PS50005; TNFR_NGFR_2; 2.
SMART; SM0005; DEATH; 1.
Glycoprotein; Repeat; Cytokine; Signal.
                                                                                                                                                             TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                   L -> R
SWISS)
                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                17.8%;
26.5%;
                                                                                              Pfam; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                                                                                                              401 AA; 45923
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                       165
                                                                                                                                                                                                                                                                                       288
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                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                    97 VFPGNKTHNAVC 108
                                                                                                                                                                                                                                                                                                                                                                                                           : || ||: ||
IQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                            22
23
23
64
107
306
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VARIANT
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Gaps
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          09Y606;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. BRL; AF018253; AAB86809.1; -. HSSP, P25942; 1CDF. MIM; 603499; -. MIM; 6034999; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 LVAVVAGNSTTPRRCACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAG
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.8%; Score 131; DB 4; Length 616; 24.1%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 HTTRCCR-----DYPGEECCSEWDCMCVQPEFHCG------DPC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E3DE9A7A08196F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Glycoprotein; Transmembrane; Signal; Repeat. SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS.
616 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00050; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
SMART; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
23
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1113
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"Cloning and characterization of the gene encoding human osteoprotegerin/Osteoclastogenesis-inhibitory factor.";

Eur. J. Blochem. 254.685-691(1998).

Eur. J. Blochem. 254.685-691(1998).

FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERPRING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.

-1- SUBBUILT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                        MEDLIKE-97262071; PubMed-9108485; Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                                                              Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.; Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro."; Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZZ
                                                                                                                                                                                                    Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).

**SUBCELLULAR LOCATION: EXTRACELLULAR.

**ISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROLD, SPINAL CORD AND LIVER. ALSO DETECTED A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED THE PANCHEAS OR PERIPHERAL BLOOD LYMPHOCYTES.

**IMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

EMBL, AB002146; BAA22910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
OSTEOPROTEGERIN.
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InterPro; IPR001368; -.
Prom; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
Glycoprotein; Repeat; Cytokine; Signal.
SIGNAL
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                           MEDLINE=98151033; PubMed=9492069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=PLACENTA;
MEDLINE=98351569; PubMed=9688283;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-LUNG FIBROBLAST;
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106
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                                     SEQUENCE FROM N.A.
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  NCBI_TaxID-9606;
                                                                                                                                                                                                                                              bone density
                                                              TISSUE-KIDNEY
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EMBL; U94332;
HSSP; P25942;
MIM; 602643;
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"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression in embryogenesis.";
gene 215:339-343(1998).
-- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEMLY
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STRAIN=129/OLA, AND NIH SWISS;
MEDLINE=98382527; PubMed=9714833;
Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
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SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
SYNTOMAL CELLS AND OSTEOCLAST PROGENITORS.
SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C; TISSUE-KIDNEY;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto on the state of th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
05TEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG, BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
                                                                                                                                (POTENTIAL).
                                                                                                                                                                      (POTENTIAL)
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23.8%; Pred. No. 1.8e-07;
Live 15; Mismatches 59; Indels
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EB42FA51C9D7C71E CRC64;
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BY SIMILARITY.

N-LINKED (GLCNAC...) (
A-> D (IN REF. 2 AND 3)
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Best Local Similarity 23.8
Matches 38; Conservative
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-1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.

-1- SUBDINIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                              Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs·S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                               Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL: U94330; ARB53707.1; --
HSSP; P25942; LCDF.
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                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
74 TFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVC---VPG-SPPAEP 117
              158 YFSDAFSSTDKCRPWINCTFLGKRVEHHGTEKSDAVCSSSLPARKPPNEP 207
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N-LINKED (GLCNAC...
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BY SIMILARITY.

OSTEOPROTEGERIN.
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TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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InterPro; IPR001368; -
InterPro; IPR001368; -
InterPro; IPR001368; -
InterPro; IPR00120; INFR_G6; 4.
PROSITE; PS00652; INFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; INFR_NGFR_2; 2.
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                                                                                                                  Created)
                                                                                                                                                                                                                                                                      TISSUE=INTESTINE; MEDLINE=97262071; Pubmed=9108485;
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(TrEMBLrel. 04, I
(TrEMBLrel. 16, I
                                                                                       PRELIMINARY;
                                                                                                                                                                                         Rattus norvegicus (Rat).
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289
401 AA;
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                                                                                                                                                                               TNFRSF11B OR OPG
                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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01-JUL-1997
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                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 RHGNATHNTVCQC-RAGMHCSDASCQTCVENEPCKQGFGFVAAMAEARMTSPCEPCAEGT 151
                                                                                                                                                                       36 CGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFG 93
                                                                                   -----CMCVQPEFH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CMCVQPEFHCGDPCCTTC-RHHPCPPGQG-VQSQGKFSFGFQCIDCASGT 74
                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
17.7%; Score 130.5; DB 11; Length 401; 28.1%; Pred. No. 9.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBL: AJ293700; CAC220218.1; -.
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 276;
                                         53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Last annotation update)
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                                                                                   4 CCRVHTTRC--CRDY------PGEEC-----CSEWD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FS--GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Query Match 17.7
Best Local Similarity 28.1
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.4
Matches 38; Conservative
                                                                                                                                                                                                                                                                                   | : || ||: ||
171 LLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                           94 FLTVFPGNKTHNAVC 108
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN CD40-HOMOLOGUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     09DDD2;
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TNFRSF18

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------TQFGFLTVFPGNKTHNAVC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLGTGTDARCCRVHTTRCCRD
                                                                                                                   61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nocential G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL: AF229433; AAF61567.1; -.
InterPro: IPR000561;
SMART: SM00181; EGF: 1.
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Last annotation update)
FAMILY RELATED PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 AA; 24450 MW; 594932BA425A79CA CRC64;
                                                                                                                                                                                                                                                                                              121 SGGHEGHCKPWTDCCWRCRRPKTPEAASSPRKSGASDRQRRRGGWET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                      SGGHEGHCK PWTDC-
                                                                                                                                                                                                                                                                                                                                                                                                  172 EPGRPPGPP 180
                                                                                                                                                                                                                                                                                                                                                             154 VPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
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1D AC 035714
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPEQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
Curr. Biol. 0:0-0(1999).
InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Warksryota's Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi;
Catarrhini, Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 979; DB 4;
100.0%; Pred. No. 2.8e-95;
ive 0; Mismatches 0;
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GITR-D.

Homo saplens (Human).

Eukaryota; Metazoa; Chordata;

Mammalla; Eutherla; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
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Best Local Similarity 75.1
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 164; Conservative
                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Local

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QUANGO

121

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musculu musculu

salvelinus

sapien homo sapien homo sapien

088734 mus m 016042 homo s 000508 homo s 075412 homo s

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

057484 gallus gall 061204 mus musculu. 022685 caenorhabdi 094438 chironomus 022048 caenorhabdi 099383 drosophila

088281 rattus norv 008999 mus musculu

Q9gpm8 caenorhabdi Q9vrO8 drosophila O02660 bos taurus

Q18238 caenorhabdi Q9vxm0 drosophila Q9r172 rattus norv

Q9xvx3 caenorhabdi Q9xsv8 bos taurus O35806 rattus norv Q9xwd6 caenorhabdi

Oggwwd rattus sp. Ogwuh9 rattus norv Ogxvx3 caenorhabdi

	RR PSEQUENCE FROM N.A. RX MEDLINE-9156876; PubMed-10037686; RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y RA Liu D., Wang S.X., Kwon B.S.; RY "Identification of a novel activation-inducible pro			SMAKI; SMOUZOO; INFK; I. Receptor.	SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CR		. Query Match 100.0%; Score 979; DB 4; Le	%	Matches 164; Conservative 0; Mismatches 0;		VY 1 MAZHOAMGAFRALCGLALLCALSLOGURTGGFGCGFGRLLLGTGTT	Db 1 MAQHGAMGAFRALCGLALLCALSLGORPTGGPGCGPGRLLLGTGTI	•	Qy 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK1		DD 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKI		Qy 121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG		Db 121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG
	edicted by chance to have a ore of the result being printed, al score distribution.		Description	095851 homo sapien	Q9y5u5 homo sapien	Qynyjy nomo sapien Q9jkr2 mus musculu	035714 mus musculu	Q9jkr3 mus musculu	09jkrl mus musculu	002/64 oryctolagus	O95407 homo sapien	008727 rattus norv	008712 mus musculu	Q9y6q6 homo sapien	Q9uhp4 homo sapien	000300 homo sapien	075509 homo sapien	Obepus musculu	035305 mus musculu	09jkeO rattus norv
<pre>11: sp_rodent:* 12: sp_unclassified:* 13: sp_vertebrate:* 14: sp_virus:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES & SUMMARIES	Score Match Length DB ID	4	241	52.1 222 11	52.1 228 11	52.1 294 11	38.8 132 11		3 15.6 300 4 0	401 11	14.2 401 11	14.1 616 4 (	4	14.0 401 4	13.2 655 4 0	125 12.8 655 11	12.6 625 11	12.5

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Gaps

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Length 234; Indels

25110 MW; 55DB593CD0B1DB45 CRC64;

SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164 

1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

MEDLINE-99156876; PubMed-10037686; Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Liu D., Wang S.X., Kwon B.S.; "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand."; J. Blol. Chem. 274:6056-6061(1999).
EMBL; AF117297; AA019694.1; -.

Homo sapiens (Human). Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;

01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

234 AA.

PRT;

PRELIMINARY;

095851

AC DIT DIT DIT DIT DIT DIT OS

RESULT 095851

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*

sp\_organelle:\*

sp\_plant:\*

sp\_phage: \* sp\_mhc: \*

sp\_archea:\* sp\_bacteria:\* sp\_fungi:\*

SPTREMBL\_16:\*

Database

us-09-512-363-2\_copy\_1\_164.rspt

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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A. "Genomic amplification of a decoy receptor for Fas ligand in lung and
  110 HCSDASCQTCVENEPCKQGFGFVAAMAEARMISPCEPCAEGTFSNVSSKTEPCHFWISCE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PANCREAS;
MEDLINE-20122600; PubMed-10655513;
Bal C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
Soderman A., Galloway S.M., Liu O., Austin C.P., Caskey C.T.;
"Overexpression of M68/DcR3 in human gastrointestinal tract tumors
independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor
Superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1)
DCR3 OR TR6 OR TNFRSF6B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
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Pred. No. 1.9e-08;
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ProDom; PD000711; -; 1.

PROSITE: PS01186; BGF_2; UNKNOWN_1.

PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE: PS00050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF134240; AAD29688.1; -.
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EMBL, AF217794; AAF33685.1; --
EMBL, AF217794; CAC03668.1; --
EMBL, AL121845; CAC03668.1; --
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26.3%;
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                                                                       136 QFGFLTVFPGNKTHNAVC 153
                                                                                                        170 EKGLVVKVKGTNTSDVIC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 396:699-703(1998).
                                                                                                                                                                                                                                           PRELIMINARY;
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InterPro; IPR000561; -.
InterPro; IPR001368; -.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YPG--EECCSEWDCM-CVQ-----PEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 FOCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC------VPGSPPAE 161
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AALGLALLLGLLLGAEPR--PDCVGDTYPGGDRCCLECQPGYGMVSRCNRSQDTICHPC 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBL: AJ293700; CAC220218.1; -
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.5%; Score 171.5; DB 6; Length Best Local Similarity 32.6%; Pred. No. 2e-10; Matches 59; Conservative 11; Mismatches 74; Indels
              Isonor T., Seto. A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO0311; BAA20059.1; -.
HSSP; P19438; IEXT.
InterPro; IPR001368; -.
Pfam; PP00202; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                         267
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19 2
267 AA;
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STRAIN-CHBB: HM
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SIGNAL
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66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
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                                                                7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
                                                                                      7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL, AF229434; AAF61568.1;
InterPro: IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.8%; Score 380; DB 11; Length 132; 50.4%; Pred. No. 1.4e-32; ive 21; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14106 MW; F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                            126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
        Pred. No. 6.1e-46;
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54.1%; Pred. No. + ive 25; Mismatches
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Best Local Similarity 50.4%
Matches 64; Conservative
      L Similarity 54.1
86; Conservative
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SEQUENCE FROM N.A.
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        Best Local
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Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Riccardi C.;
Gene structure and chromosomal assignment of GITR, a mouse member of
"Gene structure and chromosomal assignment of GITR, a mouse member of
the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                          STRAIN-C3H/HEN;

MDEDINE-97322352; pubMed-9177197;

Nocentini G., Glunchi L., Ronchetti S., Krausz L.T., Bartoli A.,

Moraca R., Migliorati G., Riccardi C.;

Moraca R., Migliorati G., Riccardi C.;

A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis.";

Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino I Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL, AF229432; AAF615661;
EINTEFPRO; IPROBO0561;
SMART; SMO0181; EGF; 1.
SEQUENCE 294 AA; 33258 MW; FE0D4AEGA007BA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
GLUCOCORTICOID INDUCED TNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.1%; Score 510; DB 11; Length 294;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.1%; Score 510; DB 11;
11arity 54.1%; Pred. No. 4.9e-46;
Conservative 25; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELATED PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 AA;
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Best Local Similarity
Matches 86; Conserv
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SUBCELLULAR LOCATION: EXPRACELLULAR.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
PLACENTA. NOT DETECTED IN SPLEEN.
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
15 TO DAY 17.
                                                                                                                                                                                                                                                                                                                                                                                                           71 DCMCVQP-----EFHCGDPCCTTC------RHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                            15 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEW---- 70
                                                                                                                                                                                                                                                                                                                                                                                       36 GHQLLC------DKCAPGTYL-----KQHCTVRRKTLCVPCPDHSYTDSWHTSD 78
                                           SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
R -> P (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                     I -> R (IN STRAINS 129/OLA AND NIH SWISS).
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                                                                                                                                                                                                                                                                                                                        R (IN STRAINS 129/OLA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                  GFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
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SIMILARITY
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Best Local Similarity
Matches 43; Conservi
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                                               01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. REMEL; AF018253; AAB86809.1; -. HSSP. P25542; 1CDF. MIM; 603499; -. MIM; 603499; -.
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N-INKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .)
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                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
RECEPTOR ACTIVATOR OF NF-KAPPA-B.
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 138.5; DB 4; Length 616; 24.1%; Pred. No. 1.2e-06; Live 14; Mismatches 69; Indels 81
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS00605; TNFR_NGFR_2; 1.
RROSITE; ROSO0; TNFR, 1.
Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
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E3DE9A7A08196F81 CRC64;
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CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                    INDUCED CYTOKINE RECEPTOR) (RANK).
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                               (TrEMBLrel. 12,
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PRELIMINARY;
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                                                                                                                    TNFRSF11A OR RANK.
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01-NOV-1999 (
01-NOV-1999 (
01-MAR-2001 (
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Mus musculus
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-I- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INTERIPT IN VITRO OSTEOCLASTOGENESIS BY INTERIPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.

-I- SUBDINIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: EXTRACELLULAR.

-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97262071; PubMed=9108485; Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luuethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimmanoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;

"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                       RCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQ 146
                                                                                                             GFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVC------VP 155
                                                                   -CVQPEFHCGD-----PCCTT-----CR------HHPCPPGGGVQSQGKFSF 108
 Gaps
                       GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM- 73
                                             GERLVCA------QCPPGTFV-----QRPCRRDSPTTCGPCPPRHYTQFWNYLE 86
                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 26;
  Indels
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 Mismatches
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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ProDom; PD000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
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 14;
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  Conservative
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                                                                                                                                                                                                                                                                                                                 INFRSF11B OR OPG.
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-INTESTINE;
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                                                                                                                                                                              GAEECE 212
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 49;
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REPEAT
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Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 CYYCSPVCKELQTVKQECNRTHNRVCECEEGRYLELEFC---LKHRSCPPGLGVLQAGTP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 C-----CSEWD-----CMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRC--CRDY-----PGEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
Gene 215:339-343(1998).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 GROLLC------DKCAPGTYL----KQHCTVRRKTLCVPCPDYSYTDSWHTSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997. (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                   . . .) (POTENTIAL). . . .) (POTENTIAL). . . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 141.5; DB 11; Length 401; 27.2%; Pred. No. 4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 SFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 ERNTVCKRCPDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                          FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                  (GLCNAC
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                                                                                                                                                                                                                                                                                                  N-LINKED
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01-701-1997 (TrEMBLrel. 04, Created)
01-701-1997 (TrEMBLrel. 04, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last and
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MEDLINE=97262071; PubMed=9108485;
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MEDLINE=98382527; PubMed=9714833;
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Cell 89:309-319(1997).
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mes 46; Conserv
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                                                                                                                                                                                                                                        88 -----TC-----RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GH 124
                                                                                                                                                                 Gaps
                                                                                                                                                                                                       | | | : | | : | : | : | : | 37 HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 96
                                                                                                                                                                                           --- 87
BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

A -> D (IN REF. 2 AND 3).

M-S D (IN REF. 2 AND 3).
                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                   48;
                                                                                                                                       Query Match
Best Local Similarity 23.8%; Pred. No. 1.2e-06;
Matches 38; Conservative 15; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                         45996 MW;
 142
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401 AA;
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Search completed: September 4, 2001, 16:14:34 Job time: 1221 sec

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NCBI_TaxID=9606;
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DOMAIN
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   OOX ARABAY ARABA
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                                                        56 MSSKCTTTSDSVCLP----CGPDEYLDSWNEEDKCLLHKVCDTGKALVAVVAGNSTTPRR 111
                                                                                                                      -----CTTCRHH-PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKP 130
                                                                                                                                                            112 CACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFSSTDKCRP 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TC----TC------RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GH 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Clothing and Expression of Osteoprotegerin from Homo sapiens.";
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
EMBL; AF134187; AAF20168.1; -.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
05TEOPHOTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS EACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
THERSF11B OR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 137; DB 4;
23.8%; Pred. No. 1.1e-06;
tive 15; Mismatches 59
                                                                                                                                                                                                                                       131 WTDCTQFGFLTVFPGNKTHNAVC---VPG-SPPAEP 162
                                                                                                                                                                                                                                                                                                  172 WINCTFLGKRVEHHGTEKSDAVCSSSLPARKPPNEP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 AA.
PGEECCSEWDCMCVQPEFHCG-------DPC-
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PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSTEOPROTEGERIN (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P25942; ICDF.
Interpro; IPR000488; -.
Interpro; IPR001368; -.
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nes 38; Conserv
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O00300; O60236;
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SEQUENCE
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Matches
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MEDLIRE=97262071; PubMed=9108485; Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Lucety R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shinamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                    Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaquchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Hiqashio K.; Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitto."; Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z Z
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"Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROLD, SPINAL CORD AND LIVER. ALSO DETECTED A NUMBER OF OTHER HEMATOPOPLETU IMMUNE ORGANS. NOT DETECTED THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AB002146; BAA25910.1; -.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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PRODOM: PD000771; -; 1.
PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE: PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
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-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
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MEDLINE=98351569; PubMed=9688283;
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TISSUE=LUNG FIBROBLAST;
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SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR000561; -
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Matches 74; Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
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Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
Curr. Biol. 0:0-0(11999).
InterPro: IPR001368:
                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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81.7%; Score 687; DB 4; Length 255;
Best Local Similarity 71.3%; Pred. No. 7e-67;
Matches 117; Conservative 2; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00208; TNFR; 1.
SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) GLUCCCORTICOID-INDUCED TNFR-RELATED PROTEIN.
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Last sequence update)
Last annotation update)
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                                                                           241
                                                                                                               Created)
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                                                                   Q9Y5U5 PRELIMINARY;
Q9Y5U5;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2001 (TrEMBLRel. 16,
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Best Local Similarity 100.
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                 TISSUE-BONE MARROW;
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                                                                                                                                                                                                                                                         NCBI_TaxID-9606;
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RESULT 100 N 100

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67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNA 126
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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Sciurognathi; Muridae; Murinae; Mus.
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Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2098 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOID INDUCED THER FAMILY RELATED PROTEIN PRECURSOR.
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SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TQFGFLTVFPGNKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 EAASSPRKSGASDRQRRRGGWET-----CGCEPGRPPGPP 180
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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MEDLINE-97322352; PubMed-9177197;
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Q62327 mus musculu O88734 mus musculu

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Ogbus Salvelius
Ogwx3 caenorhabdi
Ogxw4 catuus
Ogyw4 rattus sp.
Ogv383 drosophila
O8281 rattus norv
Ogwub9 rattus norv
O22048 caenorhabdi
O9508 homo sapien
O2568 caenorhabdi
O95914 phytolacca
O75412 homo sapien
O9515 homo sapien
O9515 homo sapien
O97515 homo sapien
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002660 bos taurus
057484 gallus gall
                                    Q16042 homo sapien
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Q18238 caenorhabdi
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Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

Kwon B., Yu K.Y., Ni J., Yu G.L.,

Liu D., Wang S.X., Kwon B.S.;

"Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";

J. Biol. Chem. 274:6056-6061(1999).

EMBL, AF117297; AAD19694.1;

InterPro; IPR001368;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 841; DB 4; Length 234; 100.0%; Pred. No. 1.4e-83; Live 0; Mismatches 0; Indels (
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Q9V383
Q88281
Q62327
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Q16042
Q9PUSO
Q9XVX3
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Q22048
Q9GPM8
Q9G438
Q20508
Q20585
Q9S9F4
Q75412
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Matches 137; Conservative
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095407 homo sapien
008727 rattus norv
09ddd2 gallus gall
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                                                                                                                                                                                                                      1 QRPTGGPGCGPGRLLLGTGT......FPGNKTHNAVCVPGSPPAEP 137
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                                   Compugen Ltd
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
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MEDLINE-99087326; PubMed-9872321;
MEDLINE-99087326; PubMed-9872321;
Ditti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
"Genomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                                    95 HTRDTVCR---CRP--GTQPLNGYKHGVDCAPCPQGHFSEGNNRACRPWTNCTLAGKRTL 149
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                                                                                                                                                                                                                                                                                   9 CGPGRLLLGTGTGARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQ------PEFHCG 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bal C., Connolly B., Metzker M.L., Hilllard C.A., Liu X., Sandig V. Soderman A., Galloway S.M., Liu Q., Austlu C.P., Caskey C.T.; "Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                            40 CQP-----GYGMVSRCNRSQDTICHPCEPGFYNEAVNYQACKPCTQCNRRSGSEPQQECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostoml;
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                DB 6; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu K.Y., Kwon B., NI J., Zhal Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor
auppresses LICHT-mediated apoptosis.";
J. Balol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                          62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mathews L.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104419; AAD03056.1; -.
EMBL; AF134240; AAD29688.1; -.
                                                                                                                            A8B4CD3173C9500B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1)
DCR3 OR TR6 OR TNFRSF6B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000)
                                                                                                                                                                                           s; Score 154.5; DB 6b; Pred. No. 3.6e-09; 11; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 AA.
                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 FPGNKTHNAVC-----VPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 QPASSISDAVCEDRSSLATQPWETPSAP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11550E=FANCKEAS;
MEDLINE=20122600; PubMed=10655513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BLOOD;
MEDLINE-99253915; Pubmed-10318773;
PROSITE; PS50050; TNFR_NGFR_2;
SMART; SM00208; TNFR; 1.
                                                                                                                                   28489 MW;
                                                                                                                                                                                                18.4%;
31.1%;
                                                                                                                                                                                                                                          46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 396:699-703(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                                                              267 AA;
                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                   1977
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                                                                                                                                   SEQUENCE
                                                                                                                                                                                                Query Match
                                          Signal.
NON_TER
SIGNAL
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                                                                                                          CHAIN
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Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89:309-310(1997).
FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 HATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTOCOPCPPGTFSASSSSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTT-----CR-----HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_raxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTBOCLASSYGGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTBOCLAST PROGENITORS.

1. SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM--CVQPEFHCGD-----PC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
03-MAR-2001 (TrEMBLRel. 16, Last annotation update)
05-EOPROFECERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 -HCKPWTDCTQFGFLTVFPGNKTHNAVC-------VPGSPPAE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AA; 32679 MW; F90AEE33718449AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.9%; Score 150.5; DB 4 Best Local Similarity 26.9%; Pred. No. 1.1e-08; Matches 45; Conservative 13; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 AA
                                                                                                                                                                                                                              Pfam: PF00020; TNFR_c6; 4.

ProDom; PD00071; -; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS50065; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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EMBL; AF217796; AAF35244.1; -
EMBL; AF217793; AAF33685.1; -
EMBL; AF217794, AAF33686.1; -
EMBL; AL121845; CAC03668.1; -
HSSP; P25942; 1CDF.
InterPro; IPR001368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U94330; AAB53707.1;
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000488;
InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFRSF11B OR OPG.
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HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNA 126
                                                                                 27 PGCGPGKVQNGSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 PGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66
                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0X40 PRECURSOR (FRAGMENT).
0X40 PRECURSOR (Rabbit).
0xyctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Migliorati G., Riccardi C.;
Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isono T., Seto A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003911; BAA20059.1; -.
HSSP; BAB. 1EXT.
InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AA; 14106 MW; F586A5404B1DFEDE CRC64;
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 339.5; DB 1
Pred. No. 1.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 AA.
                                                                                                                                                                                                                                                                     132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.4%;
52.5%;
                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-MAR-2001 (TrEMBLrel, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF229434; AAF61568.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.55
Matches 53; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO00561;
SMART; SM00181; EGF;
SEQUENCE 132 AA; 1
                                                                                                                                                             127 VCVPGSPPAE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                    TNFRSF18
                                                                                                                                                                                                                                                                                         Q9JKR1;
                                                                                                                                                                                                                                                                   Q9JKR1
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                                                                                                                                                                                  "Gene structure and chromosomal assignment of GITR, a mouse member of the tumor necrosis factor/nerve growth factor receptor family."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: U82534; AABB1243.1; -
EMBL: AF109216; AAF14231.1; -
MGD: MGI: 894675; Tnfrsf18.
InterPro: IPR000561; -
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 PGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Migliorati G., Riccardi C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Nocentini G., Glunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.; A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                STRAIN-BALB/C;
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Riccardi C.;
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. GLUCOCORTICOID INDUCED THER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%; Score 465.5; DB 11; Length 56.9%; Pred. No. 7.9e-43; ive 21; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of three novel mRNA splice variants of Cell Death Differ. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                     50D8C275D9C56259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.4%; Score 465.5; DB 11; Best Local Similarity 56.9%; Pred. No. 6.3e-43; Matches 74; Conservative 21; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                     RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                       228 AA; 25334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF229432; AAF61566.1; -. InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TIEMBLIEL 15, 01-0CT-2000 (TIEMBLIEL 15, 01-MAR-2001 (TIEMBLIEL 16, GITR-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00181; EGF;
SEQUENCE 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 VCVPGSPPAE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 VCIPEPLPTE 149
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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TNFRSF18.

**Q9JKR3** Q9JKR3; φ

RESULT 09JKR3

SEQUENCE

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Gaps

7;

Pfam; PF00020; TNFR\_c6; 3. PROSITE; PS00652; TNFR\_NGFR\_1;

7 PGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66

Matches

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Length 132;

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EMBL; AF134187; AAF20168.1;
HSSP; P25942; ICDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                000300
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000300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; .Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEW----DCMCVQP-----EFHC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 NRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 CAPGTYL-----KQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0STEOPROTECERIN (FRAGWENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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TISSUE-PLACENTA;
He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and Expression of Osteoprotegerin from Homo saplens.";
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                           -> P (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> D (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> A (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.5%; Score 139; DB 11; Length 401; 26.4%; Pred. No. 2.4e-07; 1ve 10; Mismatches 65; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA6102D3B312470 CRC64;
                                                                                                                                                                                                                                                                                                                                                           OSTEOPROTEGERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA
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SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                          DEATH DOMAIN.
                                                                                                                                                                       TNFR-CYS 3.
TNFR-CYS 3.
Prodom; PD000771; -; 1.
PROSITE; PS50017; PS674—DOMAIN; 1.
PROSITE; PS50052; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 AA; 45923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.48
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                    401
201
63
106
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23
23
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DISULFID
DISULFID
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CARBOHYD
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REPEAT
                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                          DOMAIN
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Q9UHP4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.; "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoclastogenesis in vitro."; Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTTRCCRDYPG----EECCSEWDCMCV-----QPEFHCGDPC--CT------ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TC-----RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000300; 060256; 01-JUL-1997 (TrEMBLR-I) 04, Created) 01-JUL-1997 (TrEMBLR-I) 04, Last sequence update) 01-JUL-1997 (TrEMBLR-I) 04, Last annotation update) 01-MAR-2001 (TrEMBLR-I) 16, Last annotation update) 025EOPROTEGRAIN PRECURSOR (OSTEGOCLASTOGENESIS INHIBITORY FACTOR) (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.; "Cloning and characterization of the gene encoding human
                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 133; DB 4; Length 372;
24.2%; Pred. No. 1e-06;
live 14; Mismatches 51; Indels
                                                                                                                                                                                                                                                        372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 AA
InterPro; IPR000488; -.
InterPro; IPR001368; -.
InterPro; IPR001368; -.
PROSTE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSTE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 EGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97262071; PubMed-9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LUNG FIBROBLAST;
MEDLINE-98151033; PubMed-9492069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PLACENTA;
MEDLINE-98351569; PubMed-9688283;
                                                                                                                                                                                                                                                                                                                                                               Ouery Match 15.8%
Best Local Similarity 24.2%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
PLACENTA. NOT DETECTED IN SPLEBN.
BEVELOPMENTAL STAGE: IN SPLEBN.
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
15 TO DAY 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
                                                                                    73 KERHCTPHEICEDNAGLIVKRHGNATHNTVCQC-RAGMHCSDASCQTCVENEPCKQGFGF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suggs S., Boyle W.J.;
"Osfeoproceagerin: a novel secreted protein involved in the regulation of bone deserts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis."; Gene 215:339.343(1998).

-i- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMILATION OF NEWLY SYNTHESIZED BONE AND CARTICAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROCEDINGS.
-i- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
       LLLGCGQPGDAVNCSDKQYEHKGRCCNRCQPGKKLASECNDTEDSVCTPCENGQYQHSWT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Lucthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto Derose M., Ellott R., Colombero A., Tan H.-L., Trail G., Sullivan Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                        -----CMCVQPEFHCGDPCCTTC-RHHPCPPGQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                    75 VQSQGKFSFGFQCIDCASGTFS--GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB013899; BAA33388.1; JOINED.
EMBL, AB013900; BAA33388.1; JOINED.
EMBL, AB013901; BAA33388.1; JOINED.
EMBL, AB013902; BAA33388.1; JOINED.
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-KIDNEY;
MEDLINE-97262071; PubMed-9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-129/OLA, AND NIH SWISS;
MEDLINE-98382527; PubMed-9714833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U94331; AAB53708.1; -.
EMBL; AB013898; BAA28269.1; -.
EMBL; AB013903; BAA33388.1; -.
                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:109587; Tnfrsf11b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Monse)
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InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P25942; 1CDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFRSF11B OR OPG.
                                                                                                                                                                                                                                                                                                                                                      008712; 070202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                             008712
                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--G 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CGPGRLLLGTGTDARCCRVHTTRC--CRDY------PGEEC-----CSEWD------ 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPGTYL-----KOHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSPVCKELQTVKQECN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · · · ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM
EMBL; AJ293700; CAC20218.1; -.
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Score 140; DB 11; Length 401; 28.0%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 276;
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                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
N-LINED GLCONC. . . ) (POT N-LINKED (GLCONC. . . ) (POT M-LINKED (GLCONC. . ) (POT M-LINKED (GLCONC. . . ) (POT M-LINKED (GLCONC
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Last annotation update)
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Llarity 26.1%; Pred. No. 1.8e-07;
Conservative 10; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLGTGT - - DARCCR - - - - VHTTRCC - RDYPGEECCSE - - -
                                                                                                                        Cytokine; Signal.

BY SIMILARITY.

OSTEOPROTEGERIN.
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                                                                                                                                                                                                  4 X TNFR-CYS.
TNFR-CYS 1.
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TNFR-CYS 3.
TNFR-CYS 4.
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                 Prodom; PD000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
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TNFR C6; 4.
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                                                                                                                     Repeat;
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Matches 42; Conserv
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46; Conserv
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Pfam; PF00020;
                                                                                                                             Glycoprotein;
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TRANSMEM
DOMAIN
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osteoprotegerin/osteoclastogenesis-inhibitory factor.";
Eur. J. Blochem. 254.585-61(1998).
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                              -!- SUBSCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROLD, SPINAL CORD AND LIVER. ALSO DETECTED
A NUMBER OF OTHER HEMATOPOLIETIC AND IMMUNE ORGANS. NOT DETECTED
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL, AB008822; BAA32976.1; -.
EMBL, AB008821; BAA32976.1; -.
EMBL, AB08821; BAA32976.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TC----TC------RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--GH
                                                                                                       SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
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EB42FA51C9D7C71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .)
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                                                                                         STROMAL CELLS AND OSTEOCLAST PROGENITORS
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                                                                                                                                                                                                                                                                                                                                            PEGEN; PEODOLO; TNFR_C6; 3.
ProDom; PEODO071; -; 1.
PROSITE; PSO00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SWART; SM00005; DEATH; 1.
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TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Cytokine; Signal
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P25942; 1CDF.
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401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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HSSP;
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-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-!- SUBSCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLGRCCNKCEPGKYMSSKCTTTSDSVCLP----CGPDEYLDSWNEEDKCLLHKVCDTGKA 97
01-NoV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
N-LINKED (GICNAC. ..) (POTENTIAL).
N-LINKED (GICNAC. ..) (POTENTIAL).
N-LINKED (GICNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
BEMEL; AF018253; AAB86809.1; -- HSSP; PS5942; LCDF.
MIM; 603499; -- InterPro; IPR001368; -- InterPro; IPR00200; TNFR_C6; 4.
Prosite; PS00050; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS00050; TNFR_NGFR_2; 1.
SMART; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --CTTCRHH-PCPPGQGVQSQGKFSFGFQCIDCASG
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Glycoprotein; Transmembrane; Signal; Repeat. SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 4.
TNER-CYS 4.
BY SIMILARITY.
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                                                                                                                    INDUCED CYTOKINE RECEPTOR) (RANK).
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616 AA.

PRT;

PRELIMINARY;

09¥60

TNFRSF18

Q9Y5U5 Q9Y5U5;

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66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE
                                                                                                               61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                                                                                           ----TQFGFLTVFPGNKTHNAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-THYMUS;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.
Migliorati G., Riccardi C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of three novel mRNA splice variants of GITR."; cell Death Differ, 0:0-0(2000).
EMBL; AF229433; AAF61567.1; -.
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Last annotation update)
FAMILY RELATED PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 AA; 24450 MW; 594932BA425A79CA CRC64;
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Last annotation update)
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Pred. No. 8.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.2%; Scor.
54.5%; Pred. No. o...
7. 25; Mismatches
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(TrEMBLrel, 15, 1
(TrEMBLrel, 16, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00181; EGF; SEQUENCE 222 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     172 EPGRPPGPP 180
                                                                                                                                                                                                                                                                                                                                  VPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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01-OCT-2000 (
01-MAR-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
Curr. Biol. 0:0-0(1999).

EMBL: AF125304; AAD22655.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalja; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riccardi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Ri
"Identification of a soluble human GITR splicing (hGITR-D).
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF211229; AAF63506.1; - . C986552AC97AF2CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 255;
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llarity 75.1%; Pred. No. 2.7e-78;
Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90DC3B4AA7E82CBE CRC64;
                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                                                                                                               241
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SEQUENCE 241 AA; 26000 MW;
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                                                                                                               PRELIMINARY;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Simi
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09NYJ9; QUYYJ9

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022685 caenorhaddi
094438 chironomus
022048 caenorhaddi
090383 drosophila
088281 rattus norv
008999 mus musculu
099pm8 caenorhabdi
09vr08 drosophila
0018238 caenorhabdi
09338 caenorhabdi
           Q62327 mus musculu
O88734 mus musculu
                                                           Q9wuh9 rattus norv
075412 homo sapien
                                                                              Q9xvx3 caenorhabdi
Q9xsv8 bos taurus
O35806 rattus norv
                                                                                                                       057484 gallus gall
Q61204 mus musculu
                              Q16042 homo sapien
Q9qvw4 rattus sp.
000508 homo sapien
                                                                                                                                                                                                                                                      09r172 rattus norv
 Q9pusO salvelinus
Q62327 mus musculi
                                                                                                            Q9xwd6 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99156876; PubMed-10037686; Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Ciu D., Wang S.X., Kwon B.S.; "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand."; J. Biol. Chem. 274.6056-6061(1999).

EMBL, AF117297; AAD19694.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
11F RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;
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                  088734
Q16042
Q9QVW4
O00508
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O57484
Q61204
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088281
008999
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O02660
Q18238
Q9VXM0
Q9K172
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Q22048
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Best Local Sin
Matches 162;
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SEQUENCE
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                   Compugen Ltd.
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Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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sp_human:*
sp_invertebrate:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 ALCGLA-LLCALSLGQRPTGGPGC-----GPGRLLL----GTGTDARCCRVHTTRCCRD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBL: AJ293700; CAC20218.1; -.
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 17.7%; Score 171.5; DB 6; Length Best Local Similarity 32.6%; Pred. No. 1.7e-10; Matches 59; Conservative 11; Mismatches 74; Indels
                  Isono T., Seto A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AB003911. BAA20059.1;
INSP: P19438; IEXT.
InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS00050; TNFR_NGFR_1; 2.
PROSITE; PS00050; TNFR_NGFR_2; 2.
SMART; SM00208; TNFR, NGFR_2; 2.
                                                                                                                                                                                                                                                                                                               A8B4CD3173C9500B CRC64;
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Last annotation update)
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Matches 53; Conserv
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MEDLINE-99087326; PubMed-9872321;
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Goddwski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
"Genomic amplification of a decoy receptor for Fas ligand in lung and
Bai C.; Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DGR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJS83P15.1.1).
DCR3 OR TR6 OR INFRSF6B.
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Pred. No. 1.7e-08;
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PROSITE: PS01186; BGE_2; UNKNOWN_1.
PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE: PS50050; TNFR_NGFR_2; 2.
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MEDLINE-20122600; Pubmed-10655513;
                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32679 MW;
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26.3%;
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AF217794; AAF33686.1;
AL121845; CAC03668.1;
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                                                                                                                                         170 EKGLVVKVKGTNTSDVIC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF217796; AAF35244.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 396:699-703(1998).
                                                                                   136 QFGFLTVFPGNKTHNAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561; -. InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Riccardi C.;
"Gene structure and chromosomal assignment of GITR, a mouse member of
the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 48109216; AAB81243.1;
EMBL; AF109216; AAB81243.1;
InterPro; IPRO0561;
SMART; SMO0181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CCSEWDCMCVQPEFHCGDPCCTTCRHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125 | 1:1| 1| 1| 1| 1| 1| 1| 1| 1| 1| 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                             MEDLINE=9732352; PubMed=9177197;
Nocentini G., Glunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
Moraca R., Migliorati G., Riccardi C.;
A new member of the tumor necrosis factor/nerve growth factor
receptor family inhibits T cell receptor-induced apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                  GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0:0-0(2000).
EMBL; AF229432; AAF61566.1; -.
Interpro; IRR00561; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 228;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 52.2%; Score 506; DB 11; Best Local Similarity 54.5%; Pred. No. 8.8e-46; Matches 85; Conservative 25; Mismatches 38;
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(TrEMBLrel. 15, I
(TrEMBLrel. 16, I
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SEQUENCE 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA;
[1]
SEQUENCE FROM N.A.
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TISSUE-THYMUS;
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01-0CT-2000 (
01-MAR-2001 (
GITR-B.
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Length 294;

DB 11;

52.2%; Score 506;

Query Match

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                           Gaps
                                                    7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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50.4%; Pred. No. 1e-32;
ive 21; Mismatches 34; Indels
                         38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of Cell Death Differ. 0:0-0(2000).
EMBL; AF224341, AAF61568.1; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F586A5404B1DFEDE CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0X40 PRECURSOR (FRAGMENT).
           Pred. No. 1.1e-45;
; Mismatches 38
                                                                                                                                                                             114 GHCRLWINCSQFGFLIMFPGNKIHNAVCIPEPLPTE 149
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54.5%; Pic. 25;
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Best Local Similarity 50.49
Matches 64; Conservative
                         Conservative
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           Similarity
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|114 GHCRLWT 120
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01-JUL-1997
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Matches 85
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6
SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECITATIOY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
PLACENTA. NOT DETECTED IN SPLEEN.
BEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
15 TO DAY 17.
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                                                         -i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; 194331; AAA28269.1; -
EMBL; AB013809; BAA3388.1; -
EMBL; AB013809; BAA33388.1; -
EMBL; AB013900; BAA33388.1; -
EMBL; AB013900; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
HSSP; P25942; ICDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.4%; Score 139.5; DB 11; Length 401; 25.7%; Pred. No. 5.8e-07; tive 10; Mismatches 69; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS).
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N-LINKED (GLCNAC...
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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SWISS).
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InterPro; IPR000488; -
FAM: PR001088; -
Pr00000; THRR_G6; 3.
Pr000m; PD000771; -; 1.
PR0SITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_GRE_1; 1.
PROSITE; PS50050; THRR_NGFR_1; 1.
PROSITE; PS50050; THRR_NGFR_1; 2.
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SWISS).
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Best Local Si
Matches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
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                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                    REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
RECEPTOR ACTIVATOR OF WE-KAPPA-B PRECURSOR (TWF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUFR-CYS 3.

TUFR-CYS 3.

TUFR-CYS 4.

BY SIMILARITY.

BY SIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AF018253; AAB86809.1; -.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCR----VHTTRCCR-----DY
                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%; Score 138.5; DB 4; Length 24.1%; Pred. No. 1.1e-06; tive 14; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603499; -.
InterPro; IPR001368; -.
Pfam, PF00020; TNFR_c6; 4.
PROSTIE; PS50050; TNFR_NGFR_1; UNKNOWN_1.
SMART; SM0208; TNFR; 1.
SMART; SM0208; TNFR; 1.
PROSPICT; DS50050; TNFR; 1.
PROSPICT; Glycoprotein; Transmembrane; Signal; Repeat.
SIGNAL 1 22 POTENTIAL.
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TNFR-CYS 1.
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                TNFRSF11A OR RANK.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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234
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Best Local Si
Matches 52;
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DOMAIN
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CARBOHYD
SEQUENCE
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REPEAT
                            09x606;
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09Y60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMILATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                              Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                            GFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVC------VP 155
                                                                 -CVQPEFHCGD-----PCCTT-----CR------HHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                      15 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM- 73
                                           GERLVCA------QCPPGTFV----QRPCRRDSPTTCGPCPPRHYTQFWNYLE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: EXTRACELLULAR.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
Embl; 094330; AAB53707.1; -.
HSSP; P25542; 1CDF.
                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 26;
 Indels
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
OSTEOPROTEGERIN.
                                                                                                                                                                                                                                    401 AA
 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEATH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; -; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine; Signal.
                                                                                                                                                                                                                                                        (TrEMBLrel. 04, Created) (TrEMBLrel. 04, Last sequ
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97262071; PubMed-9108485;
 Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000488; -. InterPro; IPR001368; -.
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Glycoprotein; Repeat; C
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201
201
63
106
143
201
365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                               TNFRSF11B OR OPG.
                                                                                                                                                       156 GSPPAE 161
                                                                                                                                                                            GAEECE 212
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                                                                                                                                                                                                                                                         01-JUL-1997
01-JUL-1997
 49;
                                                                                                                                                                                                                                  008727
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OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERPUTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
-!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C: TISSUE-KIDNEY;
MEDLINE-97262071; PubMed-9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Osteoprotegarin: a novel secreted protein involved in the regulation of bone density."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 C-----CSEWD-----CMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRC--CRDY-----PGEE 65
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"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLEEL. 04, Last sequence update)
01-MAR-2001 (TrEMBLEEL. 16, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 SFGFQCIDCASGTFSG -- GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 ERNTVCKRCPDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                     63; Indels
                                                                                                                                                                                                                                                                             FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                  14.6%; Score 141.5; DB 1.
27.2%; Pred. No. 3.6e-07;
tive 11; Mismatches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene and its expression in embryogenesis."; Gene 215:339-343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/OLA, AND NIH SWISS;
MEDLINE=98382527; PubMed=9714833;
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                             46192
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFRSF11B OR OPG.
                                                     DISULFID
                                                                                                     DISULFID
                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                        DISULFID
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                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | : | | : | : | 37 HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 96
                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 24.2%; Pred. No. 2.8e-06;
Matches 36; Conservative 14; Mismatches 51; Indels
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BY SIMILARITY.

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401 AA;
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CONFLICT
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Search completed: September 4, 2001, 16:14:30 Job time: 1217 sec

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NCBI_TaxID=9606;
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                                   TISSUE=KIDNEY
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  ;
                                             -----CTTCRHH-PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKP 130
                                                          MSSKCTTTSDSVCLP----CGPDEYLDSWNEEDKCLLHKVCDTGKALVAVVAGNSTTPRR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSS 135
 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 75
                                                                                                                                                                                                                                                                                         N | 11)

P SEQUENCE FROM N.A.

C TISSUE-PLACENTA;

A He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;

"Cloning and Expression of Osteoprotegerin from Homo sapiens.";

L Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).

R EMBL; AF144187; AAF20168.1;

R EMBL; AF144187; AAF20168.1;

PR HSCP; P25942; 1CDF.

DR InterPro; IPR001488;

DR InterPro; IPR001368;

DR Pfam; PF00020; TNPR_C6; 3.

DR POSITE; PS00652; TNPR_NGFR_1; UNKNOWN_1.

DR PROSITE; PS500652; TNPR_NGFR_2; 2.
                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000300; 060236; 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MR-2001 (TrEMBLRel. 16, Last annotation update)
05TEOPROTECREIN PRECURSOR (OSTEOCLASTOGRNESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 13.7%; Score 133; DB 4; Length 372; 1 Similarity 24.2%; Pred. No. 2.6e-06; 36; Conservative 14; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                       131 WTDCTQFGFLTVFPGNKTHNAVC---VPG-SPPAEP 162
                                                                                                              172 WINCTFLGKRVEHHGTEKSDAVCSSSLPARKPPNEP 207
                                                                                                                                                                       372 AA.
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PGEECCSEWDCMCVQPEFHCG------DPC--
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                                                                                                                                                                                                                             OSTEOPROTEGERIN (FRAGMENT).
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NON_TER 1 1
SEQUENCE 372 AA; 42758
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Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Suggs S., Boyle W.J.;
"Osteoprotegarin: a novel secreted protein involved in the regulation
of bone density.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDZINE=98151033; PubMed=9492069;
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Yasuda H., Shima N., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and osteochegerin (OPG): a mechanism by which OPG/OCIF inhibits coteoclastogenesis in vitro.";
Endocrinology 139:1329-1337(1998).
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MIM; 602643; -
InterPro; IPR000488; -
InterPro; IPR001368; -
Pfam; PF00020; TNFR_C6; 3.
PROSITE; PS00672; -; 1.
PROSITE; PS50050; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SMART; SM00005; DEATH; 1.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                            MEDLINE=97262071; PubMed=9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=PLACENTA;
MEDLINE=98351569; PubMed=9688283;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                              121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTF 120
                                                Gaps
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                           1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-4NG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-4NG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-007-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.9%; Score 187; DB 3; L
Best Local Similarity 100.0%; Pred. No. 3.8e-173;
Matches 187; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08911423 Patent No. 6111090 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34,090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,(
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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TYPE: amino acid
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California
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US-08-911-423-8
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                                                                                                                                                                                                                                                                          HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLG 186
                                                                                                                                                                                   CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
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                                                                                         7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Locinik, Albert
TITLE OF INVENTION: MANMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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    Length 228;
                                                                                                                                                                                                                                                                                                                                                               LHIWOLRKTOLLLEVPPSTEDARSCOFPEERGERSAEEKGRLGDLWV 234
                                                                                                                                                                                                                                                                                                                                                                                      Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-40G-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-40G-1996
PRIOR APPLICATION NUMBER: US 60/027,901
APPLICATION NUMBER: US 60/027,901
APPLICATION NUMBER: US 60/027,901
APPLICATION NUMBER: US 60/027,901
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
Query Match 97.4%; Score 228; DB 3; Le Best Local Similarity 100.0%; Pred. No. 6.4e-213; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: protein US-08-911-423-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:14; Search time 12.35 Seconds

(without alignments)
390.133 Million cell updates/sec
105.09-512-363-2

Perfect score: 234
Sequence: 1 MAQHGAMGAFRALCGLALLC......EEERGERSAEEKGRLGDLWV 234
Scoring table: 0LIGO
Gapop 60.0, Gapext 60.0
Searched: 197339 seqs, 20590346 residues
Word size: 0
Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum DB seq length: 2000000000 Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

Score	& Query e Match	Length	DB	SUMMARIES	Description
	;	228	! ~	US-08-911-423-6	Sequence 6. Appl
~	193 82,5	241	m	US-08-911-423-4	4
-		311	m	US-08-911-423-8	ω,
-	9 42.3	232	æ	US-08-911-423-7	,
=	1 4.7	228	٣	US-08-911-423-2	7
_	3.4	782	Н	US-07-725-083-2	7
_	3.4	782	4	US-08-669-286-10	10,
_	3.4	782	4	US-09-469-253-10	10,
•	3.0	335	Н	US-08-289-699A-4	4, 7
•	3.0	335	~	US-08-878-283-4	Sequence 4, Appli
•	3.0	603	4	US-09-097-889-23	23,
•	3.0	713	-	US-08-188-228-62	62,
•	3.0	713	-	US-08-332-643-56	56,
•	3.0	713	Н	US-08-332-638-62	62,
•	3.0	751	4	US-09-036-987A-24	24,
•	3.0	1010	4	US-08-882-046-7	7, A
•	3.0	1218	7	US-08-400-159-6	9
•	3.0	1218	m	US-08-611-729A-6	9
•	3.0	1218	4	US-08-882-046-2	Sequence 2, Appl.
•	3.0	1219	4	US-08-882-046-5	5,
_	5 2.6	15	4	US-09-077-354B-6	9
_	5 2.6	15	2	PCT-US93-06751-23	23,
~	5 2.6	16	m	US-08-793-426A-4	4
_	2.6	16	4	US-09-294-565-4	Sequence 4, Appl
_	5 2.6	29	П	US:-08-376-362A-18	Sequence 18, Appl
_	2.6	34	П	US-08-190-802A-165	Sequence 165, App
_	2.6	79	9	5284931-7	Patent No. 528493

## ALIGNMENTS

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Sequence 6, Application US/08911423
Sequence 6, Application US/08911423
Fatent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Albert
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
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                                                                                                                                                                                                                                                                                                                    Length 782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09469253

Patent No. 6184352

GENERAL INPORMATION:
APPLICANT: NAKAMURA, SELJI
APPLICANT: NAKAMURA, SELJI
APPLICANT: NAKAMURA, SELJI
APPLICANT: NAKURA, TAKKSHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
INTREE OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blich, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STREET: VA
COUNTER: USA
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,253
                                                                                                                                                                                                                                                                                                                  3.4%; Score 8; DB 4;
100.0%; Pred. No. 11;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%; Score 8; DB (
100.0%; Pred. No. 11;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/669,286
APPLICATION NUMBER: US/08/669,286
FILING DATE:
NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-110P
  REFERENCE/DOCKET NUMBER: 230-110P TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Chas 8; Conservative
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100..
                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-286-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                           17 ALLCALSL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-469-253-10
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Patent No. 6130060

GENERAL INFORMATION:
APPLICANT: SAKURAL, TAKASHI
APPLICANT: SAKURAL, TAKASHI
APPLICANT: SAKURAL, TAKASHI
APPLICANT: SAKURAL, TONI-ICHI
TITLE OF INVERTION: GENE ENCODING ADSEVERIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blich, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STRET: VA
COUNTRY: USA
COUNTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,286
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,083
FILING DATE: 03-JUL-1991
CLASSIPICATION: 435
FILING DATE: 18-MS-1989
APPLICATION NUMBER: 07/353,432
FILING DATE: 18-MS-1989
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
RECISTRATION NUMBER: 29,021
RECISTRATION NUMBER: 29,021
RELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-260
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                           Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%; .Score 8; DB 1;
100.0%; Pred. No. 11;
iive 0; Mismatches
                         ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Sulte 600 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
MAMB: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 782 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.4
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11near
MOLECULE TYPE: protein
US-07-725-083-2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ALLCALSL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-08-669-286-10
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COUNTRY:
                                                                                                           RESULT 5
US-08-911-423-2
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                                                                                                                                                 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
                                                                                                                            HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLG 186
61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
FILING DATE: 14-AUG-1997
CLASSIFICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB 3; Le
Pred. No. 3.7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11arity 100.0%; Score 99; DB 10arity 100.0%; Pred. No. 3.7 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-A0G-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotník, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 99; Conserva
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                                                                                                                                                                                                                                     181 LHIWQLR 187
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Breakefield, Xandra O.
APPLICANT: Ozelius, Laurie J.
TITLE OF INVENTION: Genetic Diagnosis of Torsion Dystonia
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTON DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7%; Score 11; DB 3; Ler
100.0%; Pred. No. 0.(ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: DNAX Research Institute
STREET: 901 Callifornia Avenue
CITY: Palo Alto
STATE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DX0612K
                                                                                                                                         Sequence 2, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07725083 Patent No. 5407821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEGAT: 650-496-1200
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 228 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 11; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 FPGNKTHNAVC 141
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Gaps
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Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
ITILE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE & DEPRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                  APPLICANT: Suzuki, Shintaro
TITLE OF INVENTYON: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
. 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NO. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENDENCE/DOCKET NUMBER: 27866/30795
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELERAX: (312) 984-9740
TELEX.: (312) 984-9740
TELEX.: (32) 984-9740
TELEX: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   ; Sequence 56, Application US/08332643; Patent No. 5639634; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.0%; Sc
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 713 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-332-643-56
                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
      177. VLLLTSA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 VLLLTSA 183
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16 VLLLTSA 22
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                                                                                                             RESULT 13
US-08-332-643-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                      0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FLING DATE: 10 308/049,460
FLING APPLICATION NUMBER: US 07/872,643
APPLICATION NUMBER: US 07/872,643
FLING DATE: 17 308/049,460
FLING DATE: 17 308/049,460
FLING APPLICATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6448
TELEPHONE: (312) 474-646
TELEPHONE: (312) 474-6468
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
FWATTH. 713 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinols COUNTRY: USA
                                                                                                                                                                                                                                                            3.0%; Score 7; DB 4
100.0%; Pred. No. 82;
:1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.0%; Score 7; DB 3 Best Local Similarity 100.0%; Pred. No. 95; Matches 7; Conservative 0; Mismatches
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 713 amino acids
amino acid
                                                                                                                                                                                                                                                            Query Match 3.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-188-228-62
                                                                                                                                                                           ; TOPOLOGY: linear
US-09-097-889-23
                                                                                                                                                                                                                                                                                                                                                                        224 SAQLGLH 230
                                                                                                                                                                                                                                                                                                                                               182 SAQLGLH 188
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US-08-188-228-62
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GENERAL INFORMATION:

APPLICANT: Herrnstadt, Corrina
APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Group C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERX LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SORTWARE: PATENTION DATA: US/09/097,889
FILING DATE: 15-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.0%; Score 7; DB 2
100.0%; Pred. No. 48;
tive 0; Mismatches
                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,699
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF152
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSenman Ph.D., Stephen J.
RECISTRATION NUMBER: 43.058
REFERENCE/DOCKET NUMBER: 660088.417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09097889 Patent No. 6218117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 335 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-878-283-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                    COUNTRY: US
ZIP: 30306-3450
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216 GPGRLLL 222
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US-09-097-889-23
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                                                                                                                                              Sequence 4, Application US/08289699A
Patent No. 5695993
GENERAL INFORMATION:
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FUKUdome, Kenji
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 one Atlantic Center, 1201 West Peachtree
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,699A
FILING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 7; DB 1;
100.0%; Pred. No. 48;
1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF152
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 30306-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ACHITTER: IBM PC COMPALIBLE
PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-878-283-4
Sequence 4, Application US/08878283
Patent No. 5852171
GENERAL INFORMATION:
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100.0%; Pr.
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TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.0
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: peptide
                        CITY: Atlanta
STATE: Georgia
17 ALLCALSL 24
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                                                                                                                              US-08-289-699A-4
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Length 335; Indels

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3.0%; Score 7; DB 4; Length 751; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
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Job time: 22 sec
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,60
TELECOMMUNICATION INFORMATION:
TELEFAX: (317)337-4816
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-036-987A-24
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APPLICANT: Baltz, Richard H.
APPLICANT: Crawford, Rathryn P.
APPLICANT: Crawford, Rathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Tradway, Patti J.
APPLICANT: Tradway, Patti J.
APPLICANT: Trnner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences LLC Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION NUMBER: US 07/872,643
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%; Score 7; DB 1;
100.0%; Pred. No. 95;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acids
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-036-987A-24
; Sequence 24, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.1
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
    Illinois: USA
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EMBL; AF241229; AAF63506.1; -.
SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;
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MEDLINE-97322352; PubMed-9177197;
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                                                                                                                           Query Match
Best Local Similarity 100.
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SGGHEGHCKPWTDC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00181; EGF;
SEQUENCE 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 FPGNKTHNAVC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
Curr. Biol. 0:0-0(1999).

InterPro; IPR001368:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
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09Y5U5,
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TNFRSF18.
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Last annotation update)
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100.0%; Pred. No. 1.3e-184;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 82.5
Best Local Similarity 100.
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
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                                                                                                              Gaps
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EMBL, AF229433; AAF61567.1; -.
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Mammalla; Eutheria; Rodentia; Sclurognathl; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUCOCORTICOLD INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
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               Length 255;
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                                                     Indels
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Last annotation update)
               Score 134; DB 4; LA Pred. No. 1.1e-125;
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100.0%; Pred. No. 0.007;
tive 0; Mismatches 0.
228 AA
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streptomyce streptomyce

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pyrococcus pyrococcus

Minimum DB seq Maximum DB seq

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61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota, Viridiplantae; Core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 422;
                                                                                                                                                                                                                     Length 260;
                                                                                                                                                                                                                                                                      Indels
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL360314; CAB96664.1; ...
Hypothetical protein:
SEQUENCE 422 AA; 48570 MW; 31D1BC828F40BC39 CRC64;
                                                                                                                                                DAOF43E1197BACE1 CRC64;
the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; ALI37187; CAR69773.1; -.
InterPro: IPR002781; -.
Pfam; PF01925; DUF81; 2.
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NCBI_TaxID=10320;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 48.6 KDA PROTEIN.
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Last annotation update)
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100.0%; Pred. No. 12;
vative 0; Mismatches
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100.0%; Pred. No. 7.5
rative 0; Mismatches
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MEDLINE=95313343; PubMed=7793062;
                                                                                                                     Hypothetical protein.
SEQUENCE 260 AA; 25996 MW;
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14,
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                                                                                                                                                                                                                   Query Match 3.4
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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SEQUENCE FROM N.A.
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112 VVLLAVAA 119
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039493
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MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                              Gaps
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2010 (TrEMBLrel. 16, Last annotation update)
SC748.24C.
SC748.24C.
Streptomyces coelicolor.
Bacterla, Firmicutes, Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                               Length 241
                                                                                                                                           0; Indels
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TISSUE-SALIVARY GLAND;
Verma R.S., Elwood P.C.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF000380; AAB1377.1; -
SEQUENCE 245 AA; 26268 MW; BA36B7DB95FC0E20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Oliver K., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                        B9432671E3308A77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
FOLATE BINDING PROTEIN.
                                                                                             DB 2;
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100.0%; Pred. No. 7.5;
tive 0; Mismatches
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100.0%; Pred. No. 7.4
cive 0; Mismatches
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Hypothetical protein.
SEQUENCE 241 AA; 27514 MW;
                                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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014596;
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Aquifex aeolicus.
Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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100.0%; Pred. No. 6.8;
tive 0; Mismatches
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   Created)
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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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EMBL; AE000766; AAC07762.1;
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                          Caenorhabditis elegans
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                                              R160.6 PROTEIN.
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Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Migliorati G., Riccardi C.;
Migliorati G., Riccardi C.;
Gene structure and chromosomal assignment of GITR, a mouse member of
"Gene structure and chromosomal assignment of GITR, a mouse member of
the tumor necrosis factor/nerve growth factor receptor family.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; M2554; AAB81243.1;
EMBL; AF109216; AAF14231.1;
MGD; MGI:894675; Infrafi8.
InterPro; IPR000561;
SMART; SM00181; EGF;
SMART; SM00181; EGF;
Signal; Receptor.
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Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D., Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 0.0-0(2000).
EMBL; AF229432; AAF61566.1; -.
InterPro; IPR000561; -.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.; An ew member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                    GLUCOCORTICOLD INDUCED TNFR FAMILY RELATED PROTEIN. 50D8C275D9C56259 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     228 AA; 25334 MW;
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Matches 11; Conservative
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Q9TZD2;
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Q9TZD2
ID Q9TZD2
AC Q9TZD2;
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Q9JKR3 9

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MEDINE-94150718; Pubmed-7906398; MEDINE-94150718; Pubmed-7906398; MEDINE-94150718; Pubmed-7906398; MEDINE-94150718; Pubmed-7906398; Milson R., Ainscough R., Anderson K., Baynes C., Berks M., Milson R., Ainscough R., Connell M., Copsey T., Cooper-J., Coulson A., Crambon M., Dear S., Du Z., Durbin R., Favello A., Fulton L., A Gardner A., Green P., Hawkins T., Hilier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister M., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., A Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Analdon N., Smith A., Sonhammer E., Staden R., Suiston J., Anterry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; R. Legans."
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MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Deckert G., Warren P.V., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN-BRISTOL N2;
Waterston R.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF099001; AAC68733.1; -.
SEQUENCE 215 AA; 24502 MW; OAAC4FFF27914F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 27.5 KDA PROTEIN.
Last sequence update)
Last annotation update)
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RT "A set of ordered cosmids and a detailed genetic and physical map for RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL MOI. Microbiol. 21:77-96(1996).
DR KMI. A1445503; CAC13089.1; -...
KW Kinase.
SQ SEQUENCE 548 AA; 58276 MW; 72F37F817FD5D8E9 CRC64;
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2 SEQUENCE 548 AA; 58276 MW; 72F37F817F05D8E9 CRC64;
Query Match
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: September 5, 2001, 09:47:57 Job time: 98 sec

168 VVLLAVAA 175 |||||||| 24 VVLLAVAA 31

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STRAIN-A3(2);
Saunders D.C.,
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Letchworth G.J., Schwyzer M.; "Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus I genome which exhibits a colinear gene arrangement with the UL1 to UL4 genes of herpes simplex virus."; virology 210:100-108(1995).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; AC004877; AAC36300.1; -.
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Pfam; PF00096, zf-C2H2; 12.
PRINTS; PR00048; zINC_FINGER.
PROSITE; PS00028; ZINC_FINGER_C2H2; 12.
RART; SM00355; ZINC_FINGER_C2H2; 12.
DNA-Dinding; Metal-Dinding; Nuclear protein; Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                 Schwyzer M., Paces V., Letchworth G.J., Misra V., Buhk H. Lowery D.E., Simard C., Bello L.J., Thiry E., Vloek C.; Submitted (EEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AJ004801; CAA06124.1; -InterPro: IPR00785; -Pfam; PF01528; Herpes, glycop; 1. PF01528; Herpes, glycop; 1. PR010333; HSVINTEGRLMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leonard S., Graves T., Strowmatt C.; "The sequence of Homo sapiens PAC clone DJ0751H13."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.H.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        45517 MW; 4E7C7FA64FAAEFC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
WUGSC:H_DJ0751H13.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%; Score 8; DB 4;
100.0%; Pred. No. 14;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   504 AA.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                            Query Match 3.4
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                         438 AA;
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                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            168 VVLLAVAA 175
                                                                                                                                                                                                                                                                                                    93 VVLLAVAA 100
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317 GGPGCGPG 324
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                                                                                        STRAIN-JURA;
                                                                                                                                                                                        SEQUENCE
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075850
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J.E.,
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                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harriss Gordon S.V., Eiglmeier R., Gas S., Barry C.E. III, Tekaia F., Bacham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;

"Descipharing the blology of Mycobacterium tuberculosis from the nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID=1902;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 509;
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Sauntited (OCT-2000) to the EMBL/GenBank/DDBJ databases
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                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 53.2 KDA PROTEIN.
RV3887C OR MTCX15F10.25.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE TWO COMPONENT SYSTEM HISTIDINE KINASE.
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100.0%; Pred. No. 14;
iive 0; Mismatches
509 AA
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    PRT;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987; PubMed-9634230;
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Tuberculist; Rv3887c; -.
Hypothetical protein.
SEQUENCE 509 AA; 53278 MW.
                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 8; Conservative
    PRELIMINARY;
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205 VVLLAVAA 212
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/label- TR11
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                                                                                                                                                                    Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory condition.
                                                                                                                                                           Best Local Similarity
                                                                                                                        234 AA;
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                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                   AAY52158;
                                                                                                                                                   Query Match
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TRII activated NF-kappaB through a TRAP2-mediated mechanism.

Expression is activation-inducible. The TRI1 ligand is constitutively expressed in an endothelial cell line. This suggests that TRI1 and its ligand may be involved in activated T-cell trafficking. The invention provides TRI1, TRISVI and TRIISV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly and/or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                "conserved domain CD-VII
..113
te= "conserved domain CD-IV"
                                              "conserved domain CD-VI"
                                                                                  "conserved domain CD-IX"
                                                                                                                     "epitope-bearing region"
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                                                                                                                                                                                                region"
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                 128..134
/note= "conserved domain CD-V"
                                                                                        ..233
te- "conserved domain CD-X"
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hte= "epitope-bearing
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re- "epitope-bearing
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                                                                                                                                                                                                                                                                                                                                                                                           99US-0134172.
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                                                                       . 209
                                    .160
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                                                                                                                                                                                                        99..107
                                              /note=
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59..67
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222..23
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                                                                                                     'note
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Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                               defloiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                           arthitis, systemic liques erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicalular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TSAQLGLHIWQLRKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLWV 234
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immunodeficiency, especially common variable immunodeficiency
x-linked agammaglobulinemia, severe combined immunodeficiency
(SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 234; DB 21;
100.0%; Pred. No. 5.8e-214;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      agonist/antagonist compounds are also provided.
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163..179
/note= "Transmembrane domain"
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September 5, 2001, 09:46:14 ; Search time 20.66 Seconds
(without alignments)
686.641 Million cell updates/sec
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234
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Database

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human tumour necro	Tumour necrosis fa	Truncated human 31	Amino acid sequenc	Human TNF receptor	Human protein PRO3	Human PRO364 prote	Human tumour necro	Human PRO364 prote	Human PRO364 prote	Human immunostimul
SUMMARIES	. ~	AAY52158	AAW37840	AAW37839	AAY06605	AAB27651	AAB33431	AAY95895	AAB24409	AAY71467	AAB20115
igth DB	234 21	234 21	228 19	241 19	241 20	241 21	241 21	241 21	241 21	241 21	241 22
% Query e Match Length DB	100.0	100.0	97.4	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5
Score	234	234	228	193	193	193	193	193	193	193	193
Result No.	H	7	3	4	Ŋ	9	7	80	6	10	11

	9	ς.	241	22	AAB4	7054	Human PRO364. Hom
	S.	ς.	241	22	AAB5	0910	
	σ	ä	241	22	AAB5	0982	Human PRO364 prote
	σ	ά.	241	22	AAB5	3090	Human angiogenesis
	œ	φ.	235	21	AAY4	4825	Human molecule ass
•	œ	φ.	311	19	AAW3	7842	Human 312C2 protei
	~	щ.	240	21	AAY9	5881	Human tumour necro
	7	ω.	240	21	AAY5	2160	TR11SV2 amino acid
	139	•	317	20	AAY0	6645	PRO364-related EST
	m	φ.	316	22	AAB4	7055	Polypeptide encode
	3	9	241	21	AAY9	5880	
	3	9	241	21	AAY5	2159	TR11SV1 amino acid
24	66	42.3	232	19	AAW3	AAW37841	Human 312C2 protei
25	11		222	19	AAW4	9018	
26	11	4.7	228	19	AAW4	9016	Mouse glucocortico
27	11	٠	228	19	AAW3	7838	Amino acid sequenc
. 28	11	•	294	19	AAW4	9017	Mouse glucocortico
29	7	•	20	20	AAY1	1945	Human 5' EST secre
30	7	•	61	21	AAY6	5057	Human 5' EST relat
31	7	•	79	19	AAW7	0320	Secreted protein B
32	7	3.0	79	20	AAY5		Secreted protein 1
33	7	•	79	20	AAY5	9026	Secreted protein 4
34	7	•	120	21	AAB4	AAB41195	ORF
35	7		138	13	AAR2	6820	
36	7	•	242	21	AAB0	0040	Human COMP/TSP-1 c
37	7	•	297	20	AAY0	7078	Renal cancer assoc
38	7		299	22	AAB6	AAB61485	Murine TANGO 300 e
39	7		300	21	AAB0	0041	Human COMP/TSP-2 c
40	7	•	307	21	AAG4	4824	Zea mays protein f
41	7	•	312	21	AAG448	4823	Zea mays protein f
42	7		341	22	AAB61	46	) signal
43	7	•	355	22	<b>AAB500</b>	0055	Murine Dendritic C
44	7	•	361	21	AAB2	361	Human secreted pro
4.5	7		361	22	AAB6	142	ANGO 300
					*	O MARCON CO.	
					2	ALIGNMENTS	
RESULT 1							
AAY95879 ID AAY95879		standard;	Protein;		234 A	AA.	

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AAY!	AAY95879 TD AAY95879 stan	standard. Protein. 234 AA
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AC	AAY95879;	
<b>4</b> E	20-NOV-2000	(first eptro)
X		/ Tono 2011
DE	Human tumour	Human tumour necrosis factor receptor-like protein TR11.
××		•
ΚW	TR11; human;	TR11; human; tumour necrosis factor receptor-like protein
ΚW	immunodeficiency;	ncy; autoimmune disease; rheumatoid arthrit:
ΚW	immunosuppres	antiarthritic;
ΚW	dermatologica	dermatological; antiinflammatory; therapy; diagnosis.
×		
SO	Homo sapiens.	
XX	•	
FH	Key	Location/Qualifiers
FT	Peptide	125
ΕŢ		/label= Signal_peptide
ĿΤ	Protein	26234
ΕŢ		/label= Mature_protein
ΕŢ	Domain	26162
FT		/label= Extracellular_domain
ΕŢ	Domain	163179
ΕŢ		/label= Transmembrane_domain
FT	Domain	180234
FŢ		/label= Intracellular domain
FT	Modified-site	146
FT		/note= "N-qlycosylated"
FT	Domain	7281
FΤ		/note= "conserved domain CD-II"
FT	Domain	

/note= "conserved domain CD-III"

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protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen specific proliferation and cytckine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoletic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                     Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence encoding the human 312C2 T cell
                                                                                                                                                                                                                                                                                Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Pages 59-60; 71pp; English.
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1..726
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                                                                  AAW37839 standard; Protein; 241 AA.
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96US-0689943
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                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis; cancer; has autoimmune disorders.
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N-PSDB; AAV19153.
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16-AUG-1996;
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                                                                                                                                        AAW37839;
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                             AAW37839
RESULT
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Tumour necrosis factor receptor homologue – useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or
                                                                                                                                                                                                                        Claim 17; Fig 2A; 104pp; English.
                                                                                                                                                               autoimmune responses
WPI; 1999-494296/41.
                                 N-PSDB; AAX87670.
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Gaps

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Length 241; Indels 1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

82.5%; Score 193; DB 19; I 100.0%; Pred. No. 4.4e-175; iive 0; Mismatches 0;

Best Local Similarity 100. Matches 193; Conservative

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Query Match

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61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

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The present sequence represents human PRO364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO.

Escherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-x, 26-241 (i.e. the resemble protein) and 26 x of the present sequence, where x is any one of amino acid respdies 157-167 of PRO364. PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammallan cells (claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin Fc region are also claimed. PRO364 can be used in sasays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or also be combined with an agent that is cytotoxic, chemotherapeutic
PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-glycosylated"
162..180
                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                            /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL,
                                                                                                                                                                                                               Human TNF receptor homologue PRO364.
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                 AAY06605 standard; Protein; 241 AA.
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                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                      181 TSAQLGLHIWQLR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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Pitti RM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                          AAY06605;
                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                              181
                                                                                                        RESULT
AAY06605
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standard; Protein; 228 AA.

(first entry)

28-JUL-1998

AAW37840;

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AAW37840
 AAW37840
                                                      curvival. They can be used for treating immune deficiency disorders, beginning a syndrome, HIV infection, severe combined immunodeficiency (SCID), wiskert-Aldrich disorder, blood coaquiation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia. Theumatoid arthrilis, Goodpastures syndrome, Grave's disease, multiple sclerosis, mysthenta gravis, Stiff-Man syndrome, gystemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent disease, multiple sclerosis, mysthenta gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent disease, not autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cycokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager syndrome). The products can also be used for detection, diagnosis and prognosis.
                                                                                                                                                                                                                                                              This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TR11 receptor). The invention relates to TR11 and two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were determined by sequencing cloned cDNAs AA237765-237766. The TR11 receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GITR). TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/Antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell
                                                                                                                                                                           New tumour necrosis factor receptor-like polypeptides used to, e.g.
                                                                                                                                                                                                                                Claim 14; Fig 1; 167pp; English
                                                   (HUMA-) HUMAN GENOME SCI INC.
                97US-0063212.
                                                                                                                                                                                                treat Digeorge syndrome
                                                                                                                      2000-061922/05.
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                                                                                     Ruben SM;
                21-OCT-1997;
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                                                                                                                                            YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                             61 ypgeeccsewdcmcvqpefhcgdpccttcrhhpcppgqgvqsqgkfsfgfqcidcasgtf 120
                                                                                                                                                                                                                  SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                      Gaps
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                                                                                        1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                  121 sggheghckpwtdctqfgfltvfpgnkthnavcvpgsppaeplgwltvvllavaacvlll
                                                                                                                                                               tsaqlglhlwqlrktqlllevppstedarscqfpeergersaeekgrlgdlwv 234
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   Length 234;
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                                    Indels
100.0%; Score 234; DB 21;
100.0%; Pred. No. 5.8e-214;
ive 0; Mismatches 0;
                                   Conservative
                Similarity
                                   234;
Query Match
Best Local 9
                                   Matches
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                                               Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoietic cells; lymphoid cell;
autoimmune disorders.
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Truncated human 312C2 protein from clone_A8 amino acid sequence.
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100.0%; Pred. No. 2.8e-208;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHE ) SCHERING CORP.
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                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY95895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henzel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hebert C, Ho
JL, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an J, Pennica D, Shelton DL, Watanabe CK, Wood WI, Yan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 33; Fig 36; 309pp; English
                                                       99WO-US05028.
99US-0123618.
99US-0123957.
99US-0125775.
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2000WO-US04341.
2000WO-US04342.
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99US-0132371.
99US-0134287.
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99US-0144758.
99US-0145698.
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                              2000WO-US05841
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Kabakoff RC, Lu Y, Pan
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                             02-MAR-2000;
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16-DEC-1999;
20-DEC-1999;
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06-JAN-2000;
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18-FEB-2000;
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14-SEP-2000
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04-MAY-1999
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diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB3347 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                  Length 241;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                  82.5%; Score 193; DB 21; 1 100.0%; Pred. No. 4.4e-175;
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Best Local Similarity
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WPI; 2000-611444/58
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                                                                           Gaps
                                                                                                1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as inhibitors.
                                                                                                                                                                                                                                                                                              Cardiovascular; endothelial; angiogenic disorder; PR0179; PR0238; PR0364; PR0844; PR0846; PR01760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885; PR0887;
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                                                           Length 241;
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                                                          Score 193; DB 20; I
Pred. No. 4.4e-175;
0; Mismatches 0;
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Goddard A, Gurney AL, Hillan KJ, Marsters SA,
Watanabe CK, Williams PM, Wood WI;
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/label- "Signal peptide"
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100.0%; Pre
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99WO-US12252.
99US-0144758.
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Matches 193; Conserv
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                                      Sequence
                                                           Query Match
Best Local
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Peptide
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                                                                  Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
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                                                                                                                                                                                                                              Claim 71; Fig 6; 181pp; English.
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Best Local Similarity
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N-PSDB; AAA99903
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                                         tumour;
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                           PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumous breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expresed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GTR protein homologue.
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or
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/note= "Leucine zipper pattern"
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/label- Signal_peptide
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98US-0112850.
98US-0113296.
99US-0144758.
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         Human PRO364 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-412325/35.
N-PSDB; AAD01240.
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                                                                                                                                                                                                                                                                       Modified-site
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                                                                                           Homo saptens
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homology to members of the TNFR family and mouse GITR protein. This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO565, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast,
                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                            Gaps
                                                                                                                                                                                                             9
                                                                  prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
                                                                                                                                                                                                  61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                                                                                                                  SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                    1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                 Length 241;
                                                                                                                                                          Indels
                                                                                                                                              4.4e-175;
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                                                                                                                                 DB 21;
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                                                                                                                                         100.0%; Preu. ...
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/note= "N-myristoylation
                                                                                                                                 Score 193;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26..241
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20115 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunostimulant PRO364.
                                                                                                                                 82.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                          193; Conservative
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                                                                                                                                             Local Similarity
                                                                                            241 AA
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                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20115;
                                                                                                                                 Query Match
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showing identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The invention provides highly conserved TRII, TRIISVI and TRIISV2 proteins (see AAY9581), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISV1 and/or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency. X-IInked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency of the hyper Igw. TRIISV1 and/or TRIISV2 and/or TRIISV2 and/or Gardiciency with hyper Igw. TRII, TRIISV1 and/or TRIISV2 and/or diagnose an autoimmune disease, especially rheumatcid arthritis, systemic lupus erythematosus, thrombocytopenia purpura or Igh nephropathy. The polypeptides provides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the contraction of the contractio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO; promotion; inhibition; anglogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; anglogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ypgeeccsewdcmcvqpefhcgdpccttcrhhpcppgqgvqsqgkfsfgfqcldcasgtf 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARĆCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                   82.5%; Score 193; DB 21; L 100.0%; Pred. No. 4.4e-175; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             agonist/antagonist compounds are also provided.
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98US-0112850.
99WS-011554.
99WS-0123957.
99US-0131445.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.
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08-MAR-1999;
12-MAR-1999;
28-APR-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 193;
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16-DEC-1998
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenic disorder in mammals by modulating cell proliferation, and indigonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atheroscierosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB2438 to AAB2438 bro Present nucleotide and protein sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                            Goddard A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and treating diagnosing a cardiovascular, endothelial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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Kuo SS, Paoni NF, Smith V;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO polypeptides useful for preventing
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                                                                                                                                                                                                                                                                                                          Baker KP, Ferrara N,
Surney AL, Klein RD,
Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 72; Fig 44; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing and treating diagnosi angiogenic disorders in mammals
                                                                                                                                                      99WO-US21547.
99WO-US23089.
99US-0162506.
99US-0144758.
                                                    99WO-US20111.
                                                                               99WO-US20594
                                                                                                         99WO-US20944
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Williams PM,
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Best Local Similarity 100.
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
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Watanabe CK,
  20-JUL-1999;
                             26-JUL-1999;
                                                                               08-SEP-1999;
                                                    01-SEP-1999;
                                                                                                      13-SEP-1999;
                                                                                                                                 15-SEP-1999;
                                                                                                                                                        15-SEP-1999;
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us-09-512-363-2.oli.rag

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cardiovascular, endothelial, angiogenic or angiostatic disorder. The PRO364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The tumour necrosis factor receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was 1solated from a library of cDNA fragments derived from human umbilical vain endothelial cells (HUVEC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced alsorder. PRO364 or PRO175 is useful for inhibiting angiogenesis induced disorder. PRO364 or PRO175, or their antagonists, are useful for vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vascularides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; antiinflammatory; dermatological; antiarthritic;
antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
antiallergic; antiasthmatic; immune related disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB50910 standard; Protein; 241 AA
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99US-0144732.
99US-0144758.
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Best Local Similarity 100.
Matches 193; Conservative
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20-JUL-1999;
20-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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The present sequence is one of thirty three novel PRO polypeptides.

The PRO polypeptides, anti-PRO antibodies, agonists and antegonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sogren's systemic vaculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary clirhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's diseases, autoimmune or immune-mediated skin diseases (such as such as asthma, allergic chimitis, atopic dermatitis, food hypersensitivity and urricaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumoniis), transplantation associated diseases including graft rejection and graft-versus-host diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                 , Gurney AL;
Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.5%; Score 193; DB 22; I
100.0%; Pred. No. 4.4e-175;
Live 0; Mismatches 0;
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Shelton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                 AJ, Baker KP, Chan B,
Henzel W, Kabakoff RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 58; Fig 18; 218pp; English.
                                                                                99WO-US28313.
                                                                                                                                2000WO-US30911,
                                                                                                                                                                                                2000WO-US04341.
2000WO-US04342.
                                                                                                                 99US-0170262
                                                                                                                                                                 2000WO-US00376
                                99WO-US21090
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Best Local Similarity
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                                                                                                                                                             06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
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24-FEB-2000;
15-MAR-2000;
20-MAR-2000;
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17-MAY-2000;
22-MAY-2000;
                                            15-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
09-DEC-1999;
20-DEC-1999;
05-JAN-2000;
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Wood WI;
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Matches
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The present sequence is that of novel human immunomodulator PR0364 (16 kDa) isolated from a sequence from cDNA (see AAF30057) isolated from a small intestine library. PR0364 (26 kDa) p16.34) shows sequence homology to mouse GITR protein and may be its human counterpart. The invention provides polynuclectides (see AAF30050.62) encoding novel human PR0 proteins (see AAB20108-20) including PR0364.

Claimed compositions comprising the proliferation of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune response, or increasing the proliferation of T-lymphocytes in a response to an antigen. Claimed compositions comprising a PR0 polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a TCC claimed method for treating an immune related disorder, such as a TCC claimed method for treating an immune related disorder, such as a relibody or an antagonist antibody. The disorder is selected from systemic inpus erythematosus, rheumatorid arthritis, osteoarthritis, of call disorder inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, cautoimmune chronic active hepatitis, primary bilitus, immune-mediated renal disease, demyelinated disease, (such as multiple sclerosis), autoimmatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative collitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, cautoimmune mediated skin diseases (such as bullous skin disease, captoin multiperme and psoriasis), allergic diseases (the lung and transplantation associated diseases (such as suchman allergic thinitis, and graditismed methods of diseases) (autoimmune mediated securing the level of expression of the PRO gene. Also colaimed are a method as graft rejection and graft-versus'host diseases on method of diseases is not a method of diseases of the methods 
                                                                                                                                                                                                                                                                                                                                                                       Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T lymphocytes
                                            /note= "prokaryotic membrane lipoprotein lipid
                                                                                  171..193
/note= "leucine zipper pattern"
/note= "Asn is N-glycosylated"
166..177
                                                                                                                                                                                                                                                                                                                                                                     Goddard A,
Pitti RM,
                                                                  attachment site"
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ck MR, Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Fig 16; 127pp; English.
                                                                                                                                                                                                                                        15-MAR-2000; 2000WO-US06884.
                                                                                                                                                                                                                                                                                99US-0144758
                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                             Mark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-103149/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AA;
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                                                                                                                                                   WO200105972-A1.
                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ,
                                                                                                                                                                                                                                                                                20-JUL-1999;
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                                                                                                                                                                                             25-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                      Peptide
                                                                                       Peptide
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Composition for diagnosing and treating cardiovascular, endothelial and anglogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                         PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGITR; ligand; hGITR; pRO175; tumour necrosis factor receptor; TNFR; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF_2alpha; trauma; cancer; anglogenesis;
                                                                           SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                         YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents PRO364 polypeptide, which is a human gluco-corticoid-induced tumor necrosis factor receptor (hGTTR). The corresponding ligand (hGTTR), PRO175, is given in AAB47056. PRO364 and PRO375 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a
            MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Potential signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylated"
162..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ocation/Qualifiers
                                                                                                                                                                                                                                                                                    AAB47054 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2000; 2000WO-US18867.
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                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                181 TSAQLGLHIWQLR 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-138257/14.
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                                                                                                                                                                                                                                                                                                                                                                             Human PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                   AAB47054;
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                   Qγ
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Gaps

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Length 241; Indels

82.5%; Score 193; DB 22; I 100.0%; Pred. No. 4.4e-175; tive 0; Mismatches 0;

Query Match 82.5 Best Local Similarity 100. Matches 193; Conservative

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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, protein, agonists or antagonists of a PRO protein, agonists or antagonists of a PRO protein, agonists or antagonists of a PRO protein, adonists of a PRO protein, adonists of a PRO protein, agonists or antagonists of a PRO protein, adonists of a PRO protein, adonists of a PRO protein, adonisting a compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial call growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof.

PRO nucleic acids, PRO protein, or an agonist or antagonist thereof.

PRO nucleic acids, PRO protein, and becades therapeutic agents to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate colNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the
                                                                                                                                                                                Goddard A;
                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                                                                                                Mark MR, Ma
1, Wood WI;
                                                                                                                                                                                       N, Gerber H, Go
J, Kuo SS, Mark
Williams PM, W
                                                                                                                                                                                          Baker KP, Ferrara N, surney AL, Hillan KJ,
                                                                                                                                                                                                                                     Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 69; Fig 54; 293pp; English.
99WO-US23089.
99WO-US28313.
99WO-US28409.
99WO-US28564.
                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                       Ashkenazi AJ, Baker
Godowski PJ, Gurney
Paoni NF, Pitti RM,
                                                                                                                                                                                                                                                                                 WPI; 2001-090793/10.
N-PSDB; AAC97479.
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                                                30-NOV-1999;
02-DEC-1999;
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Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-175;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy I MAQHGAMGAFRALGGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

181 TSAQLGLHIWQLR 193

 Search completed: September 5, 2001, 09:47:03 Job time: 49 sec

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28-FEB-2001
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15-SEP-1999
                                                                                                 Sequence
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                                                                                                                          Query Match
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                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                         Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of seventeen novel PRO polypeptides. The PRO
61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
       Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mark MR, Marsters SA;
4, Wood WI;
                                SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP, Ferrara N, Gerber H,
Howski PJ, Gurney AL, Kuo SS, Ma
11 RM, Watanabe CK, Williams PM,
                                                                                                                          AAB50982 standard; Protein; 241 AA
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                                                                                                                                                                                                                                                                                                                                                          99WO-US28313.
99WO-US28409.
99WO-US28565.
99WO-US30095.
2000WO-US03565.
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2000WO-US04342.
2000WO-US05004.
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2000WO-US06319.
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99US-0141037.
99US-0144758.
99US-0145698.
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2000WO-US08439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski PJ
                                                                         181 TSAQLGLHIWQLR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I A, GOUCHAN, NF, Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GETH ) GENENTECH INC
                                                                                                                                                                          Human PRO364 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-025251/03.
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                                                                                                                                                                                                                                                          WO200073445-A2.
                                                                                                                                                                                                                           wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000;
10-MAR-2000;
15-MAR-2000;
                                                                                                                                                                                                                                           Homo sapiens
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02-DEC-1999;
16-DEC-1999;
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30-MAR-2000;
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nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma. cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
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0
                                                                                                                                                                                                                                                                                                                                                                                          Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Le
                                                                                                                                                                                                                                                                                                                                                                                          82.5%; Score 193; DB
100.0%; Pred. No. 4.4
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB53090 standard; Protein; 241 AA
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99US-0134287.
99US-0134287.
99US-0141037.
99US-0144758.
99US-0145698.
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Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSAQLGLHIWQLR 193
                                                                                                                                                                                                                                                                                                                   241 AA;
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12-MAR-1999;
14-MAY-1999;
02-JUN-1999;
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01-SEP-1999;
08-SEP-1999;
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us-09-512-363-2.oli.rag

us-09-512-363-2.rag

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mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist: a retroviral gene therapy vector comprising a PRO andleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof.

PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as a therosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, come therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the devalopment and screents a PRO protein of the therapy. PRO nucleic agence represents a PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 maghgamgafralcglallcals1gqrptggpgcgpgrll1gtgtdarccrvhttrccrd 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1322.5; DE
Pred. No. 1e-99;
1; Mismatches
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Best Local Similarity 96.7%;
Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         241 AA;
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This is the amino acid sequence of the truncated human 312C2 T cell protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoletic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66
                                                                                                                                                                       Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
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                                                                                                                                                                                                                                             Disclosure; Pages 61-62; 71pp; English.
                                                                                      Zlotnik A;
 96US-0027901.
96US-0689943.
                                                                                      Randall TD,
                                                    (SCHE ) SCHERING CORP
                                                                                                                      WPI; 1998-159534/14.
N-PSDB; AAV19154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AA
07-OCT-1996;
16-AUG-1996;
                                                                                      Gorman DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                          The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial infarctions, Reynaud's disease, rheumatoid arthritis, angina, myocardial antagonists are also used to prevent tumour anglogenests and for treating periodontal diseases. The PRO nucleic acids, polypeptides and prisue regeneration. The PRO nucleic acids, polypeptides and antibodies are useful for diagnosing a cardiovascular, endothelial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233
                                                                                                                                                                                                                                  SA;
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                                                                                                                                                                                                                                                                                        Seventeen nucleic acids encoding PRO polypeptides which are useful ir diagnosis and treatment of cardiovascular, endothelial or angiogenic
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Kuo SS, Mark MR, Marsters
illiams PM, Wood WI;
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Watanabe CK, Williams PM,
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Pred. No. 1e-99;
; Mismatches
                                                                                                                                                                                                                       Ferrara N,
Gurney AL,
                                                                                                                                                                                                                                                                                                                            Claim 71; Fig 8; 182pp; English.
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                                                               99WO-US20111.
99WO-US28313.
99WO-US28409.
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96.7%;
2000WO-US13705
                           99US-0141037
99US-0144758
                                             99US-0145698
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2000WO-US04341
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                                                      99US-0146222
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                                                                                                                                                                                                                                                                                                          disorders in a mammal
                                                                                                                                                                                                                                 Godowski
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Paoni NF, Pitti RM,
                                                                                                                                                                                                                                                           WPI; 2001-025251/03.
N-PSDB; AAC90566.
                                                                                                                                                                                                                                                                                                                                                                                                                                               anglogenic disorder,
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                                                                                                                             18-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                       Ashkenazi AJ,
17-MAY-2000;
                                                                                                                                                       10-MAR-2000;
                                                                                                                                                                  15-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                     30-MAR-2000;
                                                                                                           11-FEB-2000;
                                                     28-JUL-1999;
01-SEP-1999;
                                                                       30-NOV-1999;
                                                                                         02-DEC-1999;
16-DEC-1999;
                                             26-JUL-1999
                                    20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233;
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Best Local S
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Matches
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Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; mycardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; enen therapy; transgenic animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A;
rrk MR, Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                                                                                                                                                                                Human angiogenesis-associated protein PRO364, SEQ ID NO:142
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Williams PM,
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AL, Hillan KJ,
Watanabe CK, Wi
                                                                                                                                     AAB53090 standard; Protein; 241 AA.
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99US-0123957.
99US-0134287.
99WO-US12252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ, Baker KP,
Godowski PJ, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-090793/10
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26-JUL-1999;
01-SEP-1999;
08-SEP-1999;
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02-JUN-1999;
23-JUN-1999;
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12-MAR-1999;
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30-NOV-1999
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241 v 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO364; human, glucocorticoid-induced tumor necrosis factor; receptor; hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm;
                                                                                                                                                                                                                                                                                                                                                                                         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                     SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                  9
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                                              granulomatous hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative collitis and Crohn's disease), gluten sensitive enteropathy, Whipple's disease, (auto)immuno-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersonsitivity and uricaria), immunologic aliseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host diseases) (all claimed). Claimed methods of diagnosing these disorders comprise detecting
                                                                                                                                                                        the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T lymphocytes
idiopathic inflammatory myopathy, Sjogren's syndrome, systemic asculitts, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyrodiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as multiple sclerosis),
                                                                                                                                                                                                                                                                                                                                        MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                      181 TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                          DB 22; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arterial restenosis; thrombophlebitis; tumor anglogenesis;
lung; llver; flbrosis; neuropathy; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Potential signal peptide"
                                                                                                                                                                                                                                                                                       Score 1322.5; DB
Pred. No. 1e-99;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB47054 standard; Protein; 241 AA.
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                                                                                                                                                                                                                                                                                       98.78;
96.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                    241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          saptens
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                                                                                                                                                                                                                                                                                                                233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 V 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 v 241
                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB47054;
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                 Matches
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corticoid-induced tumor necrosis factor receptor (hGTTR).

Corresponding ligand (hGTTR), PR0175, is given in AAB47056.

Rosissa and PR0175 may be used in a mixture with a cardiovascular, endothelial, anglogenic or anglostatic agent for the treatment of a cardiovascular, endothelial, anglostatic agent for the treatment of a cardiovascular, endothelial, anglostatic agent for the treatment of a cardiovascular, endothelial, anglostatic or anglostatic disorder. The PR0364 cDNA sequence was isolated from an expressed sequence tag (EST) at ababase as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PR0175 cDNA sequence was isolated from an library of cDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PR0364 or PR0175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGE_Zalpha), characterized by the presence of an elevated level of page_Zalpha), characterized by the presence of an elevated level of page_Zalpha), charactering a therapeutically effective amount of an antibody that binds PR0364 or PR0175 in a human suffering from a tumor or a retinal disorder. PR0364 or PR0175, or their antagonists, are useful for vascular-related drug targeting or as therapeutic trargets for the presence of an antibody is the presence of an subman suffering the page.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents PRO364 polypeptide, which is a human gluco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCOFPEEERGERSAEEKGRLGDLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system disease and neuropathies and rheumatoid arthritis.
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                                    162..180 - /note= "Potential transmembrane domain"
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96.7%; Pred. No. 1e-99;
iive 1; Mismatches
/note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 76pp; English.
                                                                                                                                                                                                                                                                                                                    11-JUL-2000; 2000WO-US18867.
                                                                                                                                                                                                                                                                                                                                                                                                     99US-0143304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-138257/14.
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                                                                                                                                                              WO200103720-A2
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                                                                                                                                                                                                                                                                                                                                                                                                     12-JUL-1999;
                                                                                                                                                                                                                                           18-JAN-2001
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                                                Domain
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Wed Sep

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, Gurney AL;
Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO; antiinflammatory; dermatological; antiarthritic; antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antialabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
181 tsaqlglhiwqlrsqcmwpretqlllevppstedarscqfpeeergersaeekgrlgdlw 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A, G
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Kabakoff RC,
                                                                                                                                                                                                                    AAB50910 standard; Protein; 241 AA.
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99US-0144758.
99US-0146222.
99WO-US20111.
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99US-0162506
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99WO-US30911
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99WO-US28634
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                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J, Baker KP,
Henzel W, Kab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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N-PSDB; AAC91469.
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                                                                                                                                                                                                                                                                                                                                                                      Human PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                    21-MAR-2001
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                                                234 V 234
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                                                                                                                                                                                                                                                                 AAB50910;
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AAB 50 910

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AAB 50 A
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The present sequence is one of thirty three novel PRO polypeptides.

The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, costeoarthritis, juvenile chronic arthritis, spondyloarthropathies, Slogrem's systemic vasculitis, sarcoidosis, autoimmune heemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, autoimmune or immune-mediated skin diseases, such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung (such as ecsinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary fibrosis including graft rejection and graft-versus-host diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; PRO; cardiant; antianglogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiarthriticametory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 241;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.7%; Score 1322.5; 96.7%; Pred. No. 1e-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB50982 standard; Protein; 241 AA.
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Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO364 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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241

AAY71467 standard; Protein; 241 AA.

(first entry)

08-NOV-2000 Human PRO364

AAY71467;

protein.

180 180 233

61 ypgeeccsewdcmcvqpefhcgdpccttcrhhpcppgqgvqsqgkfsfgfqcidcasgtf 120

SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 181 TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCOFPEEERGERSAEEKGRLGDLW

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RESULT
AAY71467
 cardiant; cardiovascular; antiatherosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing; a cardiovascular, endothelial or anglogenic disorder in mammals by modulating cell proliferation, anglogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiar hypertrophy). For example, the nucleic acids (NCs) and vectors cardiar hypertrophy). For example, the nucleic acids (NCs) and vectors associated with decreased PRO expression. AAA77510 to AAA77721 and AAB4138 to AAB4135 represent nucleotide and protein sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillan KJ, Godd
oni NF, Smith V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerber H,
Kuo SS, Pao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrara N,
Klein RD, K
1, Wood WI;
anglogenic; proliferative; cardia
cytostatic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 72; Fig 44; 315pp; English.
                                                                                                                                                    98WO-US25108.
98US-0112850.
99US-0115554.
                                                                                                                                                                                               99WO-US05028.
99US-0123957.
99US-0131445.
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99WO-US20111
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99WO-US23089
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Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412154/35.
N-PSDB; AAA77604.
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                                                                     40200032221-A2
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                                           Homo sapiens.
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Watanabe CK,
                                                                                                                          30-NOV-1999;
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PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                      site"
                                                                                                                                                                                                                                                                                                        "N-myristoylation site"
                                                                                                                                                                                 /note= "N-myristoylation site"
                                                                                                                                                                                                                         /note- "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation, site"
                                                                                                                                                                                                                                             /label- Mature_PRO364_protein
                                                                                                                                                                                                                                                                                                                                                                                     /label Transmembrane_domain 166..177
                                                                                                                                                                                                     /note= "N-myristoylation
                                                                                                                                                                                                                                                                 /note= "N-myristoylation
                                                                                                                                                                                                                                                                                   /note= "N-myristoylation
                                                                                                                                                     1..25
/label- Signal_peptide
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    attachment site
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98US-0112850.
98US-0113296.
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122..128
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                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
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16-DEC-1998;
22-DEC-1998;
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                                                                                                                                                   Peptide
                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                              Domain
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7; Gaps 9 9

DB 21; Length 241; 0; Indels

Score 1322.5; DE Pred. No. 1e-99; 1; Mismatches

98.78; 96.78;

Query Match Best Local Similarity 96.7 Matches 233; Conservative

YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSGGKFSFGFQCIDCASGTF 120

MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 

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Homo sapiens.
                                                                                                                                                                                                                                                                                                               clone, designated as DNA47365-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA4825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNRR) family of polypettides. PR0364 sequence also shows homology to members of the TNRR family and mouse GITR protein.

This clone is assigned the ATCC deposit No: 209436. PR0364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PR0655, PR0364 and PR0344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
                                                                                                                                                                                                                                                                                                  The present sequence is the human PRO364 protein, encoded by the cDNA
                                                                                                                                                                                      for
or
                                                                                                                                                                                    seful for inhibiting neoplastic cell growth and comprises PRO655, PRO344 or PRO364 polypeptide
                                                                                              Wood WI;
                                                                                              Napier M,
                                                                                            Gurney AL, Hillan K,
                                                                                                                                                                                                                                                             Claim 31; Fig 4; 108pp; English.
99US-0144758
99US-0145698
                                                                                                                                                                                      composition useful
                                                       (GETH ) GENENTECH INC
                                                                                              Goddard A,
                                                                                                                            WPI; 2000-412325/35
                                                                                                                                                                                                         treating cancers,
their antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AA;
                                                                                                                                                N-PSDB; AAD01240
 20-JUL-1999;
                   26-JUL-1999;
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                                                                                          Chen J,
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1;
                                                                                                                                                                                                            121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                   61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                   181 TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233
                                                                                                                                        1 maqhgamgafralcglallcalslgqrptggpgcgpgrlllgtgtdarccrvhttrccrd 60
                                                   Gaps
                                                                                           1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                                                                   DB 21; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO364; UNO319; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallergic; immunostimulant.
                                            0; Indels
Score 1322.5; D
Pred. No. 1e-99;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20115 standard; Protein; 241 AA.
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98.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                          Matches 233; Conservative
                         Best Local Similarity
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  Query Match
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PJ, Gurney Al
Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of novel human immunomodulator PRO364 (UNQ319), as deduced from CDNA (see AAF30057) isolated from a small intestine library. PRO364 (26 kDa, pt 6.34) shows sequence homology to mouse GITR protein and may be its human counterpart. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO364. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response, or increasing the proliferation of \bar{r}-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "prokaryotic membrane lipoprotein lipid
   attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski E
Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                                          note= "N-myristoylation site"
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146..150
                                                                                                                                                                                                                                                                                                                                                                          /note= "Asn is N-glycosylated"
166..177
                                                                                                                                               note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
Pitti RM,
                                                                                                                    'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                 "N-myristoylation
                                                                                                                                                                                                         'note= "N-myristoylation
                                                                       86..241
/label= Mature_protein
                                                       'label= Signal_peptide
                             Cocation/Qualifiers
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Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Fig 16; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2000; 2000WO-US06884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144758
                                                                                                                                                                                                                                                                                                            ..128
                                                                                                                                                                                                                                                                                  118..124
                                                                                                                                                                                                                                                                                                                                           156..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                 171..193
                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                   'note=
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                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                         Peptide
                                                                                                      Domain
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Homo sapiens
                                                                                                                                02-MAR-2000;
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20-APR-1999;
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05-JAN-2000;
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20-DEC-1999;
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15-SEP-1999;
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29-NOV-1999
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12-MAR-1999
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                                                                                                       Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
                                                                                                                                                                       The present invention relates to methods for stimulating or inhibiting anglogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO238, PRO364, PRO844, PRO846, PRO845, PRO815, PRO311, PRO333, PRO840, PRO877, PRO877, PRO879, PRO882, PRO885 or PRO387. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothelial or angiogenic disorders. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyrold; antidiabetic; nootropic; neuroprofective; antianamic; hepatotropic; virucide; antipsoriatic; antiallergic; antianathmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; didopathic inflammatory myopathy; sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease;
                                          RM;
                                                                                                                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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                                Gerritsen ME;
Paoni NF, Pitti
                                                                                                                                                                                                                                                                                                                                                                         MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                    DB 21; Length 241;
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                              , Ferrara N, Gerber H,
Hillan KJ, Marsters SA,
PM, Wood WI;
                                                                                                                                                                                                                                                                                                                  , Match 98.7%; Score 1322.5; Di Local Similarity 96.7%; Pred. No. 1e-99; nes 233; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO364 protein UNQ319 SEQ ID NO:92.
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                                                                                                                                                    Claim 71; Fig 6; 181pp; English
                                          Gurney AL, Hil
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                               Baker KP,
          (GETH ) GENENTECH INC.
                                                                         2000-611444/58.
                                                                                                                                                                                                                                                                                    241 AA;
                                                                                    N-PSDB; AAA99903
                               Ashkenazi AJ,
                                          Goddard A, G
Watanabe CK,
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Matches
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Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.
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L, Smith V;
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Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney AL,
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an J, Pennica I
Watanabe CK, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 33; Fig 36; 309pp; English.
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99US-0123957.
99US-0125775.
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99US-0131445.
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99US-0146222
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Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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N-PSDB; AAC58596.
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Kabakoff RC, I
Stewart TA, Tu
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18-FEB-2000;
22-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic sclenosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic andmannia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyellating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACSB397 to AACSB378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACSB579 to AACSB642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                  61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                              SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
             spondyloarthropathies,
                                                                                                                                                                                                                         DB 21; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor receptor-like protein TR11 mutein.
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                                                                                                                                                                                                                                              0; Indels
from systemic lupus erythematosus, rheumatoid
nritis, juvenile chronic arthritis, spondyloart
                                                                                                                                                                                                                                  Pred. No. 1e-99;
1; Mismatches
                                                                                                                                                                                                                       98.7%; Score 1322.5; 96.7%; Pred. No. 1e-9
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99US-0134172.
99US-0144076.
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                                                                                                                                                                                                                                   Best Local Similarity 96.7
Matches 233; Conservative
  selected from sy
osteoarthritis,
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16-JUL-1999;
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241 v 241
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receptor-like protein TRII (see also ARY95879), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The invention provides chighly conserved TRII, TRIISVI and TRIISV2 proteins (see ARY95879-81), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency, Kscht-Aldrich syndrome or X-linked immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency with hyper IgM. TRII, TRIISVI and/or TRIISV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose andyor diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lugus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in polypeptides may also be used Methods for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
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                                                                                                                                                 diagnosis, prevention and treatment of disease states associated aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 241;
                                                                                                                             Human tumor necrosis factor receptor-like proteins useful for
                                                                                                                                                                                                                                                                                                                                                    present sequence is that of human tumour necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agonist/antagonist compounds are also provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1322.5; DE
Pred. No. 1e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO364 protein sequence SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                  Disclosure; 294-295; 278pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 233; Conservative
                                                           WPI; 2000-572072/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AA;
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SM,
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   Ruben
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AAW37839
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TRII, TRIISVI and TRISVI polypeptides may be involved in the requiation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/Antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, blood pistolet disorders by wounds resulting immune deficiency disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat hear attacks, strokes, Addison's disease, heamolytic anamemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, mysathenia gravis Stiff-Man syndrome, disease, multiple sclerosis, mysathenia gravis Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent chance, or autoimnume inflammatory peripheral necepticion or graft versus host disease, inflammatory conditions, ischaemia-reperfusion or graft versus host disease, inflammatory conditions, ischaemia-reperfusion chances and central nervous system disease, emperpriblicative disorders, or infections and central nervous system disease, emperpending and central nervous system disease, and central nervous system disease, emperenced for repair and entral nervous systemic sequenced for challers and central nervous systemic sequenced for challers and entral nervous systemic sequenced for challers and entral nervous systemic sequenced for challers and entra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tumour necrosis factor receptor-like polypeptides used to, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Fig 1; 167pp; English
                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                       97US-0063212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treat Digeorge syndrome -
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-061922/05.
N-PSDB; AAZ37762.
                                                                                                                                                                                                                                                            Ni J, Ruben SM;
                                 21-OCT-1997;
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234 AA; Seguence

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                                                                                                   SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                    1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                TSAQLGLHIWQLRKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLWV 234
                                                                                                                                                                                                                   100.0%; Score 1340; DB 21; Length 234; 100.0%; Pred. No. 3.7e-101; tive 0; Mismatches 0; Indels 0;
                           Conservative
              Local Similarity
              Best Local Sim
Matches 234;
  Query Match
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181

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protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoletic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                            Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence encoding the human 312C2 T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                              Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                                                                            /*tag= a
/product= "human 312C2 protein"
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1; Mismatches
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                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zlotnik A;
AAW37839 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                        97WO-US13931
                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0027901
96US-0689943
                                                                (first entry)
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Matches 233; Conservative
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                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCHE ) SCHERING CORP.
                                                                                                                                                                            autoimmune disorders.
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                                                               28-JUL-1998
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                                 AAW37839;
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       Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
                                                                                                                                                                                                    PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gurney AL, Marsters SA;
                                                                                                                                                                                                                                                                                                                         /note= "N-glycosylated"
162..180
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                             /note= "mature protein"
146
                                                                                                                                                                                                                                                                                   /note= "signal peptide"
                                                                                                                                                                                 Human TNF receptor homologue PRO364.
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                     AAY06605 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Fig 2A; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US02642.
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                                                                                                                                                             (first entry)
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N-PSDB; AAX87670.
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Pitti RM, Wood WI;
                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                             26-OCT-1999
                                                                                                                                                                                                                                             Homo sapiens
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                                               234 V 234
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                     agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                      1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                        TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
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                                                                                                                                                                      Length 241;
                                                                                                                                                                                                     0; Indels
                                                                                                                                                                      DB 20;
                                                                                                                                                                   Score 1322.5; Dl
Pred. No. 1e-99;
1; Mismatches
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/label= "Signal peptide"
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                                                                                                                                                                     98.7%;
96.7%;
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99US-0144758.
99US-014698.
99WO-US21011.
99WO-US2813.
99WO-US28409.
99WO-US28409.
99WO-US28465.
2000WO-US28555.
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                                                                                                                                                                     Query Match
Best Local Similarity 96.7
Matches 233; Conservative
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                                                                                                                      241 AA;
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22-FEB-2000;
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                                                                                                                      Sequence
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Skin cell protein, 4-1BB receptor pro Murine 4-1BB polyp

Mouse receptor 4-1 Mouse 4-1BB recept Murine CD137 prote Mouse Receptor 4-1 H4-1BB receptor pr

Human tumour necro

TR11SV1 amino acid PRO364-related EST

Human tumour necro FR11SV2 amino acid Human molecule ass Human 312C2 protei

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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Polypeptide encode
Mouse glucocortico
Amino acid sequenc
Mouse glucocortico
Mouse glucocortico
Human 312C2 protei
Murine TNF-alpha f
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Human 4-1BB recept
Human CD137 protei
Human receptor pro
Human tumour necro
 Human PRO364 prote
Human PRO364 prote
Human anglogenesis
Truncated human 31
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/note= "conserved domain CD-II"
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/label- Mature_protein
26..162
/label- Extracellular_domain
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146
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                                                                                                                                                                                                                                                                                                                                                                              AAY33215
AAY28687
AAR70977
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/label- Signal_peptide
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AAX06645
AAB47055
AAW49016
AAW37838
AAW49017
AAW49018
AAW37841
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AAR70978
AAR64199
AAW04173
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AAW26658
AAY33214
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AAB50521
AAW31759
AAW92523
AAW92524
                  AAB50982
AAB53090
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   (first entry)
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 Modified-site
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1322.5
1322.5
1323.5
1232.1
1292.1
1292.1
1293.5
992.5
992.5
905.6
1093.6
1093.6
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Tumour necrosis fa
Amino acid sequenc
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Human PRO364 prote
Human tumour necro
Human PRO364 prote
Human pRO364 prote
Human pRO364 prote
Human pRO364 prote
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(without alignments)
112.480 Million cell updates/sec
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                4.5
Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
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1340
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                                                                                                                 September
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100876321

Score

Result ç N

A novel human h4-1 Human h4-1BBSV rec Human h4-1BBSV rec

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The present sequence is that of human tumour necrosis factor receptor-like protein TRII, a novel 25 kDa protein which shows for receptor family related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library. TRII activated NF kappas Hrough a TRAE-mediated mechanism.

Expression is activation-inducible. The TRII ligand is constitutively expressed in an endothelial cell line. This suggests that TRII and its invention provides TRII, TRIISVI and TRIISVI and TRIISVI and See AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/Or TRIISVI polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                       .151
:e= "epitope-bearing region"
                                                          CD-VI"
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te- "conserved domain CD-IX"
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/note= "epitope-bearing
59..67
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                                   "conserved
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99US-0144076.
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                                  /note=
153..16
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176..18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HV1; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
                                                                                                                                                                                                                                                                                                                                                             61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                       1 MAOHGAMGAFRALCGLALLCALSLGORPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                         (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                   arthritis, systemic lupus erythematosus, thrombocytopenia purpura or 1gA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
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                                                                                                                                                                                                                               DB 21; Length 234;
immunodeficiency, especially common variable immunodeficiency X-linked agammaglobulinemia, severe combined immunodeficiency
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                                                                                                                                                                                                                               100.0%; Score 1340; DB 21;
100.0%; Pred. No. 3.7e-101;
iive 0; Mismatches 0;
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26..162
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Matches 234; Conservative
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160 AEPLGWLTVVLLAVAACVLLTSAQLGLHIW----QLRKTQLLLEVPPS---TEDARSCQ 212
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                                                                                                                                                                                                                                                                                                                                    NOT TATE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immune* A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
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                                                                                                                                                                                                                                                                Sequence 7, Application US/08097827
Patent No. 5457035
GENERAL INFORMATION:
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ATTORNEY/ACENT INFORMATION:
NAME: PERKINS, PARTICLA A.
RECISTRATION NUMBER: 34 693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 266-587-0730
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACERISTICS:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Baum, Peter
APPLICANT: Goddwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 545703
                                                                                                                                                                    222 APEAE 226
                                                                                                                               213 FPEEE 217
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APPLICANT: F
APPLICANT: G
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Search completed: September 4, 2001, 15:57:34 Job time: 376 sec

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100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPP 159
                                                                                                                              59 LC-----HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 VQSQCKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 QOPT-----ALLLIGLTLGVTARRINCVKHTYPSGHKCCRECOPGHGMVNRCDHTRDT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for TITLE OF INVENTION: 0X40
CORPRESS: 13
                                                                                                     160 AEPLGWLTVVLLAVAACVLLLTSAQLGLHIW----QLRKTQLLLEVPPS---TEDARSCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 438;
                                                            111 PRODSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%; Score 175.5; DB 1
27.3%; Pred. No. 1.7e-08;
Live 17; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           ; Sequence 11, Application US/08494574
; Patent No. 5783665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FELECOMMUNICATION INFORMATION: TELEPHONE: 206-587-0730
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 438 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-494-574-11
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ADDRESSEE: Immunex C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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Best Local Similarity
Matches 67; Conserva
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                         222 APEAE 226
                                                                                                                                                                                213 FPEEE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
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                                                                                                                                                                                                                                                                                      RESULT 14
US-08-494-574-11
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  48; Gaps
                                       58 CRDYPG-----EECCS----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFS 107
                                                                                                                                                           81 ----CKDCCFGTFNDQKRGICRPWINCSLDGKSVLVNGTKERDVVCGPSSADLSPGASSV 136
                                                                                                                                                                                                                           LC-----HPCETGFYNEAVNYDICKQCTQCNHRSGSELKQNCTPTQDIVCRCRPGTQ 110
                                                                26 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QOPT-----ALLLIGLTLGVTARRINCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for NUMBER OF SEQUENCES: 13
CORRESPONDENCE: 13
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                   158 -PPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH---IWQLRKTQLLLEVPP----
                                                                                                                    108 FGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGS-----
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indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE:
  70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.1%; Score 175.5; DB 1
27.3%; Pred. No. 1.7e-08;
Live 17; Mismatches 84
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Immunex Corporation 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: PERKIALS, PALTICIDA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
19;
                                                                                                                                                                                                                                                                                                          197 QTTQEEDGCSCRFPEEEEG 215
                                                                                                                                                                                                                                                                                 204 --- STEDARSCOFPEERG 219
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Matches 67; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-097-827-11
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STREET: 51 Univ
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
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62;
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-097-827-11
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  Matches
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REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08816605
Patent No. 5874240
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-236-918A-8
                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                       TOPOLOGY:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-816-605-9
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 RHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 -EKDCRPGQELTKQG------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 HNAVCVP-------GSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHI--W 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : || | : | | : | : | : | : | 104 KDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKW 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smitch, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.2e-11;
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SOFTWARE: Microsoft Word, Version #6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 201.5; 1 28.7%; Pred. No. 4.2e. Live 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1934
            APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFCATION: 435
                                                                                                                                   NAME: Michaels, Christopher A RECISTRATION NUMBER: 34,390
REPERENCE/DOCKET NUMBER: KWO5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEPAX: 607-273-1711
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08236918A Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 28.7%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03965-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 28101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                            85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                     34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDP 84
Query Match 14.7%; Score 197; DB 1; Length 255; Best Local Similarity 30.2%; Pred. No. 1.1e-10; Matches 67; Conservative 20; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTKI.

ZIP: 20850
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 ---IWQLRKTQLLLEVPP-----STEDARSCQFPEEERG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 FSVVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG 251
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SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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US-08-816-605-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-816-605-2
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                                                                                                                                                                                                                                                                                                                              98 GCSMC-EQDCKQGQELTKKG------CKDCCFGTFNDQKRGICRPWINCSLDGKSVLVN 149
                                                                                                                                                                                                                                                                                                                                                                                                           145 GNKTHNAVCVPG-----SPPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH 188
                                                                                                                                                                                                                                                                                                      85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                       34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
                                                                                                                                                      Length 255;
                                                                                                                                                                                         81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Monoclonal antibody against human TITLE OF INVENTION: receptor 4-1BB NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 --- IMQLRKTQLLLEVPP-----STEDARSCQFPEEERG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                  14.7%; Score 197; DB 2;
30.2%; Pred. No. 1.1e-10;
tive 20; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-58P-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/267,577 FILING DATE: 07-NOV-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application PC/TUS9603965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: KWO5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-605-9
                                                                                                                                              Query Match
Best Local Similarity 30.2 Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 607-273-2609 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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PCT-US96-03965-8
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                                                                                                                                                                                                              34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
                                                                                                                                                                                                                                                        48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA
                                                                                                                                                                      54;
                                                                                                                       14.7%; Score 197; DB 5; Length 255; 30.2%; Pred. No. 1.1e-10; Live 20; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 4-IBB Receptor Splicing Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 ---IWQLRKTQLLLEVPP-----STEDARSCQFPEERG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 FSVVKRGRKKLLYIFKOPFMRPVQTTQEEDGCSCRFPEEEEG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 194; DB 2;
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THER: US/08/816,605
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08816605
Patent No. 587420
GENERAL INFORMATION:
APPLICANT: Ni, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                   Query Match
Best Local Similarity 30.2%
Matches 67, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 amino acids
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APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301-309-8512
           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03965-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                                                                                                                126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185
                                          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MGAFRALCGLALLCALSLGQRPTGGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC
                                                                                                                                                                                                                                                                 186 GLHIWQLRK-----TQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233
                                                                                                                                                                                                                                                                                         APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.1%; Score 605; DB 3; Length 232; Best Local Similarity 78.1%; Pred. No. 7.7e-48; Matches 107; Conservative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STALLY
COMPUTRY: USA
ZIP: 94304-1104
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FTLING TATON: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-A0C-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: DNAX Research Institute
901 California Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 232 amino acids amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-911-423-7
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                                                                                                                                                                                HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLG 186
                                                                                                                                                                                                                                                               Gaps
                                                                                                  1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 60
                                                                            7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX RESEARCH INSTITUTE
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; Score 703; DB 3; Length 228; 54.9%; Pred. No. 9.4e-57; 1ve 32; Mismatches 58; Indels
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: E. FLOPPY disk
MEDIUM TYPE: F. FLOPPY disk
MEDIUM TYPE: F. FLOPPY disk
MEDIUM TYPE: F. FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY AGENT INFORMATION:
NAMME: Ching, EG411 P.
NAMME: Ching, EG411 P.
REGISTRATION NUMBER: DX0612K
TELECOMMUNICATION NUMBER: DX0612K
TELECOMMUNICATION NUMBER: DX0612K
TELECOMMUNICATION NUMBER: DX0612K
              Pred. No. 4.6e-92;
Mismatches 0;
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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650-496-1200
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Best Local Similarity 54.9
Matches 129; Conservative
            Best Local Similarity 100.
Matches 187; Conservative
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STATE: Callfornia
                                                                                                                                                                                                                                                                                                                           LHIWOLR 193
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US-08-911-423-2
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APPLICATION NUMBER: PCT/US96/03965 FILING DATE:
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
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APPLICATION NUMBER: US 08/012,269 FILING DATE: 01-FEB-1993
                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2801
TELECOMMUNICATION INFORMATION:
TELEPRIONE: (206) 287-0430
TELEPRIONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                            : 256 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-236-918A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 62; Conserva
                                                                                                                                                                                                                                                                                                                                          linear
                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
PCT-US96-03965-2
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                                                                                                                                                                                                                                                                                          LENGTH:
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                                         CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI----DCASGTFSG 122
                                                              61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQCVQSQGK---SWRCLWESTQARGSTRAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66
1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%; Score 255; DB 4; Length 89; 46.3%; Pred. No. 1.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated From Skin Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytckine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From S
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/236,918A FILING DATE: 06-May-1994
                                                                                                                                                                                                                                                                       Sequence 191, Application US/09188930A Patent No. 6150502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08236918A Patent No. 5674704 GENERAL INFORMATION:
                                                                                                                           123 GH-EGHCKPWTDCTQFG 138
                                                                                                                                                                    118 GRARGHRCPARTCGVWG 134
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.0
Best Local Similarity 46.3
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 51 Un:
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mouse US-09-188-930-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98101
                                                                                                                                                                                                                                                   US-09-188-930-191
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US-08-236-918A-6
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Gaps
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                                                                                                                                                                                                                                                                                                          102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                                                                                                                                                                                                                                                                          149 HNAVCVP------GSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHI--W 190
                                                                                                                                                                                                                                                                                                                                                                                                                                154 KDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKW 213
                                                                                                                        34 CGPGRL-LLGTGTDDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
                                                               43;
Length 256;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9603965
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yull
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, Brown & Michaels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
15.0%; Score 201.5; DB 1
28.7%; Pred. No. 4.2e-11;
Live 26; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 IRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 QLRKTQLLLEVP-----PSTEDARSCQFPEEERG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
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10;

us-09-512-363-2.rai

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

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Sequence 7, Appli
Sequence 8, Appli
Sequence 13, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appl
Sequence 12, Appli
Sequence 12, Appli
Sequence 15, Appli
Sequence 23, Appli
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Sequence 7, Ap
Sequence 8, Ap
Sequence 1, Ap
Sequence 2, Ap
Sequence 2, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08911423

Patent No. 6111090...
GENERAL INFORMATION...
APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Lord INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
COUNTRY: OSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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ZIP: 94304-1104

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: US-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CALIA, EQWIN D.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä,
US-08-995-659-2
US-08-974-022-2
US-09-042-785A-7
US-08-974-022-4
US-09-042-785A-13
US-08-385-22
US-08-650-000-2
US-08-650-000-2
US-08-477-347-3
S395760-2
US-09-042-785A-11
US-09-042-785A-12
US-08-997-022-6
US-08-997-022-6
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
US-09-042-785A-4
US-09-042-785A-3
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LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4
     RESULT 1
US-08-911-423-4
     142.5
141.5
141.5
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     ; Search time 65.86 Seconds (without alignments) 73.157 Million cell updates/sec
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Sequence 6, Appli
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-911-423-8
US-08-911-423-9
US-08-911-423-7
US-08-911-423-7
US-08-918-930-191
US-08-236-918A-6
PCT-US-6-605-9
US-08-816-605-2
US-08-816-605-2
US-08-94-574-11
US-08-94-574-7
US-08-974-022-52
US-08-996-139-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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1340
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Match Length D
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us-09-512-363-2.rai

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TOPOLOGY:
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US-08-911-423-8
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                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                    181 TSAQLGLHIWQLRSQCWWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
                                                                                                                                      61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSGGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                    SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                      Gaps
                                                             1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRD 60
                                                                               181 TSAQLGLHIWQL-----RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
  Pred. No. 4.8e-113;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AGC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
Best Local Similarity 96.7%;
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gorman
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CLASSIFICATION:
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US-08-911-423-6
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67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
                                                                                                                                                                                                        HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLG 186
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                           1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC
                                                                                              7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
               Length 228;
                                                                                                                                                                                                                                                                                                                                                       187 LHIWQLRKTQLLLEVPPSTEDARSCQFPEERGERSAEEKGRLGDLWV 234
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-40G-1997
CLASSIFICATION: 536
                 Score 1308; DB 3; I
Pred. No. 9.3e-112;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
97.6%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotnik, Albert TITLE OF INVENTION: RANDALIA TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P. REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                          Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650-496-1200
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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STATE: California
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                                    Similarity
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DB 3; Length 311;

81.6%; Score 1093;

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Domain
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                                                     protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or applicals. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                         Gaps
                                             the amino acid sequence of the truncated human 312C2 T cell
auto-immune disorders, transplantation rejection and
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                                                                                                                                                                                      100.0%; Score 246; DB 19; Length 228; 100.0%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                   TRI1; human; tumour necrosis factor receptor-like protein; immunodeficiency; autolimune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                 necrosis factor receptor-like protein TR11,
                                                                                                                                                                                                                                    108 dcasgtfsggheghckpwtdctqfgfltvfpgnkthnavcv 148
                                                                                                                                                                                                                           1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "conserved domain CD-VII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "conserved domain CD-VI"
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                                                                                                                                                                                                        0; Mismatches
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128..134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "N-glycosylated"
                           Disclosure; Pages 61-62; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- Mature_protein
26..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                l..25
/label- Signal_peptide
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204..209
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e.g. cancers, auto-imm
other T cell disorders
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                                                                                                                                                           228 AA;
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Best Local S:
Matches 41
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                                             This is
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receptor-like protein TRII, a note; 125 kDa protein which shows
58.6% identity to murine glucocorticoid induced tumour necrosis
cator receptor family-related gene. The sequence was deduced from
a count clone (see AAA50304) discovered in a Thelper cell library.
TRII activated NF-kappaB through a TRAF2-mediated mechanism.
TRII activated NF-kappaB through a TRAF2-mediated mechanism.
Expression is activation-inducible. The TRII ligand is constitutively expressed in an endothelial cell line. This suggests that TRII and
its ligand may be involved in activated T-cell trafficking.
The invention provides TRII, TRIISVI and TRIISV2 nucleic acids
(see AAA50304-06) and highly conserved encoded proteins (see
AAA50304-06) and highly conserved encoded proteins (see
AAY5079-81), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/or TRIISV2 polypeptides are useful
for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency
x-linked agammaglobulinemia, severe combined immunodeficiency
(SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency
antagonists (e.g. antibodies) are used to treat, prevent, prognose
and/or diagnose an autolimmune disease, especially rheumatoid
arthritis, systemic lupus erythematosus, thrombocytopenia purpura
or IgA nephropathy. The polypeptides and/or antibodies can be administered to cells in vitro, ex vivo or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156..164
/note= "epitope-bearing region"
203..21
/note= "epitope-bearing region"
222..230
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                                                               "epitope-bearing region"
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"conserved domain CD-X"
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                                                                                                                                                                                                                                                                                                                                                                                                               125..133
/note= "epitope-bearing
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/note= "epitope-bearing
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/note= "epitope-bearing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0121648.
99US-0134172.
99US-0144076.
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                                                                                                                                                                                                                                                                                                                                                       99..107
                                                                                                                              /note=
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16-JUL-1999;
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Human 312C2 protei Polypeptide encode PRO364-related

glucocortico

Mouse

prote Hom

prote

PRO364 PRO364

Human

Human Human

rR11SV1 amino acid

Human immunostimul

Mouse glucocortico Amino acid sequenc Mouse glucocortico ACT-4 cell surface ACT-4-h-1 receptor

Human OX40 protein Human tumour necro Mouse type-II memb Mouse OX40 extrace

Deduced sequence e Plasmid pDC406/OX4 OX40/Fc mutein. C A novel human h4-1

Human h4-1BBSV rec Human h4-1BBSV rec H4-1BB receptor pr

Human receptor

Human 4-1BB polype Human 4-1BB recept Human CD137 protei Human receptor pro

Post-processing:

Database

seg

Minimum DB : Maximum DB :

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Isolated 312C2 T cell gene - used to develop products for treating,

Score

Result No.

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dermatological; antiinflammatory; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  "conserved domain CD-III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "conserved domain CD-VI"
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                                                                                                                                                                                                                                                                                                                                                                                           "conserved domain CD-II"
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                                                                                                                                                                                                                                                                                                                                                     'note- "conserved domain CD-I"
                                                                                                                                                                                                                 169..185
/label- Transmembrane_domain
                                                                                                                                                                                                label- Extracellular_domain
                                                                                                                                                                                                                                                       186..240
/label= Intracellular domain
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hte= "conserved domain
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e= "epitope-bearing
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                                                                                                                                                                                                                                                                                                                'note- "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "epitope-bearing
                                                                                                                                      10..240
|abel= Mature_protein
                                                                                                                 label- Signal_peptide
                                                                               .ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200050459-A1
                                                                                                                                                                                                                                                                                            Modified-site
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                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-2000
                                                                               Key
Peptide
                                                                                                                                      Protein
                                                                                                                                                                                                                                                           Doma i.n
                                                                                                                                                                                                                                                                                                                                    Domain'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA library. This sequence is expressed in cardiovascular and haematopoidetic/immune tissues. MACP shows antiarteriosclerotic, antiating hepatotropic, antiafilammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic, immunosuppressive, osteopathic, antiatritic, uropathic, antiulicer, and ophthalmological activities. The present sequence is useful in the adiagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arterlosclerosis, atherosclerosis, bursatis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TR11SV2; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumour necrosis factor receptor-like protein TR11SV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patterson C,
'note= "Potential phosphorylation site"
                                        note- "Potential phosphorylation site"
                                                                             "Potential phosphorylation site"
                                                                                                               note "Potential phosphorylation site"
                                                                                                                                                                                            'note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 dcasgtfsggheghckpwtdctqfgfltvfpgnkthnavcv 148
                                                                                                                                                          'note- "Potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 246; DB 21; 100.0%; Pred. No. 2.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corley NC,
                                                                                                                                                                                                                                   /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Pages 64-65; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                       99WO-US16637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC
                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-182699/16.
N-PSDB; AAZ49948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 AA;
                                                                                                                                                                                                                                                                            WO200005374-A2
                    Modified-site
                                                        Mod1fled-site
                                                                                               Addified-site
                                                                                                                                      Modified-site
                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1998;
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Modified-site
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        AAY44825;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRII receptor). The invention relates to TRII and two splice variants TRIISVI and TRIISV2. The nucleotide sequences were determined by sequencing cloned cDNAs AAZ37765-237766. The TRII receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GITR). TRII. TRIISVI and TRIISV2 polypeptides may be involved in the regulation
                                                                                                                                                                                                                      Tumour necrosis factor receptor-like protein (TR11) amino acid sequence
                                                                                                                                                                                                                                       Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tumour necrosis factor receptor-like polypeptides used to,
                                                         Length 234;
polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
                                                                            Indels
                                                                                                       100.0%; Score 246; DB 21; 100.0%; Pred. No. 2.6e-24;
                                                                                            1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                        26..234
/label- TR11
/o.162
/note- "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                            163..179
/note= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "Intracellular domain"
                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                              /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                               AAY52158 standard; Protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Fig 1; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US22085
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treat Digeorge syndrome -
                                                                           41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               180..234
                                                                                                                                                                                                                                                                                       condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-061922/05.
                                                                 Local Similarity
                            234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AA237762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Ruben SM;
                                                                                                                                                                                                                                                                                        inflammatory
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9920758-A1
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                                                                                                                                                                                                    01-FEB-2000
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                                                                                                                                                                                  AAY52158;
                             Sequence
                                                         Query Match
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                                                                           Matches
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survival. They can be used for treating immune deficiency disorders, .
Digeorge syndrome, HIV infection, severe combined immunodeficiency
(SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, the mamonlytic angemia, rheumatoid arthritis, Goodpastures syndrome, Crave's disease, multiple sclerosis, mysathenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephiritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; molecule associated with cell proliferation; MACP-5; Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-inflammatcry; antipsoriatic; anti-INV; antiasthmatic; anaemia; dermatchlogical; antidiabelic; nephrotropic; antithyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; burstits; hepatitis; Crohn's disease; amyloidosis.
of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 246; DB 21;
100.0%; Pred. No. 2.6e-24;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signature_sequence
165..186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection, diagnosis and prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 AA;
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/note= "mature protein"

146

1..25 /note= "signal peptide"

Location/Qualifiers

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inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
                                                                                                          Mod1fled-site
                                 Homo sapiens
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                                                                                                                                                                                                                                                                                     Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                Peptide
                                                                                      Protein
                                                                                                                                Domain
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ID AAB2
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                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                       Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoietic cells; lymphoid cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                 Isolated 312C2 T cell gene - used to develop products for treating,
e.g. cancers, auto-immune disorders, transplantation rejection and
other T cell disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO364; tumour necrosis factor receptor; human; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                    Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 246; DB 19; Best Local Similarity 100.0%; Pred. No. 2.7e-24; Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                         /*tag= a
/product= "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TNF receptor homologue PRO364.
                                                                                                                Location/Qualifiers
1..726
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Pages 59-60; 71pp; English
                                                                                                                                                                                                                                                                                              Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06605 standard; Protein; 241 AA.
                                                                                                                                                                                                                    97WO-US13931
                                                                                                                                                                                                                                         96US-0027901
96US-0689943
28-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                              Gorman DM, Randall TD,
                                                                                                                                                                                                                                                                         (SCHE ) SCHERING CORP.
                                                                          autoimmune disorders.
                                                                                                                                                                                                                                                                                                                  WPI; 1998-159534/14.
N-PSDB; AAV19153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AA;
                                                                                               Homo sapiens
                                                                                                                                                                                                                    14-AUG-1997;
                                                                                                                                                                          WO9806842-A1
                                                                                                                                                                                                                                        07-OCT-1996;
                                                                                                                                                                                                                                                   16-AUG-1996;
                                                                                                                                                                                              19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY06605;
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AAY06605
ID AAY0
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AC AAY0
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DT 26-0
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calaimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin For region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor homologue – useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%; Pred. No. 2.7e-24;
ive 0; Mismatches 0;
                                                                                  /note= "transmembrane domain"
/note= "N-glycosylated"
162..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB27651 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Fig 2A; 104pp; English.
                                                                                                                                                                                                                                                                     99WO-US02642.
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Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-494296/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX87670
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ,
                                                                                                                                                                                                                                                                        09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                     09-FEB-1998;
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RESULT
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                                                                                                                                                                                                                                               The present sequence is that of human tumour necrosis factor receptor-like protein TR118V2, a novel 26 kDa protein which shows 18.68 identify to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50306) discovered in an activated T-cell library. The invention provides TR11, TR118V1 and TR118V2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50809-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR118V1 and/or TR118V2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency action of the transportance of the creat, prevent, prognose an autoimmune disease, especially prevent, prognose can autoimmune disease, especially remains and the contract of the creat, prevent, prognose can autoimmune disease, especially remains and the contract of the creat of the creat of the contract 
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                                                     Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arthritis, systemic lupus erythematosus, thrombocytopenia purpura or iga nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
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re= "Transmembrane domain"
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                                                                                                                                                                                                  Claim 14(n); Fig 3A-B; 278pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY52160 standard; Protein; 240 AA.
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/label= TR11SV2
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169..18
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N-PSDB; AAA50306
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Best Local Simi
Matches 41;
                                                                                                                                         arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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AC AAY5;
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DT 01-FF
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DE TRII;
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KW DIGGE
KW ALZh
KW AL
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This is the amino acid sequence of the human tumour necrosis factor receptor-like protein splice variant 2 (TRIISV2 receptor). The invention claims to TRII and two splice variants TRIISV1 and TRIISV2. The invention uncleotide sequences were determined by sequencing cloned cDNAs nucleotide sequences were determined by sequencing cloned cDNAs AA237765-Z37766. The TRII receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family related gene (GITR). TRII, TRIISV1 and TRIISV2 polypeptides may be involved in the regulation of cell type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, blood platelet disorders or wounds resulting from trauma or immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatosia gravis, surgery can also mania, inheumatosia gravis, syndrome, grave's disease, multiple sclerosis, mysthemia gravis, stiff-Man syndrome, systemic alpuse erythematosus, Guillain Barre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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llarity 100.0%; Pred. No. 2.6e-24;
Conservative 0; Mismatches 0;
/note= "Intracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                         97US-0063212.
                                                                                                                                                                                                                                                          98WO-US22085
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Matches 41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ37764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J, Ruben SM;
                                                                                       W09920758-A1
                                                                                                                                                                                                                                                          21-OCT-1998;
                                                                                                                                                                                                                                                                                                                                             21-OCT-1997;
                                                                                                                                                                           29-APR-1999.
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"conserved domain CD-VIII'
                                                                                                                                                         "conserved domain CD-III"
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/note= "epitope-bearing region"
                                                                                                                                                                                                                                                                                       ..160
te= "conserved domain CD-VI"
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/note= "conserved domain CD-IX"
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ce= "epitope-bearing region"
                                                                                                        "conserved domain CD-II"
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/note= "conserved domain CD-X"
                                                      "conserved domain CD-I"
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/note= "epitope-bearing
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     "N-glycosylated"
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99US-0134172.
99US-0144076.
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176..186
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16-JUL-1999;
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     PY CONTRACTOR OF THE CONTRACT 
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present inference of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic selected from systemic inflammatory myopathies, sjopen's systemic solections, diopathic inflammatory myopathies, sjopen's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, and peripheral nervous systems, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central cand peripheral nervous systems, hepatobiliary diseases, disease, cutoimmune or immune-mediated skin diseases, allergic diseases, immune-mediated skin diseases, allergic diseases, cancoimmune or immune-mediated skin diseases, allergic diseases.

Cantoimmune or immune-mediated skin diseases, allergic diseases.

Immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

Cantoimmune or shuman PRO sequences AAC58679 to AAC58642 and AAC58678 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                               Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes sixty four human PRO proteins which can
                                                                          Gurney AL, Hebert C, Henzel W;
), Shelton DL, Smith V;
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 246; DB 21; Length 241; 100.0%; Pred. No. 2.7e-24;
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                                                                                                     D, Shelto
Wood WI,
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/label- Transmembrane_domain
180..241
1abel- Intracellular domain
146
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1...162
/label- Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                          Ashkenazi AJ, Baker KP, Goddard A,
Kabakoff RC, Lu Y, Pan J, Pennica
Stewart TA, Tumas D, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY95880 standard; Protein; 241 AA.
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Best Local Similarity 100..
"These 41; Conservative
                           (GETH ) GENENTECH INC.
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N-PSDB; AAC58596.
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Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis.
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(HUMA-) HUMAN GENOME SCI INC
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02-MAR-2000;
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12-MAR-1999;
12-APR-1999;
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02-JUN-1999;
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15-SEP-1999;
15-SEP-1999;
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30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
02-DEC-1999;
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28-JUL-1999
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08-SEP-1999
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02-DEC-1999
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                                                               AAB33431;
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                           AAB33431
             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to methods for stimulating or inhibiting anglogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO238, PRO346, PRO846, PRO846, PRO205, PRO205, PRO321, PRO333, PRO8410, PRO846, PRO845, PRO885 or PRO367. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothelial or anglogenic disorders. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen ME;
Paoni NF, Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                    Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara N, Gerber H,
Illan KJ, Marsters SA,
                                                                                                                                                                            Location/Qualifiers
1..25
/label= "Signal peptide"
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PM, Wood WI;
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99WO-US28565.
2000WO-US04342.
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99US-0145698
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99WO-US21090
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Watanabe CK, Williams PM,
                                    26-JAN-2001 (first entry)
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Matches 41; Conservative
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                                                               Human protein PRO364.
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                                                                                                                           gene therapy.
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22-FEB-2000;
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             AAB27651;
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1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41

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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; didopathic inflammatory myopathy; systemic sclerosis; sarcoidosis; systemic vasculitis; autoimmune hemolytic anaemia; diabetes mellitus; autoimmune hemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobillary disease; Mhipple's disease;
                                                                                                                                                                                                                    inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease;
                                                                                                                                                                                                                                                       graft rejection; graft-versus-host-disease
                                                                      Human PRO364 protein UNQ319 SEQ ID NO:92.
AAB33431 standard; Protein; 241 AA
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2000WO-US04342.
2000WO-US04414.
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                                                (first entry)
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                                                                                                                                                                                                                                                                                                       WO200053758-A2.
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20-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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18-FEB-2000;
22-FEB-2000;
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Modified-site
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Best Local Si
Matches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                        Chen J,
                      Protein
                                                                                                                                                                      Domain
                                                                                                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                                                                                                                                                                                                                useful for preventing, disgnature and treating disgnosing a cardiovascular, endothelial or angiogenic disorder in mammals by andulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and disgnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosolerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors conclaining them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24455 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                   Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                         present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals -
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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100.0%; Pred. No. 2.7e-24;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..25
/label= Signal_peptide
5..11
                                                                                   Ferrara N,
Klein RD, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY71467 standard; Protein; 241 AA
                                                                                                                                                                                                   Claim 72; Fig 44; 315pp; English.
                                                                                  Baker KP, Fe
Gurney AL, Kl
Williams PM,
99WO-US20944.
                    99WO-US21547.
                                         99US-0162506
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                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO364 protein.
                                                              GETH ) GENENTECH INC.
                                                                                                                           WPI; 2000-412154/35.
N-PSDB; AAA77604.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   241 AA;
                                                                                  Ashkenazi AJ,
Godowski PJ,
                                                                                                        Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                  15-SEP-1999;
05-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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clone, designated as DNA4735-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA4815, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to the Incyte expressed sequence receptor (TNFR) family of polypeptides. PRO364 sequence also shows homology to members of the TNFR family and mouse GITR protein.

This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
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or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is the human PRO364 protein, encoded by the cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition useful for inhibiting neoplastic cell growth and treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide their antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Prokaryotic membrane lipoprotein lipid attachment site"
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Pred. No. 2.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Leucine zipper pattern"
                                                                                     30..36
/note= "N-myristoylation site"
                        "N-myristoylation site"
                                                                                                                                                   'note= "N-myristoylation site"
                                                                                                                                                                                                                                           /note= "N-myristoylation site"
146..150
                                                                                                                                                                                                                                                                                   /note= "Asn is N-glycosylated"
156..162
                                                                                                                                                                                                                                                                                                                                /note= "N-myristoylation site"
                                        26..241
/label- Mature_PRO364_protein
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166..177
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100.0%; Pr
Live 0;
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98US-0113296.
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99US-0145698.
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/note= "N
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25..31
/note=
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N-PSDB; AAD01240.
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                                                                                     Modified-site
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Disclosure; 294-295; 278pp; English.
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23-JUN-1999
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08-SEP-1999
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arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB24409;
                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of natural nectors raceptor-like protein TRISY1, a novel 26 to protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family related gene. The sequence was deduced from cDNA (see AAA50305) discovered in a PHA-stimulated T-cell library. The invention provides TRI1, TRIISV1 and TRIISV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) as well as vectors, host cells and recombinant methods for their production. TRII, TRIISV1 and/or TRIISV2 polypeptides are useful immunodeficiency, reating, preventing, prognosis and/or diagnosis of an immunodeficiency (SCID) Wiskott-Aldrich syndrome or X-linked immunodeficiency (SCID) Wiskott-Aldrich syndrome or X-linked immunodeficiency anthonian and antigonists (e.g. anthodies) are used to treat, prevent, prognose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                               arthritis, systemic lupus erythematosus, thrombotytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
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                                                                                                                                                                                                                                                                                                                                              Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tumor necrosis factor receptor-like proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TR11; human; tumour necrosis factor receptor-like protein;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 246; DB 21;
100.0%; Pred. No. 2.7e-24;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                               1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                agonist/antagonist compounds are also provided
           sequence is that of human tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY95895 standard; Protein; 241 AA.
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99US-0134172.
99US-0144076.
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-572072/53.
                                                                                                                                                                                                                                                                                                          241 AA;
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.13-MAY-1999;
16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY95895;
                                                                                                                                                                                                                                                                                                           Sequence
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The present sequence is that of human tumour necrosis factor receptor-like protein TRI1 (see also AAY95879), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family related gene. The invention provides factor receptor family related gene. The invention provides highly conserved TRI1, TRI1SV1 and TRI1SV2 proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TRI1, TRI1SV1 and/or TRI1SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency. Trinked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency and/or TRI1SV2 and/or diagnose an autoimmune disease, especially rheumatoid anthritis, systemic lugus erythematosus, thrombocytopenia purpura arthritis, systemic lugus erythematosus, thrombocytopenia purpura cantibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides may also be used. Methods for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agonist/antagonist compounds are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO364 protein sequence SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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99US-0141037
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99WO-US20594
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us-09-512-363-2\_copy\_114\_154.rag

congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzhelmer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.

Sequence

8.58888858888

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Gaps

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Length 241; Indels

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/note= "Extracellular domain"
                                                                                                                      /note= "Intracellular domain"
                                                                                                            "Transmembrane
                                                                                         Location/Qualifiers
         AAY52159 standard; Protein; 241 AA.
                                                                                                                                                                                                                    Claim 14; Fig 2; 167pp; English.
                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                     TR11SV1 amino acid sequence.
                                                                                                                                                  98WO-US22085
                                                                                                                                                           97US-0063212
                            (first entry)
                                                                                                       163..179
/note= "T
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                                                                                                                                                                                                           treat Digeorge syndrome
                                                                                                                                                                                       2000-061922/05.
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                                                                                                                                                                              Ruben SM;
                                                                                                                               W09920758-A1.
                                                                                Homo sapiens
                                                                                                                                                  21-OCT-1998;
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                            01-FEB-2000
                   AAY52159;
                                                                                              Domain
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RESULT 15
                                                                                           Key
     AAY52159
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100.0%; Score 246; DB 21;
100.0%; Pred. No. 2.7e-24;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                   1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
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Job time: 341 sec
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Best Local Similarity
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Tumour necrosis factor receptor-like protein; TRI1; TRI1SV1; GITR; growth; differentiation; cell death; immune deficiency disorder; bigeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; inflammatory condition.
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Domain
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                                                      protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of hematopoletic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                          Gaps
                                               This is the amino acid sequence of the truncated human 312C2 T cell
e.g. cancers, auto-immune disorders, transplantation rejection and other \tau cell disorders
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                                                                                                                                                                                     100.0%; Score 252; DB 19; Length 228; 100.0%; Pred. No. 4e-20; 1.ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                TRII; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                Human tumour necrosis factor receptor-like protein TR11.
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/label- Extracellular_domain
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/label- Transmembrane_domain
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hte= "conserved domain
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                           Disclosure; Pages 61-62; 71pp; English.
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/label- Mature_protein
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153..16
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128..13
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les 40; Conserv
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Matches 40
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receptor-like protein TRII, a nowel 25 kpa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library. TRII activated NF-kappaB through a TRAF2-mediated mechanism characterization-inducible. The TRII ligand is constitutively expression is activation-inducible. The TRII ligand is constitutively expressed in an endothelial cell line. This suggests that TRII and its ligand may be involved in activated T-cell trafficking. The invention provides TRII, TRIISVI and TRIISV2 notclet acids (see AAA50304-06) and highly conserved encoded proteins (see Contine TRII, TRIISVI and/or TRIISV2 polypeptides are useful their production. TRII, TRIISVI and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, contined agammaglobulinemia, severe combined immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated aberrant cell survival such as autoimmune disease and rheumatoid
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222..230
/note= "epitope-bearing region"
                                                       "epitope-bearing region"
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"conserved domain CD-X"
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/note= "epitope-bearing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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/note=
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16-JUL-1999;
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Human angiogenesis
Human 312C2 protei
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PRO364-related EST
Human 312C2 protei
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Mouse gluccocrtico
Amino acid sequenc
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Human PRO364 prote
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41bb protein. Uni
4-1BB receptor pro
Murine 4-1BB polyp
Mouse receptor 4-1
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Soluble herpesviru
Soluble herpesviru
Soluble herpesviru
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Murine TNF-alpha f
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EGF receptor relat
                              FR11SV1 amino acid
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Murine CD137 prote
Mouse Receptor 4-1
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antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoietic cells; lymphoid cell;
autolumune disorders.
         Human PRO364
Human PRO364
  Human tumour
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                                                                             AAB53090
AAW37842
AAB47055
AAY06645
AAW37841
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AAW49016
AAW37838
AAW49017
AAY76013
AAB55952
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AAY58212
AAB48033
AAW60046
AAY94716
AAY79206
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AAY33215
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 97WO-US13931
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96US-0689943
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                                                                                                                      (SCHE ) SCHERING CORP
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N-PSDB; AAV19154.
Homo sapiens
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16-AUG-1996;
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 RESULT
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Human TNF receptor
Human protein PRO3
Human PRO364 prote
Human tumour necro
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Human tumour necro
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                                                                  4, 2001, 15:56:24; Search time 126.12 Seconds (without alignments) 19.227 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                      /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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SUMMARIES

score greater than or equal to and is derived by analysis of

is the

Pred. No.

AAW37840 AAY95879

DB

Score

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Result

% Query Match Length D

AAY52158 AAY44825 AAY95881 AAY52160 AAW37839 AAW37839 AAB27651 AAB33431 AAB33431

hits satisfying chosen parameters: 412676 segs, 60623988 residues

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Total number

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_0601:\*

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

US-09-512-363-2\_COPY\_74\_113

Perfect score:

Title:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

protein search, using sw model

OM protein

Run on:

September

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dermatological; antiinflammatory; therapy; diagnosis.
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:e= "conserved domain CD-V"
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/label= Mature_protein
20..168
/label= Extracellular_domain
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/label- Transmembrane_domain
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/label- Intracellular domain
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re= "conserved domain
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                                                                                                                  label Signal_peptide
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                                         Homo sapiens
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16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA library. This sequence is expressed in cardiovascular and haematopoletic/immune tissues. MACP shows antiarteriosclerotic, antiarthy hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic, immunosuppressive, osteopathic, antiarthitic, uropathic, antiulier, and ophthalmological activities. The present sequence is useful in the activite keratosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arterlosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
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                                     'note= "Potential phosphorylation site"
                                                                                                                  'note- "Potential phosphorylation site"
/note= "Potential phosphorylation site"
                                                                           'note- "Potential phosphorylation site"
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Pred. No. 4.1e-20;
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                                                                                                                                                                                                                                /note= "N-glycosylated"
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Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor receptor-like protein; TR11; TR11SV1; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV, SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; inflammatory condition.
                                                                                                                                                          Gaps
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                                                                                                                  Length 234;
polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
                                                                                                                                                          Indels
                                                                                                                , DB 21;
4.1e-20;
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/note= "Transmembrane domain"
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/note= "Intracellular domain"
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/note= "Extracellular domain"
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100.0%; Pred. No. 4
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/label- TR11
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ses 40; Conservative
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                                                        234 AA;
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                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                            RESULT
AAY52158
  8 \times 6 
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Digeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antiqenic molecule, organ rejection or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzhelmer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for
of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; molecule associated with cell proliferation; MACP-5; Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-inflammatory; antipsoriatic; anti-HIV; antiasthmatic; anaemia; dermatological; antidabetic; nephrotropic; antithyroid; thyromlmetic; immunosuppressive; osteopathic; antiatthritic; uropathic; antiulcer; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                          survival. They can be used for treating immune deficiency disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 21;
4.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signature_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signature_sequence 37
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/label= Signature_sequence
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/label= Signature_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signature_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 252; 100.0%; Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44825 standard; Protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection, diagnosis and prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AA;
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modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
 inflammation; antiinflammatory; NF-KB activation;
                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 2A; 104pp; English
            autoimmune disease; therapy
                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                 WPI; 1999-494296/41.
                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX87670
                                                                                                            Modified-site
                                                                                                                                                                                                                                                                               Ashkenazi AJ,
                                  Homo sapiens
                                                                                                                                                                    WO9940196-A1
                                                                                                                                                                                                             09-FEB-1999;
                                                                                                                                                                                                                                    09-FEB-1998;
                                                                                                                                                                                          12-AUG-1999.
                                                                                                                                                                                                                                                                                            Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                   Peptide
                                                                                        Protein
                                                                                                                                    Domain
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ID AAB2
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                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytckine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                        Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                          Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO364; tumour necrosis factor receptor; human; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                   Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 252; DB 19; Best Local Similarity 100.0%; Pred. No. 4.2e-20; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                               /*tag= a
/product= "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Pages 59-60; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TNF receptor homologue PRO364.
                                                                                                                        Location/Qualifiers
1..726
                                                                                                                                                                                                                                                                                                     Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06605 standard; Protein; 241 AA
                                                                                                                                                                                                                         97WO-US13931
                                                                                                                                                                                                                                              96US-0027901.
96US-0689943.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                     Gorman DM, Randall TD,
                                                                                                                                                                                                                                                                               (SCHE ) SCHERING CORP.
                                                                            autolmmune disorders.
                                                                                                                                                                                                                                                                                                                          WPI; 1998-159534/14.
N-PSDB; AAV19153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AA
28-JUL-1998
                                                                                                  Homo saptens
                                                                                                                                                                              WO9806842-A1
                                                                                                                                                                                                                         14-AUG-1997;
                                                                                                                                                                                                                                              07-OCT-1996;
16-AUG-1996;
                                                                                                                                                                                                   19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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XX
AC AAY0
XX
DT 26-0
XX
XX
Humai
XX
KW PRO3
                                                                                                                        Key
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Marsters SA;

Gurney AL,

Goddard A,

Wood WI;

/note= "transmembrane domain"

99WO-US02642 98US-0024087

/note- "N-glycosylated"

162..180

'note= "signal peptide"

26..241 /note= "mature

Location/Qualifiers 1..25

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The present sequence represents human PRO364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides. e.g. in CHO.

Escherichia coli or yeast host cells, are provided. Claimed or polypeptides comprise amino acids 1.241, 1.x, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respites 157-167 of PRO364. PRO364 polypeptides re useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells proinflammatory or autoimmune responses in mammalian cells (claimed). Chimeric molecules comprising a PRO364 polypeptide immunoglobulin For region are also claimed. PRO364 polypeptide immunoglobulin For region are also claimed. PRO364 polypeptides in theractions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic methods, purification methods and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 252; DB 20; Best Local Similarity 100.0%; Pred. No. 4.2e-20; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB27651 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitors
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/note= "Intracellular domain"

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW37839
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  Dβ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                         factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAAS0306) discovered in an activated T-cell library. The invention provides TRI1, TRIISVI and TRIISV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50819-81), as well as vectors, host cells and recombinant methods for their production. TRI1, TRIISVI and/or TRIISV2 polypeptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HUY, SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
                                          Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Allarich syndrome or X-linked immunodeficiency deficiency with hyper igm TRIISV1 and/or TRIISV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis, systemic lupus erythematosus, thrombodytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
                                                                                                                                                                                                    The present sequence is that of human tumour necrosis factor receptor-like protein TR11SV2, a novel 26 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis
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100.0%; Pred. No. 4.2e-20;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
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186..240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..19
/label= Signal_peptide
                                                                                                                                                            Claim 14(n); Fig 3A-B; 278pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY52160 standard; Protein; 240 AA.
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/label= TR11SV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TR11SV2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169..185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 AA;
N-PSDB; AAA50306.
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Trists the amino acid sequence of the human tumour necrosis factor creates to TRII and two Splice variant 2 (TRIISV2 receptor). The invention relates to TRII and two Splice variants TRIISV1 and TRIISV2. The invention sequences were determined by sequencing cloned contact of nucleotides sequences were determined by sequencing cloned contact of A237765-237766. The TRII receptor and its splice variants show homology comparing the murine glucocorticoid induced tumour necrosis factor receptor family related gene (GTTR). TRII. TRIISVI and TRIISV2 polypeptides may be involved in the requilation of cell-type specific receptor-mediated coused for screening for agonists/Antagonists. The polypeptides may be involved in the requilation of cell-type specific receptor-mediated conservant cell survival. They can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemala, rheumatoid arthritis, Goodpastures syndrome, systemic lupus erythematosus, Guillain-Barre corpus crythematory systemic lupus erythematosus, Guillain-Barre syndrome, systemic lupus erythematosus, Guillain-Barre corpus rejection or garft versus host disease, inflammatory conditions, isohaemia-reperfusion injury, complement-mediated hypersocute rejection, isoharial defects, trauma, age, disease, inflammatory conditions. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, inflammatory sortic plastic surgery, including cosmetic plastic surgery, they can also be used to repair, replace, or protect tissue damaged by comparines, neuropathies, and central nervous system disease, profiles and sentence of alsoese, Parkinson's disease, Huntington's disease, Parkinson's disease, Huntington's disease, Parkinson's and sentence or syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Ni J, Ruben SM;
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W09920758-A1
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"conserved domain CD-VIII

"conserved domain

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"conserved domain CD-VI"

"conserved domain CD-IV"

"conserved domain

"conserved domain CD-V"

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111..216
note= "conserved domain CD-IX"
331..240
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229..237
                                          72..81
/note= "conserved domain CD-II"
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                             'note- "conserved domain CD-I"
                                                                                                                                                                                                                                                                                                note- "conserved domain CD-X"
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   'note= "N-glycosylated"
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 The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-PR
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                                                                                                                                               Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                            Henzel W;
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                                          Gurney AL, Hebert C, H
D, Shelton DL, Smith V;
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TR11SV1; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumour necrosis factor receptor-like protein TR11SV1.
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100.0%; Pred. No. 4.2e-20;
tive 0; Mismatches 0;
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/label Intracellular domain
146
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/label- Extracellular_domain
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/label- Transmembrane_domain
                                         Ashkenazi AJ, Baker KP, Goddard A,
Kabakoff RC, Lu Y, Pan J, Pennica
Stewart TA, Tumas D, Watanabe CK,
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                                                                                                                                                                                                         Claim 33; Fig 36; 309pp; English.
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Best Local Similarity 100.
             (GETH ) GENENTECH INC.
                                                                                                    WPI; 2000-572271/53.
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                                                                                                                  N-PSDB; AAC58596
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Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14(i); Fig 2A-B; 278pp; English.
                                                                                                  (HUMA-) HUMAN GENOME SCI INC
99US-0134172.
99US-0144076.
                                                                                                                                                                                                                            WPI; 2000-572072/53.
N-PSDB; AAA50305.
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AAB27651;

Peptide

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antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Syogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; dlabetes mellitus; autoimmune haemolytic anaemia; dlabetes mellitus; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immuno-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.
                                                                                                                                                                                                                          Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
                                                                                                                                                                             Human PRO364 protein UNQ319 SEQ ID NO:92.
                     AAB33431 standard; Protein; 241 AA.
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99US-0123618.
99US-0123957.
99US-0125775.
99US-0128849.
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99US-0132371.
99US-0134287.
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99US-0144758
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99US-0162506
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2000WO-US04414
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                                                                                                                          (first entry)
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22-FEB-2000;
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29-0CT-1999
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                                                                        AAB33431;
AAB33431
                                                                        Y CONTROL OF THE CONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to methods for stimulating or inhibiting and cardiovascularization. The methods involve the use of pharmaceutical compositions beased on the following proteins, PRO179, PRO384, PRO844, PRO846, PRO1760, PRO205, PRO331, PRO331, PRO847, PRO879, PRO882, PRO885 or PRO887. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothelial or angiogenic disorders. The present
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                                                                                                                     Cardiovascular; endothelial; anglogenic disorder; PRO179; PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO840; PRO840; PRO877; PRO879; PRO882; PRO885; PRO887;
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Hillan KJ, Marsters SA,
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                                                                                                                                                                                                                                                                                                                                          1..25
/label- "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood WI;
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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99US-0145698.
99WO-US20111.
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99WO-US28409
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2000WO-US04342
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Watanabe CK, Williams PM,
                     26-JAN-2001 (first entry)
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                                                                        Human protein PRO364
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                                                                                                                                                                                                          gene therapy
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Modified-site
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22-DEC-1998;
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26-JUL-1999;
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                           Protein
                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                             useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosolerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                                                                             Goddard A;
                                                                                                                                                                                                                                                    present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                              Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
                                                                                             1, Hillan KJ, Godd
Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
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100.0%; Pred. No. 4.2e-20;
tive 0; Mismatches 0;
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                                                                                             Gerber 1
Kuo SS,
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/label Signal_peptide
5..11
                                                                                             Ferrara N,
                                                                                                       Klein RD,
Wood WI;
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                                                                                                                                                                                                                             Claim 72; Fig 44; 315pp; English
99WO-US20944.
99WO-US21090.
99WO-US21547.
                                                                                             Baker KP, Fe
Gurney AL, Kl
Williams PM,
                                   99WO-US23089
99US-0162506
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Best Local Similarity 100.
Watches 40; Conservative
                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO364 protein.
                                                                                                                                           WPI; 2000-412154/35.
N-PSDB; AAA77604.
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                                                                                            Ashkenazi AJ,
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                                     Watanabe CK,
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                        15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "Prokaryotic membrane lipoprotein lipid attachment site"
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100.0%; Pred. No. 4.2e-20;
ive 0; Mismatches 0;
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                       "N-myristoylation site"
                                                                                                            'note- "N-myristoylation site'
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                                                                    /label- Mature_PRO364_protein
                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane_domain
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                                                                                                                                                                                                       "N-myristoylation
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98US-0112850.
98US-0113296.
99US-0144758.
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N-PSDB; AAD01240.
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Best Local Similarity
Matches 40; Conserv
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14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1999
arthritis
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB24409;
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24409
                                                                                                                                                                                                                                                                                                                                                                                                                                  pp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor-like protein TRISY1, a novel 56 kba protein which shows receptor-like protein TRISY1, a novel 58 kb identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from cDNA (see AAA50305) discovered in a PHA-stimulated T-cell library. The invention provides TRI1, TRIISV1 and TRIISV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see that production. TRI1, TRIISV1 and/or TRIISV2 polypeptides are useful their production. TRI1, TRIISV1 and/or TRIISV2 polypeptides are useful immunodeficiency, sepecially common variable immunodeficiency.

7. Linked agammaglobulinemia, severe combined immunodeficiency (SCID), wiskott-Aldrich syndrome or X-linked immunodeficiency antagonists (e.g. antibodies) are used to treat, prevent, prognose an autoimmune disease, especially rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumour necrosis factor receptor-like protein TR11 mutein.
                                                                                                                                                                                                                                                                                                                                           Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunodeficiency; autoimmune disease; rheumatoid arthritis;
immunosuppressive; antirheumatic; antiarthritic; haemostatic;
dermatological; antiinflammatory; therapy; diagnosis; mutein;
          present sequence is that of human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TR11; human; tumour necrosis factor receptor-like protein;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 252; DB 21;
100.0%; Pred. No. 4.2e-20;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                               agonist/antagonist compounds are also provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY95895 standard; Protein; 241 AA.
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99US-0134172.
99US-0144076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2000; 2000WO-US04572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-572072/53.
                                                                                                                                                                                                                                                                                                        241 AA;
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                                                                             receptor-like grotein TRII (see also AAY95879), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family related gene. The invention provides highly conserved TRII, TRIISVI and TRIISV2 proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                      (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TRAISVI and/or FRIISVS antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in
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                                                      present sequence is that of human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soluble forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vivo or to a multicellular organism. Soluble forms of turn orly or to a multicellular organism. Methods for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 252; DB 21; 100.0%; Pred. No. 4.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agonist/antagonist compounds are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO364 protein sequence SEQ ID NO:117.
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Disclosure; 294-295; 278pp; English.
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99US-0115554
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Matches 40; Conservative
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99WO-US20594

They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.

241 AA;

Sequence

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This is the amino acid sequence of the human tumour necrosis factor
receptor-like protein splice variant 1 (TRIISVI receptor). The invention
relates to TRII and two splice variants TRIISVI and TRIISV2. The
uncleotide sequences were determined by sequencing cloned cDNAs
AZ37765-Z37766. The TRII receptor and its splice variants show homology
AZ37765-Z37766. The TRII receptor and its splice variants show homology
to the murine glucocorticoid induced tumour necrosis factor receptor
family related gene (GITR). TRII, TRIISVI and TRIISV2 polypeptides may
be involved in the requilation, and ultimately, cell death. They can be
used for screening for agonists/Antagonists. The polypeptides, agonists
or antagonists can be used for treating a disease state associated with
aberrant cell survival. They can be used for treating immune deficiency
cal disorders blood platelet disorders or wounds resulting from trauma or
disorders, blood platelet disorders or wounds resulting from trauma or
climunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation
disorders, blood platelet disorders or wounds resulting from trauma or
surgery. They can also be used to treat heart attacks, strokes,
also fave seed in the memolytic anamia, rheumatoxid arthritis, Goodpastures
Syndrome, Grave's disease, multiple sclerosis, maschhenia gravis,
stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre
contained to the plate of the plate of the plate of a particular or autoinfamune insulation
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contained the plate of the plate of the plate of a particular or autoinfamune or plateled the plate of a particular or autoinfamune of the plate of the pl
                                                                                                                                                                                                                         Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour necrosis factor receptor-like polypeptides used to, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..179
bte= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                            AAY52159 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Fig 2; 167pp; English.
                                                                                                                                                                            TR11SV1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                     (first entry)
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180..241
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                     01-FEB-2000
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                                                                                        AAY52159;
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                         AAY52159
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RESULT
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Gaps
                                   0
           Length 241;
                                   Indels
                                                                       Score 252; DB 21;
Pred. No. 4.2e-20;
0; Mismatches 0;
                                                           1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
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          100.0%;
Query Match
Best Local Similarity 100.0
The Ao to Conservative
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eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections.

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Region
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                                                                        protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Bngagement of 312C2 stimulates proliferation of T cells clones, antigan-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of heematopoletic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of the human 312C2 T cell protein from clone_A5, which is identical to sequence AAW37838 for the first 105 amino acid residues. It is thought that divergence may be due to an unspliced intron. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
                                                                                                                                                                                                                                                                  Gaps
                                                               This is the amino acid sequence of the truncated human 312C2 T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                           Length 228;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 312C2 protein from clone_A5 amino acid sequence.
                                                                                                                                                                                                                                         ch 100.0%; Score 255; DB 19; Similarity 100.0%; Pred. No. 6.1e-20; 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                      gcgpgrlllgtgtdarccrvhttrccrdypgeecsewdcm 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Pages 62-63; 71pp; English.
                                      Disclosure; Pages 61-62; 71pp; English.
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96US-0689943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis; cancer; he
autoimmune disorders.
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                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                         228 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                 AAW37841;
                                                                                                                                                                                                          Sequence
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Matches
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antigen-specific proliferation and cytokine production by T-cells, potentiates T cell expansion or apoptosis. The products can be use in the treatment of conditions associated with abnormal physiology
                                                          development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of heematopoietic cells, e.g. lymphoid which affect immunological responses, e.g. autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tumour necrosis factor receptor-like protein TR11.
                                                                                                                                                                                                                                                                                                                   27 gcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcm 67
                                                                                                                                                                                                                                                                                                 1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                  100.0%; Score 255; DB 19;
100.0%; Pred. No. 6.2e-20;
ive 0; Mismatches 0;
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/note= "conserved domain CD-IV"
128..134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "conserved domain CD-VI"
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/label- Extracellular_domain
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/label= Signal_peptide
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/label- Mature_protein
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Best Local Similarity 100.(
Matches 41; Conservative
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Murine TuF alpha f Skin cell protein, Mouse gluccocrtico Mouse gluccocrtico Amino acid sequenc Muse gluccocrtico Human tumour necro TRILSVI amino acid TRAIN-R short, sol Human nTR-5 recept Amino acid sequenc Human TRAIN-R.

Scoring table:

Searched:

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Minimum Maximum Database

Perfect score:

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Sequence:

Human angiogenesis Human 312C2 protei Polypeptide encode PRO364-related EST

Human tumour necro TR11SV2 amino acid

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Human PRO364.

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Human secreted pro Mouse STRIFE2 (Tan Mouse TNFR superfa

Human PRO4333 prot

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Novel protein

Human hAPO4-alpha

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Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autoimmune disorders.
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AAY71467
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AAB47054
                                          AAB50910
AAB50982
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AAY06645
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AAY52160
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AAB55952
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96US-0689943.
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19.708 Million cell updates/sec
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1 GCGPGRLLLGTGTDARCCRV.....TTRCCRDYPGEECCSEWDCM
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         412676 segs, 60623988 residues
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                                                                      OM protein - protein search, using sw model
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Listing first 45 summaries
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haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myaathenia gravis, Stiff-Wan syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersonsitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischemia-reperfusion chijury, complement-mediated hypercuce rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's clisease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, our operatives, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, anyotrophic lateral sciences, and Siy-longer syndrome). The products can also be used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; molecule associated with cell proliferation; MACP-5; Incyte clone 2809903; antiarteriosclarotic; hepatotropic; cytostatic; anti-filammatchory; antipsoriatic; anti-HV; antiasthmatic; anaemia; dermatological; antidiabelic; nephrotropic; antithyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer; ophthalmological; dagmosis; treatment, prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68..96
/label- Signature_sequence
109..147
/label- Signature_sequence
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/label- Signature_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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'label- Signature_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44825 standard; Protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                           diagnosis and prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           detection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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AAY44825
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The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOTO6 cDNA library. This sequence is expressed in cardiovascular and haematopoidetic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatotropic, antinflammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic, immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                            Baughn MR;
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                                                                                                                                                                                                                                                                                                            Patterson C,
223
/note= "Potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
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/product= "human 312C2 protein"
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                                                                                                                                                                                                                                                                                                            Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 255;
100.0%; Pred. No. 6.
:ive 0; Mismatches
                                                             /note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                          Lal P, Hillman JL,
                                                                                                                                                                                                                            98US-0093827
                                                                                                                                                                                   99WO-US16637
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                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. Crohn's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA;
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                                          Modified-site
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Matches 4
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The present sequence is the control of the control of the protein TRII, a novel 25 kDa protein which shows a factor receptor family related gene. The sequence was deduced from factor receptor family related gene. The sequence was deduced from a construction of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCID), Wiskott Aldrich syndrome or X-linked immunoglobulin deficiency with hyper igw. TRIL, TRILSVI and/or TRILSV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
                                                                                                                                                                                                                                                               ..211
te= "epitope-bearing region"
'note= "epitope-bearing region"
                                             "epitope-bearing region"
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                                                                                                                                                                                              "epitope-bearing
                                                                                                                                                                                                                                              "epitope-bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14(c); Fig 1A-B; 278pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0134172.
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                                                                                                                     ..133
                                                                                                                                                                   143..151
                                                                      99..107
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203..21
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222..23
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N-PSDB; AAA50304.
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This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRII receptor). The invention relates to TRII and two splice variants TRIISV1 and TRIISV2. The nucleotide sequences were determined by sequencing cloned CONAS AB277765.237766. The TRII receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GITR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRII, TRIISVI and TRIISV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and uttimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, placeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aidrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease,
                                                                                                                                                                                                                          Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.
                                                                                                                                                                                                                                                  Tumour necrosis factor receptor-like protein; TR11; TR11SV1; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tumour necrosis factor receptor-like polypeptides used to, e.g.
              33 gcgpgrlllgtgtdarccrvhttrccrdypgeecsewdcm 73
41
1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Extracellular domain"
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/note= "Transmembrane domain"
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/note= "Intracellular domain"
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                                                                                                                     AAY52158 standard; Protein; 234 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26..234
/label= TR11
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                                                                                                                                                                                        (first entry)
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/note= "
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N-PSDB; AAZ37762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ni J, Ruben SM;
                                                                                                                                                                                        01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Gaps

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Indels

100.0%; Score 255; DB 21; 100.0%; Pred. No. 6.3e-20; ive 0; Mismatches 0;

Query Match 100.
Best Local Similarity 100.
Matches 41; Conservative

Length 234;

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Homo sapiens.
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                                                                                                                                                         02-MAR-2000;
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29-NOV-1999;
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                                                                                                                                                                                                                                                                                              Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods for stimulating or inhibiting anglogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO284, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO640, PRO877, PRO876, PRO879, PRO882, PRO885 or PRO887. These proteins were identified by isolating cDNA clones encoding secreted proteins were identified by invention may be used to diagnose and treat cardiovascular, endothelial or anglogenic disorders. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                     Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                           Gerritsen ME;
Paoni NF, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 255; DB 21; Length 241; 100.0%; Pred. No. 6.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                           , Gerber H,
Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO364 protein UNQ319 SEQ ID NO:92.
/label= "Signal peptide"
                                                                                                                                                                                                                             Ferrara N,
                                                                                                                                                                                                                                    Gurney AL, Hillan KJ,
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB33431 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                   Claim 71; Fig 6; 181pp; English.
                                                                                                                                                        99WO-US28409.
99WO-US28565.
2000WO-US04342.
                                                                                                                  99US-0145698.
99WO-US20111.
99WO-US21090.
                                                                                     99US-0123957.
99WO-US12252.
99US-0144758.
                                                                                                                                               99WO-US28313
                                                          2000WO-US05004
                                                                                                                                                                                      2000WO-US04414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                 WPI; 2000-611444/58.
N-PSDB; AAA99903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AA;
                   WO200053757-A2
                                                                                                       20-JUL-1999;
26-JUL-1999;
01-58P-1999;
30-NOV-1999;
30-NOV-1999;
02-DEC-1999;
18-FEB-2000;
22-FEB-2000;
                                                                                                                                                                                                                                              Watanabe CK,
                                                                                                                                                                                                                            Ashkenazi AJ,
                                                         24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2001
                                      14-SEP-2000
                                                                            08-MAR-1999
                                                                                                                                                                                                                                      Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB33431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
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8
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Sixty four PRO polypeptides, useful in the diagnosis and treatment of Immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemis; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immuno-mediated skin disease; allergic disease; graft rejection; graft-versus-host-disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henzel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL, Hebert C, He
J, Shelton DL, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D, Shelton DL,
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an J, Pennica
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A,
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                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US05028.
99US-0123618.
99US-0123957.
99US-0125775.
99WO-US08615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US20111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US21090,
99WO-US21547.
                                                                                                                                                                                                                                                                                                                                                                     2000WO-US05841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0131445
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99US-0134287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0145698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0146222
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99WO-US28634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US00376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US04341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US04342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US28551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US28564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US00277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US04414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-572271/53.
N-PSDB; AAC58596.
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us-09-512-363-2\_copy\_33\_73.rag

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The present sequence represents human PRO364, a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO. Bscherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-x, 26-241 (i.e. the mature protein) and 26-x of the present sequence, where X is any one of amino acid respidas 157-167 of PRO364. PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells fused to a heterologous sequence souprising a PRO364 polypeptide fused to a heterologous sequence comprising a PRO364 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin Fc region are also claimed. PRO564 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cardiovascular; endothelial; angiogenic disorder; PR0179; PR0238; PR0364; PR0844; PR04760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885; PR0887;
                                                                                                                                                                                                                                            Gurney AL, Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 255; DB 20; 100.0%; Pred. No. 6.4e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB27651 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 2A; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                               99WO-US02642.
                                                                                                                                   98US-0024087
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                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein PRO364.
                                                                                                                                                                                                                                                                                                                      WPI; 1999-494296/41.
                                                                                                                                                                                                                              Ashkenazi AJ, Godaa
n:++: RM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AA;
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX87670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                               09-FEB-1999;
                                                                                                                                   09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JAN-2001
                           12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB27651;
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB27651
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     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 313C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apportosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated 312C2 T cell gene - used to develop products for treating e.g. cancers, auto-immune disorders, transplantation rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 255; DB 19;
Pred. No. 6.4e-20;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-glycosylated"
162..180
/note= "transmembrane domain"
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/note= "signal peptide"
26..241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note- "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Pages 59-60; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TNF receptor homologue PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06605 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Sillarity 100.0%; P. Conservative 0;
                                                                                                     97WO-US13931
                                                                                                                                                            96US-0027901
                                                                                                                                                                                     96US-0689943
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                                                                                                                                                                                                                                                                                                Gorman DM, Randall TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other T cell disorders
                                                                                                                                                                                                                                            (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-159534/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV19153
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WO9806842-A1
                                                                                                        14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9940196-A1
                                                                                                                                                         07-0CT-1996;
                                                                                                                                                                                     16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1999
                                                    19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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Length 241; Indels

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Modified-site
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                                                                                                                                                                                                                                                        Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                                                                                                                                                                                                                                                                                                                                                     useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorder in mammals by modulating cell proliferation, anglogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosolerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors conclaining them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 expression to the protein sequences used in the exemplification of the present invention.
                                                                                   Goddard A;
                                                                                                                                                                                                                                                                                                                                                        The present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                          Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals -
                                                                                   Gerber H, Hillan KJ, Godd
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 255; DB 21;
Llarity 100.0%; Pred. No. 6.4e-20;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.31
/note= "N-myristoylation site"
26.241
/label= Mature_PRO364_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "N-myristoylation
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/label- Signal_peptide
                                                                                 Ferrara N,
Klein RD,
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                Claim 72; Fig 44; 315pp; English
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99US-0162506
                                                                                                      Gurney AL, K
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2000 (first entry)
                                                                                 Baker KP,
                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO364 protein.
                                                                                                                                                                WPI; 2000-412154/35
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AA;
                                                                                                                                                                                        N-PSDB; AAA77604
                                                                                 Ashkenazi AJ,
                                                                                                                          Watanabe CK,
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                                                                                                      Godowski PJ,
  29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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Peptide
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AAY71467
AAX71467
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AC AAY71467
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KW PRO364,
KW NEORDIS
KW NEORD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
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                                                                                                                                                                                                                                                                                                                                /note= "Prokaryotic membrane lipoprotein lipid attachment site"
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100.0%; Pred. No. 6.4e-20;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Leucine zipper pattern"
                                                                118..124 /note= "N-myristoylation site"
                                         'note= "N-myristoylation site"
                                                                                                                                       "N-myristoylation site"
                                                                                                                                                                                      "Asn is N-glycosylated"
                                                                                                                                                                                                                                       'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                      label Transmembrane_domain
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"N-myristoylation
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98US-0112850.
98US-0113296.
99US-0144758.
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Best Local Similarity 100.
Matches 41; Conservative
                                                                                                                 122..128
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                      . . 39
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                                                                                                                                                                                           'note-
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N-PSDB; AAD01240.
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                      Modified-site
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22-DEC-1998;
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be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosting immune related discretes. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related discretes. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, solected from systemic ladopathic inflammatory myopathies, Sjoyene's systemic sclerosis, idopathic inflammatory myopathies, Sjoyene's systemic sclerosis, idopathic inflammatory morphises, Sjoyene's anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune-mediated skin diseases, allergic diseases, allergic diseases, allergic diseases, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AACSB379 to AACSB378 represent PRO primers and hybridisation probes used the isolation of human PRO polynucleotide and protein sequences glven in the exemplification of the present invention.
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 present invention describes sixty four human PRO proteins which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour necrosis factor receptor-like protein TR11 mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
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Pred. No. 6.4e-20;
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100.0%; Pred. No. 6.4
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ni J;
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                                                 showing identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The invention provides highly conserved TRII, TRISVI and TRIISV2 proteins (see AAV95879-81), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, sepecially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency, (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency antabonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis, systemic lupus erythematosus, thrombocytopenia purpura or 1gA nephropathy. The polypeptides, polynuclectides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
The present sequence is that of human tumour necrosis factor receptor-like protein TR11 (see also AAY95879), a novel protein
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100.0%; Pred. No. 6.4e-20;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
12-MAR-1999;
28-APR-1999;
14-MAY-1999;
02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999;
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12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1999
13-SEP-1999
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15-SEP-1999
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99WO-US23089

05-0CT-1999

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This sequence represents PR0364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGITR). The corresponding ligand (hGITRL), PR0175, is given in ARA47056.

PR0364 and PR02175 may be used in a mixture with a cardiovascular, endothelial, anglogenic or anglostatic agent for the treatment of a cardiovascular, endothelial, anglogenic or anglostatic disorder. The PR0364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PR0175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical veln endothelial cells (HUVEC). Administering an effective amount of PR0364 or PR0175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PR0364 or PR0175 in a human suffering from a tumor or a retinal disorder. PR0364 or PR0175, or their antagonists, are useful for tweetunes. Expended drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vascular-related drug targeting or as therapeutic targets for the thrombophlebitis, tumor anglogenesis, periodontal diseases, antersensing and peripheral nervous attraction or begeneration and treatment of bung or liver fibrosis, periodontal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                              Composition for diagnosing and treating cardiovascular, endothelial and anglogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO; antlinflammatory; dermatological; antiarthritic;
antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system disease and neuropathies and rheumatoid arthritis.
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 255; DB 22; 100.0%; Pred. No. 6.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB50910 standard; Protein; 241 AA
                                                                                                                                                                                                                                                    Claim 1; Fig 1; 76pp; English
                                                                        11-JUL-2000; 2000WO-US18867.
                                                                                                  99US-0143304
                                                                                                                                                  Williams PM, Gerritsen ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Conservative
                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO364 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                          2001-138257/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AA
                                                                                                                                                                                       N-PSDB; AAC85433
                         WO200103720-A2
                                                                                                12-JUL-1999;
                                                 18-JAN-2001
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The present sequence is one of thirty three novel PRO polypeptides.
The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related alsorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vacculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases (such as inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's diseases, eurthema multiforme, contect dermatitis, psoriasis).

The properties of the sasthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski PJ, Gurney AL;
, Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
antidiabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NJ, Baker KP, Chan B, Goddard A, G
Henzel W, Kabakoff RC, Shelton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 58; Fig 18; 218pp; English.
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99US-0146222
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                                                                                                                                                                                                                                                                                                           02-JUN-2000; 2000WO-US15264
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                                                                                                                                                                                WO200073452-A2.
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Hebert C, Hen
Wood WI;
                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2000;
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                                                                                                                                                                                                                                                   07-DEC-2000
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nvention provides polynucleotides (see AAF30050-62) en human PRO proteins (see AAB20108-20) including PRO364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB47054 standard; Protein; 241 AA.
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162..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                     PR0364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB47054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of novel human immunomodulator PR0364 (M00319), as deduced from cDNA (see AAF30057) isolated from a small intestine library. PR0364 (26 kDa, pI 6.34) shows sequence homology to mouse GITR protein and may be its human counterpart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "prokaryotic membrane lipoprotein lipid attachment site"
                                                                                  PRO364; UNQ319; human; immune disease; autoimmune disease; antirheumatic; antiaribritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallergic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                    site"
                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                            site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Asn is N-glycosylated"
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Pitti RM,
                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                               .63..183
'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                           "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                   "N-myristoylation
                                                                                                                                                                                                                        26..241
/label- Mature_protein
                                                                                                                                                                                                              /label- Signal_peptide
                                                                                                                                                                                  Location/Qualifiers
1..25
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SA,
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:k MR, Marsters
                                                              Human immunostimulant PRO364,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2000; 2000WO-US06884.
                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    'note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillan KJ, Mark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-103149/11.
N-PSDB; AAF30057.
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                                     30-APR-2001
                                                                                                                                                              Homo saptens
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             AAB20115;
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                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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craimed compositions comprising trace proteins of trainmed compositions comprising the proliferation of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune tissue of a mammal, stimulating or enhancing an immune response to an antigen. Claimed compositions comprising a PRO polypeptide or its antagonist have the opposite effect. A calaimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from a prolifer arthritis, spondyloarthropathy, systemic selected from a califormy antibodiated disorder, dispeting antibodiated arthritis, sarcoidosis, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive disease (such as asthma, allergic rhintis, atopic dermatitis, food hypersensitivity and urticaria), immunologic dermatitis, food hypersensitivity and urticaria), immunologic diseases (such as asthma, allergic rhintis, atopic can diseases (such as asthma, allergic rhintis, atopic callerder of expression of the PRO gene. Also claimed are a method of diagnosing these disorders comprise detecting and anterhod of the PRO polypeptide, vectors, host cells, antibodies, and an anthod of stimulating the proliferation of T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGITR; 11gand; hGITR; pRO175; tumour necrosis factor receptor; TNFR; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF_2alpha; trauma; cancer; anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Claimed compositions comprising these proteins or their agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          age related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 22;
6.4e-20;
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/note= "Potential signal peptide"
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0; Mismatches
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lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.
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241 AA; Sequence

ö Gaps ; 0 Ouery Match 100.0%; Score 255; DB 22; Length 241; Best Local Similarity 100.0%; Pred. No. 6.4e-20; Matches 41; Conservative 0; Mismatches 0; Indels 0;

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Search completed: September 4, 2001, 15:56:24 Job time: 341 sec

2000-061922/05.

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New tumour necrosis factor receptor-like polypeptides used to, e.g.
                                                                                                                                                Claim 14; Fig 1; 167pp; English
                                                                                                          treat Digeorge syndrome
                                            N-PSDB; AAZ37762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor receptor-like protein; TR11; TR11SV1; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV: SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                           1 GCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
(SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TRIIS'I and/or TRIIS'S antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                            arthritis, systemic lupus erythematosus, thrombocytopenia purpura or 1gA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
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                                                                                                                                                                                                                                                                                          100.0%; Score 753; DB 21; Length 234; 100.0%; Pred. No. 2.8e-55;
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                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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/label- Signal_peptide
26..234
/label- TR11
26..162
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                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                              234 AA;
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Simil
Matches 122; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saptens
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cv 154
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                                                                                                                                                                                                                                 Sequence
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This is the amino acid sequence of the human tumour necrosis factor
receptor-like protein (TRI1 receptor). The invention relates to TRI1 and
two splice variants TRISV1 and TRIISV2. The nucleotide sequences were
determined by sequencing cloned cDNAS AA237765-237766. The TRI1 receptor
and its splice variants show homology to the murine glucocorticoid
induced tumour necrosis factor receptor family-related gene (GITR).

TRIISV2 and TRISV2 bolypeptides may be involved in the regulation
of cell type specific receptor-mediated cell growth, differentiation,
and ultimately, cell death. They can be used for screening for
agonists/Antagonists. The polypeptides, agonists on thagonists can be
carrival. They can be used for treating immune deficiency disorders,
bigeorge syndrome, HIV infection, severe combined immunodeficiency
(SCID), wiskott-Aldrich disorder, blood coagulation disorders, blood
platelet disorders or wounds resulting from trauma or surgery. They can
also be used to treat heart attacks, strokes, Addison's disease,
haltple sclerosis, mysthenia gravis, Stiff-Man syndrome,
also be used to treat heart attacks, strokes, Addison's disease,
conclusion and an artiganic anthritis, Goodpastures syndrome, Insulin dependent
diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,
complement-mediated hypersourde rejection, nephritis, ortokine or
chemokine induced lung injury, inflammatory bowel disease, crohn's
confects, trauma, age, disease, aurgery, relevant enjection or graft
cused to repair replace, or protect tissue damaged by congenital
defects, trauma, age, disease, unclear, disease, enjuries,
cused to repair, resperfusion injury, peripheral nerve injuries,
cused to repair, and entry system disease, enjuries,
cused to repair, septemble with the result of an any or and relation and relation and relation and relation or graft
cused to repair reperfusion injury, seriem disease, enjuries,
confidency and entry and relation and rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human molecule associated with cell proliferation, MACP-5.
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Best Local Similarity
Matches 122; Conserv
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cv 154
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ID AAY4
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Length 235;

anaemia Region Region Region (ey 

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Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-flammatory; antipschalic; anti-HIV; antiasthmatic; anaemia; dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell proliferative disorder; actinis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; crohn's disease; amyloidosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baughn MR;
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                                                                                                                                                                                                                                  cocation/Qualifiers
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N-PSDB; AAZ49948.
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Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease Claim 1; Pages 64-65; 67pp; English.

The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA library. This sequence is expressed in cardiovascular and haematopoletic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatotropic, antiinflammatory, antiaberic, antiatistic, antiabetic, nephrotropic, antiinflyod, thyromimetic, farmannosuppressive, osteopathic, antiathoric, antiathyroid, thyromimetic, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and

235 AA; Sequence

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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Bngagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates 'T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells
                                                                                                                           Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell;
                                Gaps
                                                                                                                PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                           GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                          2 T cell gene - used to develop products for treating,
auto-immune disorders, transplantation rejection and
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                                Indels
                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the human 312C2 T cell protein.
     Score 753; DB 21;
Pred. No. 2.8e-55;
Mismatches 0;
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100.0%; Pro
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96US-0689943.
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N-PSDB; AAV19153.
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Matches 122; Conserv
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16-AUG-1996;
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Polypeptide encode PRO364-related EST Human tumour necro rR11SV1 amino acid

Human 312C2 protei Mouse glucocortico Mouse glucocortico Amino acid sequenc Mouse glucocortico Murine TNF-alpha f

Skin cell protein, Mouse type-II memb Mouse Ox40 extrace Plasmid pbC406/Ox4 Ox40/Fc mutein. C

Monkey Fas ligand Human Fas ligand i H4-1BB receptor pr

Human 4-1BB polype Human 4-1BB recept Human CD137 protei Human receptor pro Human tumour necro

Tumour necrosis fa Human FAS ligand i Human FLINT. Homo

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Minimum E Maximum E

Database

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Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoletic cells; lymphoid cell;
autolumune disorders.
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                  AAB50910
AAB50982
AAB53090
AAW37842
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AAY52160
AAB47055
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N-PSDB; AAV19154.
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acid sequenc
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                           This is the amino acid sequence of the truncated human 312C2 T cell protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the requisitive conditions of degenerative conditions.
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e.g. cancers, auto-immune disorders, transplantation rejection and
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/note= "conserved domain CD-IV"
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/label- Extracellular_domain
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/label= Intracellular domain
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                          Disclosure; Pages 61-62; 71pp; English
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/label- Signal_peptide
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         other T cell disorders
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AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful immunodeficiency, especially common variable immunodeficiency, sepecially common variable immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library. TRI1 activated NF-kappaB through a TRAF2-mediated mechanism. Expression is activation-inducible. The TRI1 ligand is constitutively expressed in an endothelial cell line. This suggests that TRI1 and its ligand may be involved in activated T-cell trafficking. The invention provides TRI1, TRI1SV1 and TRI1SV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of human tumour necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis
                                                                                                        "conserved domain CD-VII'
                                                   /note= "conserved domain CD-VI"
176..186
                                                                                                                                                           "conserved domain CD-IX"
                                                                                                                                                                                                                                                         "epitope-bearing region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "epitope-bearing region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region"
                                                                                                                                                                           ..233
te= "conserved domain CD-X"
'conserved domain CD-V"
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+e= "epitope-bearing
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re= "epitope-bearing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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156..164
                                                                                                                              .209
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        note=
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Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease;

99US-0141037 99US-0144758

23-JUN-1999 20-JUL-1999

99US-0145698 99US-0146222 99WO-US20111

2000WO-US13705

17-MAY-2000;

07-DEC-2000.

WO200073445-A2.

Homo sapiens

wound healing.

99WO-US28313

26-JUL-1999; 28-JUL-1999; 01-52P-1999; 30-NOV-1999; 16-DEC-1999; 16-DEC-1999; 11-FEB-2000;

2000WO-US03565

2000WO-US05004 2000WO-US05841 2000WO-US06884 2000WO-US07532

18-FEB-2000; 24-FEB-2000; 02-MAR-2000; 15-MAR-2000; 21-MAR-2000; 10-MAR-2000;

99WO-US28565

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The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosins manner related antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoathritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculities, aercoidosis, autoimmune haemolytic and peripheral nervous systems (such as multiple sclerosis, idiopathic immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic inflammatory demyelinating polymeuropathy), hepatobiliary diseases inflammatory demyelinating polymeuropathy), hepatobiliary diseases confined as infectious, autoimmune chronic active hepatitis, primary billary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases such as asthma, allergic rhinitis, atopic dermatitis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, con hypersensitivity and urticaria), immunological diseases of the lung (such as eoslnophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonials), transplantation associated diseases.
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0
                                                                                                                                                        Gurney AL;
Watanabe CK;
                                                                                                                                                                                                                                                                                                        Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is one of thirty three novel PRO polypeptides
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                                                                                                                                                      Godowski PJ,
                                                                                                                                                                               Tumas D,
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100.0%; Pred. No. 2.9e-55;
.tve 0; Mismatches 0;
                                                                                                                                                      Goddard A, G
Shelton DL,
                                                                                                                                             Hebert C, Henzel W, Kabakoff RC, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                    58; Fig 18; 218pp; English
21-MAR-2000; 2000WO-US07532.
30-WAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-WAY-2000; 2000WO-US14042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 122; Conservative
                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                           2001-025253/03.
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N-PSDB; AAC91469
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61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                         1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                  ||
| cv | 154
                                                                                                                               CV 122
                                                                                                                  33
                                                                                                                               121
                                                                                                                           93
                                                                                                                                   153
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g õ g ò AAB50982 standard; Protein; 241 AA.

RESULT 15

(first entry)

21-MAR-2001

XXXXXX

AAB50982;

Human PRO364 protein

The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, aganists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rhematoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating deriodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-pRO antibodies are useful for diagnosing a cardiovascular, endothelial or

angiogenic disorder

Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or anglogenic

Claim 71; Fig 8; 182pp; English.

disorders in a mammal

SA;

Marsters

, Kuo SS, Mark MR, M Williams PM, Wood WI;

J, Gurney AL, Watanabe CK,

Gerritsen ME;

Gerber H,

Ashkenazi AJ, Baker KP, Ferrara N, Goddard A, Godowski PJ, Gurney AL,

Goddard A, Godowski Paoni NF, Pitti RM, WPI; 2001-025251/03

N-PSDB; AAC90566

(GETH ) GENENTECH INC.

Gaps 1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60 Length 241; 100.0%; Score 753; DB 22; 100.0%; Pred. No. 2.9e-55; iive 0; Mismatches 0; Matches 122; Conservative Best Local Similarity 241 AA; Sequence Query Match ò g

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<sup>121</sup> CV 122 || | 153 CV 154

Search completed: September 4, 2001, 15:56:23 Job time: 340 sec

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Hillan KJ,
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                                                            Wood WI;
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Matches
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                                                    1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                            ö
                                                                                                                                                                                                            PRO364; UNQ319; human; immune disease; autoimmune disease; antiuthumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "prokaryotic membrane lipoprotein lipid
                          Length 241;
                                       Indels
                      Pred. No. 2.9e-55; mlsmatches 0: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                           note- "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asn is N-glycosylated"
166..177
                                                                                                                                                                                                                                                                                                                                     'note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                         'note- "transmembrane domain"
                                                                                                                                                                                                                                       antiasthmatic; antiallergic; immunostimulant
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                                                                                                                                                                                                                                                                                                                                                               'note- "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      attachment site
                                                                                                                                                                                                                                                                                      26..241
/label- Mature_protein
                                                                                                                                                                                                                                                                               /label- Signal_peptide
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                       AAB20115 standard; Protein; 241 AA.
                                      ö
                         100.0%;
100.0%;
                                                                                                                                                                                                Human immunostimulant PRO364.
                                                                                                                                                                                  (first entry)
                        Query Match 100.
Best Local Similarity 100.
Matches 122; Conservative
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       241
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                                                                                                                                                                                 30-APR-2001
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| cv | 154
                                                                                                         CV 122
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                                                                                                                                                                    AAB20115;
      Sequence
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                                                                                                                                                                                                                                                                                      Protein
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The present sequence is that of novel human immunomodulator PR0364 (UN0319), as deduced from cDNA (see AAF30057) isolated from a small intestine library. PR0364 (26 Kba, p16.34) shows sequence homology to mouse GITR protein and may be lits human counterpart. The invention provides polynuclectides (see AAF30050-62) encoding novel human PKO proteins (see AAB20108-20) including PR0364.

Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune a tissue of a mammal, stimulating or enhancing an immune response, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigon. Claimed compositions comprising a proposite of the proliferation of T-lymphocytes in a mammal in response to an antigonist have the opposite effect. A claimed method for treating an immune related disorder, such as a proceed involves administering a PR0 polypeptide, an agonist antibody or an antigonist antibody. The disorder is selected from systemic lupus erythemators rhematois arthritis, spendyloarthropathy, systemic sclerosis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated cutofinmune chronic active hepatitis, primary billary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel cliseases (auch as multiple sclerosis), gucton as multiple sclerosis, allergic thinitis, actoric as stime, allergic chinitis, diseases, erythema multiforme and psoriasis), allergic diseases (the lung and transplantation associated diseases (such as antimed methods of diagnosing these disorders comprise detecting the lung and cransplantation associated diseases (such as graftma, allergic chined methods of diagnosing these disorders comprise detecting the lung and cransplantation associated diseases (such as relating the expectation and graft-versus-host diseases) (all claimed methods of diagnosing these dis
                                                                                                                                                                                                                                 Gurney AL;
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Tumas D, Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 241;
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                                                                                                                                                                                                                             Goddard A,
Pitti RM,
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SA,
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0
                                                                                                                                                                                                                                 f, Baker KP, Fong
Mark MR, Marsters
15-MAR-2000; 2000WO-US06884.
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                                                                                                                                                  (GETH ) GENENTECH INC.
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les 122, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF30057
                                                                                                                                                                                                                             Ashkenazi AJ,
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This sequence represents PR0364 polypeptide, which is a human glucocatiood-induced tumor necrosis factor receptor (hGTTR). The cortseponding ligand (hGTTRL), PR0175, is given in AAB47056.

PR0364 and PR0175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a cardiovascular, endothelial, angiogenic or angiostatic disorder. The PR0364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PR0175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PR0364 or PR0175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGE_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that chinds PR0364 or PR0175 is useful for inhibiting angiogenessis induced by PR0364 or PR0175 in a human suffering from a tumor or a retinal coll sufficer. PR0364 or PR0175 to their antagonists, are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR; human umblilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF_2alphe; trauma; cancer; angiogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Potential transmembrane domain"
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/note= "Potential signal
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162.180
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                                                                                                                                                                                                             AAB47054 standard; Protein; 241 AA.
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N-PSDB; AAC85433
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| 153 cv 154
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           treatment or prevention of atherosclerosis, hypertension, inflammator vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.
                                                                                                                                                            Gaps
                                                                                                                                                                                   GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                vascular-related drug targeting or as therapeutic targets for the
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                                                                                                                                  Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; antiinflammatory; dermatological; antiarthritic;
                                                                                                                                                           Indels
                                                                                                                                  100.0%; Score 753; DB 22; 100.0%; Pred. No. 2.9e-55;
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                                                                                                                                                          Mismatches
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99WO-US28634.
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99US-0144758.
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2000WO-US03565,
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2000WO-US07377
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                                                                                                                                                        Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO364 protein.
                                                                                                                                                Similarity
                                                                                                 241 AA;
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11-FEB-2000;
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| cv | 154
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09-DEC-1999;
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Best Local
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             immune-mediated renal disease, demyelinating diseases of the central and perlpheral nervous systems, hepatobiliary diseases of the central bowel disease, jutten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AACSB37 to AACSB578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACSB579 to AACSB642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                    61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                     92
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                                                                                                                                                                                                                                                                                                      1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor receptor-like protein TR11 mutein.
                                                                                                                                                                                                                                           Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein;
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                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                      100.0%; Score 753; DB 21;
100.0%; Pred. No. 2.9e-55;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY95895 standard; Protein; 241 AA
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99US-0134172.
99US-0144076.
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                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 122; Conservative
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16-JUL-1999;
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The present sequence is that of human tumour necrosis factor receptor-like protein TR11 (see also AAY95879), a novel protein receptor-like protein TR11 (see also AAY95879), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The invention provides highly conserved TR11, TR115V1 and TR115V2 proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR115V1 and/or TR115V2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency deficiency with hyper IgM. TR115V1 and/or TR115V2 candor diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; anglogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis, systemic lupus erythematosus, thrombocytopenia purpura or iga nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 753; DB 21; 100.0%; Pred. No. 2.9e-55;
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99US-0123957.

99US-0131445.

99US-0134287.

99WO-US12252.

99US-0141037.
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98US-0112850.
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08-MAR-1999;
12-MAR-1999;
28-APR-1999;
14-MAY-1999;
02-JUN-1999;
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Chen J,
                                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                 useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenic disorder in mammals by and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB2438B NASA438 PRO PROSPECTION AND PROPERTIES OF AND PR
                                                                                                                                                                                             Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
                                                                                                                                                                                           Gerber H, Hillan KJ, Godd
(uo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 753; DB 21; 100.0%; Pred. No. 2.9e-55;
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                                                                                                                                                                                                          Kuo SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                          Ferrara N,
Klein RD, K
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71467 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                        Claim 72; Fig 44; 315pp; English.
                                            99WO-US20594.
99WO-US20944.
99WO-US21090.
99WO-US21547.
99WO-US23089.
                                 99WO-US20111
                                                                                                                              99US-0162506
                                                                                                                                                                                                          Gurney AL, K
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                          Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 122; Conservative
                                                                                                                                                            GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO364 protein.
                                                                                                                                                                                                                                                         WPI; 2000-412154/35.
N-PSDB; AAA77604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AA;
                                                                                                                                                                                          Ashkenazi AJ,
Godowski PJ, G
Watanabe CK, W
                                                                          15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
             26-JUL-1999;
01-SEP-1999;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2000
                                                                                                                            29-0CT-1999
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| cv || 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
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ID AAX7
XX AC AAY7
XX DT 08-N
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KW DECKW DECKW
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The present sequence is the human PRO364 protein, encoded by the cDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA44825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNRR) family of polypeptides. PRO364 sequence also shows homology to members of the TNRR family and mouse GITR protein. This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
tumour necrosis factor receptor; GITR protein homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Prokaryotic membrane lipoprotein lipid attachment site"
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8..14
                                                                                                                                                                                                                                                                   'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                          26..241
/label= Mature_PRO364_protein
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                   "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-myristoylation
                                                                                                                                                                      /label- Signal_peptide
                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 31; Fig 4; 108pp; English.
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99US-0144758.
99US-0145698.
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98US-0112850.
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                                                                                                                                                                                                                                                                                                  25..31
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-412325/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating cancers,
their antagonists
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20-JUL-1999;
26-JUL-1999;
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                                                                         Homo sapiens
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graft rejection; graft-versus-host-disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to methods for stimulating or inhibiting anglogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following process. PRO179, PRO384, PRO844, PRO846, PRO1760, PRO205, PRO311, PRO333, PRO8410, PRO845, PRO885, PRO885 or PRO887. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothelial or anglogenic disorders. The present sequence is one of the proteins of the invention.
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                                                                                                                                                                                                                                                                                                          Pitti RM;
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                                                                                                                                                                                                                                                                       Gerritsen ME;
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                                                                                                                                                                                                                                                                                                          Paoni NF,
                                                                                                                                                                                                                                                                Ferrara N, Gerber H,
llan KJ, Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO364 protein UNQ319 SEQ ID NO:92.
                                                                                                                                                                                                                                                                                               Hillan KJ, P
PM, Wood WI;
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30-NOV-1999; 99WO-US28409.
02-DEC-1999; 99WO-US28565.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
                                                                                                                                                                                                                                                                                                   Gurney AL, Hil
, Williams PM,
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                                                                                                                                                                                      GETH ) GENENTECH INC
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Watanabe CK,
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cv 154
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, such straintius, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henzel
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Pan J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 33; Fig 36; 309pp; English.
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2000WO-US00277.
2000WO-US00376.
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99US-0123618.
99US-0123775.
99US-0128849.
99WO-USO8615.
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99US-0134287.
99WO-US12252.
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99US-0145698.
99US-0146222.
99WO-US20111.
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99US-0162506.
99WO-US28214.
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99WO-US28409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC58596
                                   40200053758-A2
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Homo sapiens.
                                                                                                                 02-MAR-2000;
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06-JAN-2000;
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                                                                                                                                                                                                                                                                              28-APR-1
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                                                                                                                                           61 PCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTPCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                          Gaps
                                                                                                              1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents human PR0364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor homologue – useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
which affect immunological responses, e.g. autoimmune disorders.
                                                                             .;
0
                                                       Length 241;
                                                                                                                                                                                                                                                                                                                                                          PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marsters SA;
                                                       Score 753; DB 19;
Pred. No. 2.9e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-glycosylated"
162.180
/note= "transmembrane domain"
                                                                 Pred. No. 2.9
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26..241
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney AL,
                                                                                                                                                                                                                                                                                                                                    Human TNF receptor homologue PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                     AAY06605 standard; Protein; 241 AA.
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                                                      100.0%; Sc
100.0%; Pr
live 0;
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                                                                Similarity 100.
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
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Pitti RM, Wood WI;
                     241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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cv 154
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                                                                            Matches 122;
                                                                                                                                                                                                                                                                                          AAY 06605;
                        Sequence
                                                       Query Match
                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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Escherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respoises 157-167 of PRO364. PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells proinflammatory or autoimmune responses in mammalian cells claimed). Chimeric molecules comprising a PRO364 polypeptide immunoglobulin Fc region are also claimed. PRO364 polypeptide immunoglobulin Fc region are also claimed. PRO364 polypeptide interactions. This is useful for identifying inhibitors or assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                               61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                          1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                         Cardiovascular; endothelial; angiogenic disorder; PR0179; PR0238; PR0364; PR0844; PR046; PR01760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885;
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                                                                                                                                                                                                                                                                                                                 Length 241;
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                                                                                                                                                                                                                                                                                                                  DB 20;
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 753; DB 20; 100.0%; Pred. No. 2.9e-55;
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/label= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB27651 standard; Protein; 241 AA.
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99US-0145698.
99WO-US20111.
99WO-US21090.
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99WO-US12252
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein PRO364.
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                        241 AA;
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12-MAR-1999;
02-JUN-1999;
26-JUL-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CV 122
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                                                                                                                                                                                                                                           inhibitors.
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99WO-US28313

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                                                      protein from clone_AB. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Banagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60
                                                                                                                                                                                                                                                61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                      100 fsfgfqc1dcasgtfsggheghckpwtdctqfgfltvfpgnkthnavcvpgsppaeplg 158
                                               This is the amino acid sequence of the truncated human 312C2 T cell
cancers, auto-immune disorders, transplantation rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                     immunodeficiency; autoimmune disease; rheumatoid arthritis;
immunosuppressive; antirheumatic; antiarthritic; haemostatic;
dermatological; antiinflammatory; therapy; diagnosis.
                                                                                                                                                                                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor receptor-like protein;
                                                                                                                                                                                                                                                                                                                                                                                                          Human tumour necrosis factor receptor-like protein TR11.
                                                                                                                                                                                               100.0%; Score 737; DB 19; 100.0%; Pred. No. 4.9e-54;
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/note= "conserved domain CD-V"
153..160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26..234
/label- Mature_protein
26..162
/label- Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163..179
/label- Transmembrane_domain
180..234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label Intracellular domain
                                                                                                                                                                                                                  0; Mismatches
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                            Disclosure; Pages 61-62; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               AAY95879 standard; Protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
           T cell disorders
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                                                                                                                                                                  228 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lomo sapiens
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                  AAY95879;
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20.08 townstring the gracecorticota induced remains necessary and murine gracecorticota induced remains a constitutive for murine gracecore in a T-helper cell library.

TRII activated NF-kappaB through a TRAPZ-mediated mechanism.

TRII activated NF-kappaB through a TRAPZ-mediated mechanism.

Expression is activation-inducible. The TRII ligand is constitutively expressed in an endothelial cell line. This suggests that TRII and its ligand may be involved in activated T-cell trafficking.

The invention provides TRII, TRIISVI and TRIISVZ notels acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and see an autoimment disease, especially remark to reast, proposed encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of human tumour necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis
"conserved domain CD-VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..211
te= "epitope-bearing region"
                                                                                        "conserved domain CD-IX"
                                                                                                                                                                                                                                                            'note- "epitope-bearing region"
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99US-0134172.
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prote prote Human 312C2 protei Human tumour necro Human tumour necro TR11SV1 amino acid Polypeptide encode PRO364-related EST

TR11SV2 amino acid

Human anglogenesis

Human PRO364

Human

Mouse glucocortico
Mouse glucocortico
Amino acid sequenc
Mouse glucocortico
Human 312C2 protei
Murine TNF-alpha f
Skin cell protein,
H4-1BB receptor pr

Human 4-1BB polype Human 4-1BB recept Human CD137 protei

Human receptor pro

Human tumour necro A novel human h4-1 Human h4-1BBSV rec

Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Plasmid pbC406/0X4
OX40/Fc mutein. C
Human h4-1BBSV rec
Human mFLINT #2 pr

T-cell;

Mouse type-II memb Mouse OX40 extrace

Isolated 312C2 T cell gene - used to develop products for treating, WPI; 1998-159534/14. N-PSDB; AAV19154.

Zlotnik A;

Gorman DM, Randall TD,

protein PRO3 PRO364 prote necro

Human Human

AAY52158 AAY44825 AAW37839 AAY06605 AAB27651 AAB27651 AAB24409 AAY1467

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Human

Human

Human Human

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PR0364 PR0364 tumour

Amino acid sequenc

Human tumour necro necrosis fa Human molecule ass TNF receptor

Tumour

Truncated human 31

AAW37840 AAY95879

Query Match

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96US-0027901 96US-0689943

07-OCT-1996; 16-AUG-1996;

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N-PSDB; AAZ49948.
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The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA library. This sequence is expressed in cardiovascular and haematopoletic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatotropic, antinflammatory, antipsoriatic, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic, immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g.
Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                             Claim 1; Pages 64-65; 67pp; English.
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Length 235; Indels 100.0%; Score 737; DB 21; 100.0%; Pred. No. 5.1e-54; tive 0; Mismatches 0; Conservative Similarity AA; 235 Local Sim hes 119; Query Match Best Local Si Matches 119, Sequence

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FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSFPAEPLG 119

61

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Gaps

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cells This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antiqen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoletic cells, e.g. Imphoid cells which affect immunological responses, e.g. autoimmune disorders. Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autoimmune disorders. darccrvhttrccrdypgeeccsewdcmcvqpefhcgdpccttcrhhpcppgqgvqsqgk 105 Gaps DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119 Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders ö Length 241; Indels Amino acid sequence of the human 312C2 T cell protein. 100.0%; Score 737; DB 19; 100.0%; Pred. No. 5.2e-54; tive 0; Mismatches 0; "human 312C2 protein" Claim 2; Pages 59-60; 71pp; English. Location/Qualifiers Zlotnik A; Ā AAW37839 standard; Protein; 241 97WO-US13931. 96US-0027901. 96US-0689943. /\*tag= a /product= (first entry) Conservative Randall TD, (SCHE ) SCHERING CORP. WPI; 1998-159534/14. Query Match Best Local Similarity Matches 119; Conserv 241 AA; N-PSDB; AAV19153 Homo sapiens 14-AUG-1997; 28-JUL-1998 WO9806842-A1 07-0CT-1996; 16-AUG-1996; 19-FEB-1998 Gorman DM, AAW37839; Sequence 46 106 61 RESULT AAW37839 Key QQ 9 ò ò

Baughn MR;

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Patterson

Corley NC,

acid sequence of the human tumour necrosis factor

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agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, Digeorge syndrome, HIV infection, severe combined immunodeficiency of SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,
                            receptor-like protein (TRII receptor). The invention relates to TRII and determined by sequencing cloned cDNAS AA27765-237766. The TRII receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GTRR). TRII, TRIIISVI and TRIISV2 pollypetides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for
                                                                                                                                                                                                                                                                                                                                           hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperscute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be diseate, prepair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, encropathies, and central nervous system disease (e.g. Alzhehimer's disease, Parkinson's disease, Huttington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis and prognosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor-like protein; TR11; TR11SV1; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorges syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                               1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60
                                                                                                                                                                                                                                                                                               61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                  tumour necrosis factor receptor-like polypeptides used to, e.g.
arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
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                                                                                                                                                                Length 234;
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; Pred. No. 5.1e-54;
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/note= "Intracellular domain"
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/label= TR11
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                                                                                                                                                                                 Best Local Similarity 100. Matches 119; Conservative
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                                                                                             100.0%; Score 737; DB 21;
100.0%; Pred. No. 5.1e-54;
tive 0; Mismatches 0;
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                                                                                                                            Local Similarity
nes 119; Conserv
234 AA;
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                            proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothellal or anglogenic disorders. The present sequence is one of the proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 5.2e-54;
ive 0; Mismatches 0;
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99US-0128849.
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99WO-US20944
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Best Local Similarity 100.
Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2001
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                                                                                                                                                                                    Seguence
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PRO840,
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, costeoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, arcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immenia disease, gluten-sensitive enteropathy and whipple's disease, compendent and peripheral nervous systems, hepatobiliary diseases of inflammatory bowel disease, gluten-sensitive enteropathy and whipple's disease, autoimmune con immune-mediated skin diseases, allergic disease, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AACSBST to AACSBST pepresent PCR primers and hybridisation probes used the isolation of human PRO sequences AACSBST to AACSBST and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
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                                                                                                                                                                                                                                                                                                                                                                           KP, Goddard A, Gurney AL, Hebert C, He
Pan J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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                             99US-0162506.
                                                                                          99WO-US28301.
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99WO-US28409
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2000WO-US00376
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                                                                                                                                                                                                                                                                                                                                                                                                          Tumas D,
                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                            Lu Y,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                            Kabakoff RC,
                                                                                                                                                                                                                                                                 11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                               18-FEB-2000;
22-FEB-2000;
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01-DEC-1999
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                                                                                                                                                                        16-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                            Stewart TA,
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                                              NOV-1
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Gaps

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Length 241; Indels

AAY06605;

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RESULT

AAY06605

Key Peptide Protein

Domain

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Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders \,
                                                                                                           1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60
                                                                                                                                                           61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                             Cardiovascular; endothelial; angiogenic disorder; PR0179; PR0238; PR0364; PR0844; PR0846; PR01760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885; PR0887;
                Score 737; DB 20;
Pred. No. 5.2e-54;
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Ilan KJ, Marsters SA,
100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..25
/label= "Signal peptide"
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Goddard A, Gurney AL, Hillan KJ, N
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                       AAB27651 standard; Protein; 241 AA
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99WO-US12252.
99US-0144758.
99US-0145698.
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2000WO-US04342
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                                                   Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                Human protein PR0364
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                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001
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30-NOV-1999
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                Query Match
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                                                                                                                                                                                                                                                                      AAB27651
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                                                                                                                                                                                                                                                                                                           The present sequence represents human PRO364, a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claimed). Chimeric molecules comprising a PR0364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin Fc region are also claimed. PR0364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PR0364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PR0364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour necrosis factor receptor family. The sequence was deduced from a bone marrow CDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO, ESCherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respdies 157-167 of PRO364 pro364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
                                                                                                                                                                                                                 PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney AL, Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                1..25
/note= "signal peptide"
26..241
                                                                                                                                                                                                                                                                                                                                                                                               /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylated"
162..180
                                                                                                                                                                             Human TNF receptor homologue PRO364
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                      AAY06605 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Fig 2A; 104pp; English.
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                                                                                                                                                                                                                                                  autoimmune disease; therapy
                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
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N-PSDB; AAX87670.
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Pitti RM, Wood WI;
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                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                          26-0CT-1999
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The present invention relates to methods for stimulating or inhibiting anglogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,

241 AA;

Sequence

Pitti RM;

Gerritsen ME; Paoni NF, P

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30-NOV-1999;
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                                                                                                                                                                                                                                                                                                               Chen J,
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      8 X X Z X D X X D X X D X X D X X D X X D X X D X X D X X D X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D 
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associated with decreased PRO expression. AAA77510 to AAA7721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                   Length 241;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                100.0%; Score 737; DB 21;
llarity 100.0%; Pred. No. 5.2e-54;
Conservative 0; Mismatches 0;
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/note= "Leucine zipper pattern"
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/label- Mature_PRO364_protein
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1..25
/label Signal_peptide
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122..128
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                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 119; Conserv
                                                                                                                           241 AA;
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                                                                                                                           Sequence
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JUD AAY7

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clone, designated as DNA4736-TIOG. It is isolated from human small intestine tissue CDNA library, identified using probes based on the consensus sequence DNA48125, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNRR) family of polypeptides. PR0364 sequence also shows homology to members of the TNRR family and mouse GITR protein.

This clone is assigned the ATCC deposit No: 209436. PR0364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PR0555, PR0364 and PR0344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is the human PRO364 protein, encoded by the cDNA
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           new composition useful for inhibiting neoplastic cell growth and
treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide
their antagonists
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                                                                                                                                                                                                                Napier M,
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Pred. No. 5.2e-54;
; Mismatches 0;
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/label= Signal_peptide
26..241
/label= Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                           31; Fig 4; 108pp; English.
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100.0%;
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98US-0113296.
99US-0144758.
99US-0145698.
99WO-US28409
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N-PSDB; AAD01240.
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Matches 119;
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61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in
                                                                                                                                      Human tumour necrosis factor receptor-like protein TR11 mutein.
                                                                                                                                                                      TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autofinmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
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                              AAY95895 standard; Protein; 241 AA.
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99US-0134172.
99US-0144076.
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                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                               Homo sapiens.
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16-JUL-1999;
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                                                                                                   20-NOV-2000
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                                                                 AAY95895;
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              AAY95895
RESULT
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diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial anglogenic disorders in mammals -
Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoni NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerber
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                                                                                                                                                                                                                                                                                                                  Human PRO364 protein sequence SEQ ID NO:117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein RD,
, Wood WI;
                                                                                                                                                          AAB24409 standard; Protein; 241 AA
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99US-0144758.
99US-0145698.
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99US-0115554,
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Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 72; Fig 44; 315pp;
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Watanabe CK,
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Gaps

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Indels

Length 241;

46

g o

1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60

100.0%; Score 737; DB 21; 100.0%; Pred. No. 5.2e-54; iive 0; Mismatches 0;

Conservative

Local Similarity nes 119; Conserv

Best Loca Matches

Query Match

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This sequence represents PR0364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGTTR). The corresponding ligand (hGTTRL), PR015, is given in AAB47056.

PR0364 and PR0175 may be used in a mixture with a cardiovascular, endothelial, anglogenic or anglostatic disorder. The cardiovascular, cardiovascular, endothelial, anglogenic or anglostatic disorder. The PR0364 cDNA sequence was isolated from an expressed sequence tag (EST) receptor (TNRP) family of cDNA fragments derived from human unbilical vein endothelial cells (HUVEC). Administering an effective amount of PR0364 or PR0175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF_2alpha), trauma, a cancer, or age-related mecular degeneration in a human. The pr0364 or PR0175 is useful for inhibiting anglogenesis induced by PR0364 or PR0175 is useful for inhibiting anglogenesis induced by PR0364 or PR0175 is useful for inhibiting anglogenesis induced by PR0364 or PR0175 is useful for inhibiting anglogenesis induced by PR0364 or PR0175 is useful for an antibody that binds PR0364 or PR0175, or their antagonists, are useful for the enterpention of a retinal case therefore the presence of an elevated from a unmor or a retinal case mention or prevention of a theroselerosis, hypertension, inflammatory creatment or prevention of a theroselerosis, inflammatory creatment or prevention of a hearost-anenyms, are proper and the prostonists.
                          Composition for diagnosing and treating cardiovascular, endothelial and anglogenic disorders, comprises a PRO364 or PRO175 polypeptide -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuropathies and rheumatoid arthritis
                                                                                                                         Claim 1; Fig 1; 76pp; English
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241 AA; Sequence

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                                                      Gaps
                                            1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 60
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Length 241;
                       Indels
100.0%; Score 737; DB 22;
100.0%; Pred. No. 5.2e-54;
Live 0; Mismatches 0;
          Best Local Similarity 100.
Matches 119; Conservative
 Query Match
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RESULT 14 AAB50910 

AAB50910 standard; Protein; 241 AA

AAB50910;

21-MAR-2001 (first entry)

Human PRO364 protein.

Human; PRO; antiinflammatory; dermatological; antiarthritic; antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antifalbetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobillary disease; autoimmune disease; allergy.

Homo saptens

WO200073452-A2.

07-DEC-2000

02-JUN-2000; 2000WO-US15264.

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, Gurney AL;
Watanabe CK;
                                                                                                                                                                 Godowski PJ,
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                                                                                                                                                                      Shelton DL,
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                                                                                                                                                                 KP, Chan B,
Kabakoff RC,
                                                          99US-0170262.
                                                                          2000WO-US00376
                                                                                 2000WO-US03565.
           99US-0144758
                             99WO-US21090
                                                    99WO-US28634
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2000WO-US04914
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                      99WO-US20111
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                                                                                                                                                                 Ashkenazi AJ, Baker KP,
                                                                                                                                                     (GETH ) GENENTECH INC.
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                                                                                                                                                                                              N-PSDB; AAC91469
                                                                                     18-FEB-2000;
18-FEB-2000;
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                             15-SEP-1999
                                              30-NOV-1999
                                                               20-DEC-1999
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Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 58; Fig 18; 218pp; English

The present sequence is one of thirty three novel PRO polypeptides.
The PRO polypeptides, anti-PRO antibodies, agonists and antipodies and diagnosing immune related antipodies are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, Systemic sclerosis, idiopathic inflammatory myopathies, Syoren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy, hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's inflammatory bowel disease, gluten-sensitive enteropathy and whipple's diseases, autoimmune or immune-mediated skin diseases (such as such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary fibrosis including graft rejection and graft-versus-host diseases.

241 AA; Sequence

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Gaps
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  Length 241;
                                           Indels
Query Match 100.0%; Score 737; DB 22; Best Local Similarity 100.0%; Pred. No. 5.2e-54; Matches 119; Conservative 0; Mismatches 0;
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1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGK 60

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The present sequence is that of novel human immunomodulator PR0364 (UNQ319), as deduced from CDNA (see AAF30057) isolated from a small intestine library. PR0364 (26 kDa, pl 6.34) shows sequence homology to mouse GITR protein and may be its human counterpart. The invention provides polynuclectides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PR0364. Claimed compositions comprising these proteins or their agonists are useful for increasing inflirration of inflammatory cells into a tissue of a mammal stimulating or enhancing an immune response, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising a PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PRO polypeptide, an agonist antibody or an antagonist network propertied, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, of uvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, sjoarch's systemic sclerosis, idiopathic inflammatory myopathy, sjoarch's smiltiple sclerosis, idiopathic inflammatory myopathy, sjoarch's smiltiple sclerosis, can antoimmune chronic active hepatitis, primary biliary cirrhosis, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulommatous hepatitis, sclerosing cholangitis, iditematory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                                                                                                                                                                                            /note= "prokaryotic.membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                              "leucine zipper pattern"
                                                       'note- "N-myristoylation site"
                                                                                                                     "N-myristoylation site"
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166..177
                                                                                      "N-myristoylation site"
                                                                                                                                                                                       "N-myristoylation site"
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Pitti RM,
163..183
/note= "transmembrane domain"
                                                                                                                                                      "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                               attachment site"
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k MR, Marsters SA,
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                                                                                        'note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                            Peptide
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PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR;
                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               61 FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                                                                                                              enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermattis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all calmed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of I lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF_Zalpha; trauma; cancer; anglogenesis; age-related macular degeneration; antibody; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor anglogenesis;
                                                                                                                                                                                                                                                                Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lung; liver; fibrosis; neuropathy; rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide"
                                                                                                                                                                                                                                                                100.0%; Score 737; DB 22; 100.0%; Pred. No. 5.2e-54;
                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47054 standard; Protein; 241 AA
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                                                                                                                                                                                                                                                                                                   Conservative
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N-PSDB; AAC85433.
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                   241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L2-JUL-1999;
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                                                                                                                                                                                      using PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2001
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                                                                                                                                                                                                                                                                                                119;
                                                                                                                                                                                                                    Sequence
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Best Local S
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The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
                                                                                                                                                                                                                                  Human; PRO; cardiant; antianglogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -.
            darccrvhttrccrdypgeeccsewdcmcvqpefhcgdpccttcrhhpcppgggvqsggk 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Gerritsen ME;
Mark MR, Marsters SA;
4, Wood WI;
                                     FSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                KP, Ferrara N, Gerber H,
PJ, Gurney AL, Kuo SS, Ma
Watanabe CK, Williams PM,
                                                                                                                               AAB50982 standard; Protein; 241 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0141758.
99US-0144758.
99US-0145698.
99US-0116222.
99WO-US28313.
99WO-US28409.
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99WO-US30095
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2000WO-US08439
                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                          protein.
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30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
11-FEB-2000;
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15-MAR-2000;
21-MAR-2000;
30-MAR-2000;
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18-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                           Human PRO364
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infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or anglogenic disorder.
                                                                                                                                                                                                                                                                                                                 46 darccrvhttrccrdypgeeccsewdcmcvqpefhcgdpccttcrhhpcppgggygsggk 105
                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 5.2e-54;
ive 0; Mismatches 0;
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Matches 119; Conserv
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Search completed: September 4, 2001, 15:56:23 Job time: 340 sec

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The present sequence is that of human tumour necrosis factor receptor-like protein TRII, a novel 25 kDa protein which shows sequence to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library.

TRII activated NF-kappaB through a TRAF2-mediated mechanism.

Expression is activation-inducible. The TRII ligand is constitutively expressed in an endothelial cell line. This suggests that TRII and its ligand may be involved in activated T-cell trafficking. The invention provides TRII, TRISVI and TRIISV2 nucleic acids (see AAA53304-06) and highly conserved encoded proteins (see AAA53304-06) and highly conserved encoded proteins (see AAA53304-06), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/Or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis
                                                                                                                                                                                                                           /note= "epitope-bearing region" 66..71
                                                                                                                                                                                                                 region"
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           "conserved domain CD-IV"
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te= "epitope-bearing
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/note= "e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N1 7;
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16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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immunodeficiency, especially common variable immunodeficiency, x-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or x-linked immunodeficiency (SCID), Wiskott-Aldrich syndrome or x-linked immunodeficiency and solution of the series of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGRLLLGTGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 979; DB 21;
Pred. No. 3.9e-70;
; Mismatches 0;
                                                                                                                                                                                                                                                                               agonist/antagonist compounds are also provided
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100.0%;
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/label- TR11
26..162
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Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                234 AA;
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(HUMA-) HUMAN GENOME SCI INC

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Amino acid sequenc
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Mouse type II memb
Mouse Ox40 extrace
Plasmid pDC406/OX4
OX40/Fc mutein. C
Deduced sequence e
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Human 4-1BB polype
Human 4-1BB recept
Human CD137 protei
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PRO364-related EST
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Human 312C2 protei
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ACT-4-h-1 receptor
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Human 312C2 protei
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                             Fruncated human 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.
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84..93
/note= "conserved domain CD-III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26..234
/label= Mature_protein
26..162
/label= Extracellular_domain
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180..234
/label- Intracellular domain
146
                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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                                                                        AAY06645
AAB47055
AAY95880
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                                                                                                    AAY52159
AAW37841
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AAW37838
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(first entry)
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Modified-site
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RESULT
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tumour necro
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immunostimul
PRO364. Hom
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                                                              ; Search time 126.12 Seconds (without alignments) 78.832 Million cell updates/sec
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                                                                                                           979
1 MAQHGAMGAFRALCGLALLC......GNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1980. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1981. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1982. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1983. DAT: *
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                                                                                                                                                                                       412676
                  Compugen Ltd
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
       GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                    412676 seqs, 60623988 residues
                                                               4, 2001, 15:56:24
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Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
                                                                                                  US-09-512-363-2_COPY_1_164
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AAB33431
AAY95895
AAB24409
AAY71467
AAB20115
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AAW37839
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Score

Result No.

Post-processing:

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Minimum DB Maximum DB

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PR0364 polypeptides, e.g. in CHO, escherichia coll or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid responses in mammalian cells are useful for modulating apoptosis, NF-KB activation and proinfilmmanctory or autofinmune responses in mammalian cells (claimed). Chimeric molecules comprising a PR0364 polypeptide fused to a heterologous sequence such as epitope tag or funcation and assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PR0364 and also in therapy, e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents human PRO364, a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
                                                      PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;
Pitti RM, Wood WI;
                                                                                                                                                                                                                                              162..180
/note= "transmembrane domain"
                                                                                                                                                                      /note= "signal peptide"
                                                                                                                                                                                                    /note- "mature protein"
                                                                                                                                                                                                                              /note= "N-glycosylated"
                            Human TNF receptor homologue PRO364.
                                                                                                                                           Location/Qualifiers
1..25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Fig 2A; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                               98US-0024087
26-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-494296/41.
N-PSDB; AAX87670.
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                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  09-FEB-1999;
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                                                                                                                                                           Peptide
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O polypeptides and agonists and antagonists of them, used to and treat cardiovascular, endothelial and anglogenic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pitti RM;
Cardiovascular; endothelial; anglogenic disorder; PRO179; PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO811; PRO333; PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;
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Paoni NF, P
                                              SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
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SA,
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Marsters S
                                                                                                                                                                                                                                                                                                                1..25
/label= "Signal peptide"
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Hillan KJ, Ma
PM, Wood WI;
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                    AA.
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                                                                                                                  AAB27651 standard; Protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US12252.
99US-0144758.
99US-0145698.
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99WO-US21090.
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99US-0123957
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99WO-US28409
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2000WO-US04342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                          Human protein PRO364.
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                                                                                                                                                                                                                                                      gene therapy.
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Watanabe CK,
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18-FEB-2000;
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                                                                                                                                           AAB27651;
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Peptide
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100.0%; Score 979; DB 20; Length 241; 100.0%; Pred. No. 4e-70; 0; Indels 0;

Matches 164; Conservative

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Similarity

Local

Query Match

1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60 

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RESULT
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                                                                                                                                                                              This is the manno acid sequence of the numan tumour necrosis factor two splice variants TRISV1 and TRISV2. The invention relates to TRI1 and two splice variants TRISV1 and TRISV2. The nucleotide sequences were determined by sequencing cloned cDNAS AA23765.23766. The TRI1 receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GITR).

CRILI, TRISVA and TRISVA polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/Anadonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, blood capulation disorders, blood cogulation disorders, blood cogulation disorders, blood cogulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, had be used to treat heart attacks, strokes, Addison's disease, had be used to treat heart attacks, strokes, Addison's disease, had be used to treat heart attacks, strokes, Addison's disease, had an antigenic molecule, organ rejection or graft of alsease, multiple sclerosis, myasthenia gravis, Stiff wan syndrome, insulin dependent disease, inflammatory conditions, ischemiar-perfusion or diabetes mellitus or autotimmune inflammatory bowel disease, crowned alisease, conditions, ischemiar-perfusion of injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, crommed disease, anaphylaxis, complement-mediated hyperacute rejection, nephrities, cromplement-mediated hyperacute rejection, nephrities, and central nervous syndrome, surgery, inflammatory disease, wardery, disease, and central nervous syndrome, and surgery, inclamed sand central nervous syndrome, and surgery incortices and ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is the amino acid sequence of the human tumour necrosis factor
                                                                                            to, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 979; DB 21; Length 234; larity 100.0%; Pred. No. 3.9e-70; Conservative 0; Mismatches 0; Indels 0
                                                                                           New tumour necrosis factor receptor-like polypeptides used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XX
AC AAW37839;
XX Z8-JUL-1998 (first entry)
XX.
DE'', Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis and prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW37839 standard; Protein; 241 AA
                                                                                                                                        Claim 14; Fig 1; 167pp; English.
                                                                                                           treat Digeorge syndrome
                                          WPI; 2000-061922/05.
N-PSDB; AA237762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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              Ruben SM;
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Matches 164;
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cells
             antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoletic cells; lymphoid cell; autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid which affect immunological responses, e.g. autbimmune disorders.
Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 241;
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Pred. No. 4e-70;
Mismatches 0;
                                                                                                                                                                                                                                                       "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Pages 59-60; 71pp; English.
                                                                                                                                                                             Location/Qualifiers
1..726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorman DM, Randall TD, Zlotnik A;
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/product= '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-159534/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV19153
                                                                                                                                                                                                                                                                                                            WO9806842-A1.
                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local S
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                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor-like protein TRII (see also ARYSS879), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family related gene. The invention provides this mily conserved TRII, TRIISVI and TRIISV2 proteins (see ARYSS879-81), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/or TRIISV2 polypeptides are useful. Trinked agammaglosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, x-linked agammaglobulnemia, severe combined immunodeficiency, X-linked agammaglobulnemia, severe combined immunodeficiency antibudish syndrome or X-linked immunodebulin deficiency with hyper IgM. TRII, TRIISVI and/or TRIISV2 and and/or diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lupus srythematosus, thrombocytopenia purpura or IgA nephropathy. The polypetides, polynuclectides and/or antibudies can be administered to cells in vitro, ex vivo or in polypetides may also be used. Methods forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                           Human tumour necrosis factor receptor-like protein TR11 mutein
                                                                                                                                                                                                                       TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is that of human tumour necrosis factor
agonist/antagonist compounds are also provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; 294-295; 278pp; English.
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                                                                                           AAY95895 standard; Protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0121648.
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99US-0144076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, N1 J;
                                                                                                                                                                                                                                                                                                                                                       WO200050459-A1
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2000;
                                                                                                                                                            20-NOV-2000
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16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis
                                                                                                                          AAY95895;
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                                                                                                                                                                                                                                                                                          mutant.
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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; anglogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorder in mammals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                           Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                            164
                                                                                                       SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG
                                                                                                                                                                                                                                                    Human PRO364 protein sequence SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP, Ferrara N,
Surney AL, Klein RD, I
                                                                                                                                                                             AAB24409 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 72; Fig 44; 315pp; English.
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99WO-US20111.
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Williams PM,
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                                                                                                                                                                                                                          07-NOV-2000 (first entry)
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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02-JUN-1999;
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05-OCT-1999
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100.0%; Score 979; DB 21; Length 241; 100.0%; Pred. No. 4e-70; 1.4ve 0; Mismatches 0; Indels 0

Best Local Similarity 100. Matches 164; Conservative

Query Match

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                                                                                                                                       61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                 immune related disease; diagnosis; antiinflammatory; cardiant;
                                                                    Gaps
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                                                                                                autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease;
                                                                                      1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                               Length 241;
                                                                  Indels
                                                                                                                                                                    SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                             Query Match 100.0%; Score 979; DB 21; Best Local Similarity 100.0%; Pred. No. 4e-70; Matches 164; Conservative 0; Mismatches 0;
one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               graft rejection; graft-versus-host-disease.
                                                                                                                                                                                                                                                                                              protein UNQ319 SEQ ID NO:92.
                                                                                                                                                                                                                                     AAB33431 standard; Protein; 241 AA
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99US-0123618.
99US-0123957.
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99US-0134287.
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99US-0146222
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99WO-US20594
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99WO-US21090
                                                                                                                                                                                                                                                                           (first entry)
                    241 AA;
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                                                                                                                                                                                                                                                                                               Human PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                           29-JAN-2001
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13-SEP-1999;
15-SEP-1999;
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20-APR-1999;
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04-MAY-1999;
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26-JUL-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune mediated renal disease, demyelinating diseases of the central can peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AACSB378 represent PCR primers and hybridisation probes used the isolation of human PRO polynucleotide and protein sequences glven in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henzel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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D, Shelton DL, Smith V;
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 241;
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Pan J, Pennica D,
Watanabe CK, Woo
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                                                                                                                                                                                                                                                                                                                                                         2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
                                           99WO-US28313.
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2000WO-US03565.
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99WO-US28634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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Kabakoff RC,
                                                                                                                                                                                                                                                                                                                06-JAN-2000;
11-FEB-2000;
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18-FEB-2000;
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30-DEC-1999;
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29-0CT-1999
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Gurney AL;
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Tumas D, Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for as multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "prokaryotic membrane lipoprotein lipid
                                              antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuropriective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; antialergic; immunostimulant.
                                   UNQ319; human; immune disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides, nucleic acids and (ant)agonists, diagnosing and treating immune-related disorders, such sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171..193
/note= "leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                   25..31
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard A,
Pitti RM,
                                                                                                                                                                                                                                                         note- "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                           ..162
ce- "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Asn is N-glycosylated"
166..177
                                                                                                                                                                                                                                                                                                           /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                       33.39
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                                                                 'note= "N-myristoylation site"
                                                                                                                                                                                                           /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment site"
                                                                                                                                               1..25
/label- Signal_peptide
                                                                                                                                                                       26..241
/label- Mature_protein
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP, Fong S,
rk MR, Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Fig 16; 127pp; English
            Human immunostimulant PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2000; 2000WO-US06884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-014475B
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146..150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-103149/11.
N-PSDB; AAF30057.
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                                                                                                           Homo saptens
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                                                                                                                                            Peptide
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                                                                                                                                                                       Protein
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c a tissue of a mammal, stimulating or enhancing an immune
response, or increasing the proliferation of T-lymphocytes in a
mammal in response to an antigen. Claimed compositions comprising
a PRO polypeptide or its antagonist have the opposite effect. A
claimed method for treating an immune related disorder, such as a T
cell disorder, involves administering a PRO polypeptide, an agonist
antibody or an antagonist antibody. The disorder is selected from
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
invenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated
cranal disease, demyelinated diseases (such as multiple sclerosis),
autoimmune chronic active hepatitis, primary billary cirrhosis,
granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
cranal disease, collits and Crohn's disease, jquten-sensitive
enteropathy, Whipple's disease, (auto)immune-mediated skin diseases
(such as bullous skin disease, eartheme multiforme and psoriasis),
claimed methods of diagnosing these diseases (such
as graft rejection and graft-versus-host diseases (such
claimed methods of diagnosing these diseases) (all claimed)
claimed methods of diagnosing these diseases (an emethod
claimed methods of diagnosing these diseases (all method
claimed methods of diagnosing these diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO364; human; glucocorticoid-induced tumor necrosis factor; recept human umblical vein endothelial cell; HUVE; cardiac hypertrophy; human umblical vein endothelial cell; HUVE; cardiac hypertrophy; myocardial infarction; PGE Zalpha; trauma; cancer; anglogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud; disease; aneurysm; arterial restenosis; thrombophlebitis; tumor anglogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 979; DB 22; Best Local Similarity 100.0%; Pred. No. 4e-70; Matches 164; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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      Domain
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modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77711 and the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumou breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                                                                                                                                                                                                                                        61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
                                                                                                                                                                                   0;
                                                                                                                                                               Length 241;
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                                                                                                                                                                                                                                                                                       SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                             21;
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                                                                                                                                                           Score 979; DB 21
Pred. No. 4e-70;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-myristoylation site"
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'note= "N-myristoylation site"
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/note= "N-myristoylation site"
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/label- Mature_PRO364_protein
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/label= Signal_peptide
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100.0%;
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                                                                                                                                                                       Local Similarity
                                                                                                                              241 AA;
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                                                                                                                                                                                 Matches 164;
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                                                                                                                               Sequence
                                                                                                                                                               Query Match
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The present sequence is the human PRO364 protein, encoded by the CDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue CDNA library, identified using probes based on the consensus sequence DNA44825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TMRN) family of polypeptides. PRO364 sequence also shows homology to members of the TMFR family and mouse GITR protein. This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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                                                                         /note= "Prokaryotic membrane lipoprotein lipid
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                                                                                                                                                           /note= "Leucine zipper pattern"
                           Transmembrane_domain
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                                                                                                       attachment site"
171..193
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98US-0112850.
98US-0113296.
99US-0144758.
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163..183
/label= T
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                                                                                                                                                                                                                  WO200032778-A2.
                                                      Binding-site
                                                                                                                                                                                                                                                                                                                     30-NOV-1999;
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                              61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                         121 sggheghckpwtdctqfgfltvfpgnkthnavcvpgsppaeplg 164
                                                                                                                                                                                                                                               Pred. No. 4e-70;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB50982 standard; Protein; 241 AA
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99WO-US30095.
2000WO-US03565.
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99US-0141037.
99US-0144758.
99US-0146222.
99WO-US20111.
99WO-US28313.
                                                                                                                                                                                                                                             Best Local Similarity 100.08;
Matches 164; Conservative
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2000WO-US04342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO364 protein.
                                                                                                                                                                                                241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1999;
28-JUL-1999;
01-SEP-1999;
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18-FEB-2000;
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The PRO
                                                                                                                                                                                                                                                                                                                                                                                           Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                  SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                     Gerritsen ME;
irk MR, Marsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO polypeptidės.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 979; DB 22; Length 241; 100.0%; Pred. No. 4e-70; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human angiogenesis-associated protein PRO364, SEQ ID NO:142.
                                                                                                                                                                                                  (P, Ferrara N, Gerber H, Gerritsen JJ, Gurney AL, Kuo SS, Mark MR, M Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is one of seventeen novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 71; Fig 8; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB53090 standard; Protein; 241
2000MO-US06319.
2000MO-US06884.
2000MO-US07532.
2000MO-US08439.
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                                                                                                                                                                                                     r, Baker KP,
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 164; Conservative
                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                            Paoni NF, Pitti RM,
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                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC90566
10-MAR-2000;
15-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                     Ashkenazi AJ,
                                                                                     30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present
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Human; PRO; antiinflammatory; dermatological; antiarthritic; antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidiabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.

AAB50910 standard; Protein; 241 AA.

(first entry)

21-MAR-2001

AAB50910;

protein.

Human PRO364

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AAB50910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents PR0364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGTTR). The corticoid-induced tumor necrosis factor receptor (hGTTR). The corresponding ligand (hGTTRL), PR015, is given in AAB47056.

PR0364 and PR0175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic disorder. The cardiovascular, andotogenic or angiostatic disorder. The PR0364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNRR) family of polypeptides. The PR0175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PR0364 or PR0175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and trans, a cancer, or age-related macular degeneration in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Administering a therapeutically effective amount of an antibody that blinds PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering from a tumor or a retinal disorder. PRO364 or PRO175, or their antagonists, are useful for vascular related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides. Reynaud's disease, aneurysms, arterial restenosis,
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                                                                                                                            162..180
/note= "Potential transmembrane domain"
'note= "Potential signal peptide"
                                                                         /note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0143304
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N-PSDB; AAC85433.
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                                         Modified-site
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                                                                                                                                Domain
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99WO-US12252. 99US-0144732. 99US-0144758. 99US-0146222.

2000WO-US15264

02-JUN-2000;

02-JUN-1999 20-JUL-1999

07-DEC-2000.

WO200073452-A2.

Homo sapiens.

99WO-US21090 99WO-US21547

15-SEP-1999; 15-SEP-1999; 30-NOV-1999;

29-0CT-1999

01-SEP-1999

99US-0162506 99WO-US28313 99WO-US28634 99US-0170262

99WO-US20111

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, Gurney AL;
Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one of thirty three novel PRO polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard A, G
Shelton DL,
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Henzel W, Kabakoff RC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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N-PSDB; AAC91469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashkenazi AJ,
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0; Gaps

Length 241; Indels YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120 

SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164

121 121

1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRD 60 

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Query Match 100.0%; Score 979; DB 22; Best Local Similarity 100.0%; Pred. No. 4e-70; Matches 164; Conservative 0; Mismatches 0;

2000WO-USO6884. 2000WO-USO7377. 2000WO-USO7532. 2000WO-USO8439.

30-MAR-2000;

2000WO-US04414 2000WO-US04914

18-FEB-2000; 22-FEB-2000; 24-FEB-2000; 15-MAR-2000; 20-MAR-2000; 21-MAR-2000; 17-MAY-2000;

11-FEB-2000; 18-FEB-2000;

36-JAN-2000; 05-JAN-2000;

2000WO-US00376 2000WO-US03565 2000WO-US04341 2000WO-US04342

99WO-US30911

09-DEC-1999; 20-DEC-1999;

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Length 228;

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Gaps
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                  0; Indels
Query Match 96.7%; Score 947; DB 19; Best Local Similarity 100.0%; Pred. No. 1.3e-67; Matches 158; Conservative '0; Mismatches 0;
                                                                                                      HCKPWTDCTQFGFLTVFPCNKTHNAVCVPGSPPAEPLG 164
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99US-0144758.
99US-0145698.
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                                                                                                99WO-US28409
                                                                                                         99WO-US28565
                          05-JAN-2000; 2000WO-US00219
                                                 99WO-US12252
                                                                    99WO-US20111
                                                                                  99WO-US21547
                                                      99US-0141037
                                                                                                                          Baker KP,
                                                                                                                                AĽ,
                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                          Ashkenazi AJ, Baker B
Godowski PJ, Gurney P
Paoni NF, Pitti RM,
                                                                                                                                             WPI; 2001-090793/10.
                                                                                                                                                 N-PSDB; AAC97479
        WO200053753-A2.
Homo sapiens.
                                                                        08-SEP-1999
                                                                                           30-NOV-1999
                 14-SEP-2000
                                        12-MAR-1999
                                                 JUN-1999
                                                      23-JUN-1999
                                                           20-JUL-1999
                                                                26-JUL-1999
                                                                    01-SEP-1999
                                                                             15-SEP-1999
                                                                                      05-0CT-1999
                                             14-MAY-1999
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO nucleic acid, the recombinant production of a PRO comprising a PRO protein, agonists or antagonists of a PRO protein, additionally encompasses methods of identifying modulators of PRO protein additionally encompasses methods of identifying modulators of PRO comprision or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder or a the expression level of a PRO gene. The invention of angiogenic tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or CR or agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial candinistration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO protein, or an agonist or antagonist thereof candinistration of a PRO protein, or an agonist or antagonist thereof agonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as a cardiovascular, ulcers, wounds, cancer, Alzheimer's disease, psoriasis, endommetriosis, ulcers, wounds, cancer, Alzheimer's disease, hutington's alease, retrove DRO nucleic acids, processing architis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, hutington's the endometriosis, ulcers, wounds, are analytic and protein and protein and protein and protein and protein and and an appeared and proteins. disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the , Goddard A; Mark MR, Marsters SA; M, Wood WI; New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -N, Gerber H, G J, Kuo SS, Mar Williams PM, KP, Ferrara N, AL, Hillan KJ, Watanabe CK, Wi Claim 69; Fig 54; 293pp; English.

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This is the amino acid sequence of the truncated human 312C2 T cell protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haemacopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                         Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; haematopoietic cells; lymphoid cell;
                                               Gaps
                                                                            1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                            Truncated human 312C2 protein from clone_A8 amino acid sequence.
                                              ó,
              Length 241;
                                               Indels
                                                                                                                                                                                                                      121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
               DB 22;
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              Score 979; DB 2:
Pred. No. 4e-70;
100.0%; Sco...
100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zlotnik A;
                                                                                                                                                                                                                                                                                                              AAW37840 standard; Protein; 228 AA
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96US-0689943.
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                                              Matches 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disorders.
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N-PSDB; AAV19154.
               Query Match
Best Local Similarity
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16-AUG-1996;
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Human; PRO; cardiant; antianglogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen ME;
ark MR, Marsters SA;
        85
CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
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                                                                                    AAB50982 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                             990S-0146222.
99WO-US20111.
99WO-US28409.
99WO-US28565.
99WO-US28565.
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99US-0144758.
99US-0145698.
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2000WO-US08439
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                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                     Human PRO364 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni NF, Pitti RM,
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N-PSDB; AAC90566.
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24-FEB-2000;
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30-MAR-2000;
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                                                                                                   AAB50982;
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The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or anglogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, anglna, myocardial

Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic

Claim 71; Fig 8; 182pp; English.

disorders in a mammal

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infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or anglogenic disorder.
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                                                                                                                                                                    100.0%; Score 711; DB 22; 100.0%; Pred. No. 2.9e-50;
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AAB47054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                      166.177 "prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                        "leucine zipper pattern"
                                   'note- "N-myristoylation site"
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Pitti RM,
                                                          "N-myristoylation site"
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163..183
/note= "transmembrane domain"
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k MR, Marsters SA,
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/note= "N
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122..128
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receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psortasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermattis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all calmed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO364; human; glucocorticoid-induced tumor necrosis factor; recept hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNF human umbilitoal vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; GEC_2alpha; trauma; cancer; anglogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm; arreital restenosis; thrombophlebitis; tumor anglogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
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Pred. No. 2.9e-50;
Mismatches 0;
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tive 0; 1
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N-PSDB; AAC85433.
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30-NOV-1999; 01-DEC-1999; 09-DEC-1999;

99WO-US21547

2000WO-US00219 2000WO-US00376

05-JAN-2000; 06-JAN-2000; 11-FEB-2000;

20-DEC-1999

99WO-US30911

2000WO-US04342

18-FEB-2000; 18-FEB-2000; 22-FEB-2000; 24-FEB-2000; 15-MAR-2000;

2000WO-US04414 2000WO-US06884 2000WO-US07377 2000WO-US08439 2000WO-US13705 2000WO-US14042

20-MAR-2000; 30-MAR-2000;

21-MAR-2000 17-MAY-2000

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receptor (TNRFN) family of polypeptides. The profile included to a sequence was isolated from a library of cDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF_2alpha), characterized by the presence of an elevated level of PGF_2alpha), characterized by the presence of an elevated level of PGF_2alpha), characterized by the presence of an elevated level of PGF_2alpha), characterized by the presence of an elevated level of an antibody that binds PRO364 or PRO175 is useful for inhibiting amplogenessis induced disorder. PRO364 or PRO175 in a human suffering from a tumor or a retinal vascular-related drug targeting or as therapeutic targets for the vascular-related drug targeting or as therapeutic targets for the vascular-related drug targeting or as therapeutic targets for the vascular-related drug targeting or as therapeutic targets for the vasculatives, Reynaud's disease, aneurysms, arterial restenosis,
                              Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                     endothelial, anglogenic or anglostatic agent for the treatment of a cardiovascular, endothelial, anglogenic or anglostatic disorder. The PRO364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.
                                                                                                                                                                                          This sequence represents PRO364 polypeptide, which is a human gluco-corticoid-induced tumor necrosis factor receptor (hGITR). The corresponding ligand (hGITRL), PRO175, is given in AAB47056. PRO364 and PRO175 may be used in a mixture with a cardiovascular,
                                                                                                                             Claim 1; Fig 1; 76pp; English
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AL; CK;

odowski PJ, Gurney Tumas D, Watanabe

Godowski PJ,

Shelton DL, Goddard A,

AJ, Baker KP, Chan B, Henzel W, Kabakoff RC,

Ashkenazi AJ, Baker KP, (GETH ) GENENTECH INC.

Hebert C, Wood WI;

WPI; 2001-025253/03. N-PSDB; AAC91469.

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                                    Gaps
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                                                        1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                    61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
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           Length 241;
                                   Indels
           Score 711; DB 22;
Pred. No. 2.9e-50;
100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                      Best Local Similarity 100:
Matches 114; Conservative
           Query Match
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The present sequence is one of thirty three novel PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, didopathic inflammatory myopathies, Signen's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain Barre syndrome, and chronic

Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

Claim 58; Fig 18; 218pp; English.

inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and utricaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis

and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.

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Human; PRO; antiinflammatory; dermatological; antiarthritic; antihhumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidiabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.
                         AAB50910 standard; Protein; 241 AA
                                                                   (first entry)
                                                                                                  Human PRO364 protein.
                                                                                                                                                                                                                        WO200073452-A2.
                                                                         21-MAR-2001
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RESULT 1
AAB50910
ID AAB5
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02-JUN-2000; 2000WO-US15264.

07-DEC-2000.

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1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60

CITCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                         Human tumour necrosis factor receptor-like protein TR11 mutein.
                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency; autoimmune disease; rheumatoid arthritis;
immunosuppressive; antirheumatic; antiarthritic; haemostatic;
dermatological; antiinflammatory; therapy; diagnosis; mutein;
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                                                                      AAY95895 standard; Protein; 241 AA.
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99US-0144076.
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                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N1 J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200050459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               TR11; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-1999;
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16-JUL-1999;
                                                                                                                                                                                                                   20-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
                                                                                                                                            AAY95895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant.
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   RESULT
AAY95895
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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenesis and cardiovascularisation, modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerber H, Hillan KJ, Godda
Kuo SS, Paoni NF, Smith V;
Human PRO364 protein sequence SEQ ID NO:117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara N,
Klein RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood WI;
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                                                                               AAB24409 standard; Protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0115554
99WO-US05028
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Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US20594
                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-412154/35.
N-PSDB; AAA77604.
                                                                                                                                                                                                                                                                                          WO200032221-A2.
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                                                                                                                                                                                                                                                                Homo sapiens.
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Watanabe CK,
                                                                                                                                      07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999;
                                                                                                                                                                                                                                                                                                                       08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        L2-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1999
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                                                                                                            AAB24409;
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Gaps

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Indels

100.0%; Score 711; DB 21; 100.0%; Pred. No. 2.9e-50; ive 0; Mismatches 0;

Best Local Similarity 100. Matches 114; Conservative

Query Match

Length 241;

1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60

26

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30-NOV-1999;
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB20115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Peptide
                                                                                          Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                            PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                 Gaps
                                                                                                             1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Prokaryotic membrane lipoprotein lipid attachment site"
                                                              Length 241;
                                                                                 Indels
                                                              Score 711; DB 21;
Pred. No. 2.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                  26..241
/label- Mature_PRO364_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label- Transmembrane_domain
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                            1..25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                     AAY71467 standard; Protein; 241 AA
                                                             100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .150
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                                                                                 Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..124
                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                            protein.
                                                              Query Match
Best Local Similarity
                                     241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200032778-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                            Human PRO364
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                                                                                                                                                                                                                                          08-NOV-2000
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                                                                                                                                                                                                                        AAY71467;
                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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The present sequence is the human PRO364 protein, encoded by the cDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue oDNA library, identified using probes based on the consensus sequence DNA4825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNRR) family of polypeptides. PRO364 sequence also shows homology to members of the TNRR family and mouse GITR protein. This clone is assigned the ATCR deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                        for
or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC
                                                                                                                                                                                                                                                                                          New composition useful for inhibiting neoplastic cell growth and treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
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                                                                                                                                                                               Σ
                                                                                                                                                                               Napier
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                                                                                                                                                                             Hillan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                               Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20115 standard; Protein; 241
                                                                                                                                                                                                                                                                                                                                                                                 Claim 31; Fig 4; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunostimulant PRO364.
98WO-US25108.
98US-0112850.
98US-0113296.
99US-0144758.
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Matches 114; Conservative
                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                               Goddard A,
                                                                                                                                                                                                                          WPI; 2000-412325/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AA;
                                                                                                                                                                                                                                                                                                                                        their antagonists
                                                                                                                                                                                                                                               N-PSDB; AAD01240
  01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                           26-JUL-1999;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or
                                                                                                                                                                                                              PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                              /note= "signal peptide"
26..241
/note= "mature protein"
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162..180
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                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..25
                                                                                                                                                                      Human TNF receptor homologue PRO364
                                         AAY06605 standard; Protein; 241 AA.
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                                                                                                                             (first entry)
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Pitti RM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-494296/41.
N-PSDB; AAX87670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-1999
                                                                                   AAY06605;
                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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9
                     AAY06605
RESULT
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241 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to methods for stimulating or inhibiting anglogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerritsen ME;
Paoni NF, Pitti RM;
                                        Gaps
                                                                                               26 grptggpgggpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 85
                                                                          QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                                                                                                                                                                                                                               Cardiovascular; endothelial; angiogenic disorder; PR0179; PR0238; PR0364; PR0844; PR0846; PR01760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885; PR0887;
                                                                                                                                              61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                      ö
 Length 241;
                                      Indels
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Query Match 100.0%; Score 711; DB 20; Best Local Similarity 100.0%; Pred. No. 2.9e-50; Matches 114; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..25
/label= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                AAB27651 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 71; F1g 6; 181pp; English.
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99WO-US28409
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99US-0145698
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99WO-US21090
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2000WO-US04342
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                                                                                                                                                                                                                                                                                                                                                       26-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                           Human protein PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-611444/58.
N-PSDB; AAA99903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                    AAB27651;
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PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO867. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothelial or angiogenic disorders. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antialsthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic solerosis; sarcoidosis; didopathic inflammatory myopathy; systemic solerosis; sarcoidosis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whitpple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; ilmnune-mediated skin disease; allergic disease; ilmnune-mediated skin disease; allergic disease; antipuncation associated disease;
                                                                                                                                                                  Gaps
                                                                                                                                                                                           QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                       85
                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                   61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                                                                                                                  Length 241;
                                                                                                                                                               Indels
                                                                                                                                 Score 711; DB 21;
Pred. No. 2.9e-50;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    graft rejection; graft-versus-host-disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO364 protein UNQ319 SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                       AAB33431 standard; Protein; 241 AA
                                                                                                                                 100.0%;
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99WO-US08615.
99US-0131445.
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99US-0123957
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99WO-US21090
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                                                                                                                              Query Match
Best Local Similarity 100.
Matches 114; Conservative
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                                                                                         241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                 Henzel W;
V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC5837 to AAC58578 represent PCR primers and hybridisation probes in the isolation of human PRO sequences. AAC58579 to AAC58642 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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an J, Pennica D,
Watanabe CK, Woo
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                                                                 99WO-US28313
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99WO-US28565
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Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
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N-PSDB; AAC58596.
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18-FEB-2000; 2
18-FEB-2000; 2
22-FEB-2000; 3
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06-JAN-2000;
06-JAN-2000;
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30-DEC-1999;
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Sequence
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                                                                                                                                                                                                                                                                                       Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.
                                                                                                                                                                                                                                                                                                       Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorges syndrome; HV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
                                                                                                              Gaps
                                                                                                                                               85
                                                                                                                               1 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                          arthritis, systemic lupus erythematosus, thrombocytopenia purpura or igh nephropathy. The polypeptides, polynuclectides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
                                                                                                                                                                             ;
                                                                                                                                                                  61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tumour necrosis factor receptor-like polypeptides used to,
                                                                                           Length 234;
                                                                                                             Indels
                                                                                          100.0%; Score 711; DB 21;
100.0%; Pred. No. 2.9e-50;
ilve 0; Mismatches 0;
                                             agonist/antagonist compounds are also provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                        163..179
/note= "Transmembrane domain"
180..234
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/note= "Extracellular domain"
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/label- Signal_peptide
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                                                                                                                                                                                                                                AAY52158 standard; Protein; 234 AA.
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/label- TR11
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                                                                                                                                                                                                                                                                    (first entry)
                                                                                                             Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                       inflammatory condition.
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N-PSDB; AAZ37762.
                                                                                                     Similarity
                                                               234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-OCT-1998;
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                                                                Sequence
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Best Local
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This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRI) receptor). The invention relates to TRI] and two splice variants TRI] receptor). The invention relates to TRI] and two splice variants TRI] and TRISV2. The nucleotide sequences were determined by sequencing cloned conva AA23765-23766. The TRI] receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GITR).

CRII], TRISVA and TRISVA polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/andsponists. The polypeptides, agonists or antagonists can be used for treating immune deficiency disorders, blogerge syndrome, HIV infection, severe combined immunodeficiency conjugation adisease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can be used to treat heart attacks, strokes, Addison's disease, had sorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, had sorders or wounds resulting gravis, Stiff-Man syndrome, insulin dependent disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, insulin dependent disease, inflammatory conditions, ischaemia-reportion or graft versus host disease, inflammatory conditions, ischaemia-reportion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, creaming age, disease, or protect tissue damaged by congenite plastic sugatory, fibrosis, reperfusion injury, peripheral energery, inflammatory syndrome, syndrome, surgery, including cometic plastic surgery, including consentic plastic surgery, including syndrome and syndrome. Syndrome and Shapase, syndrome and shapase, energery includes and syndrome
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amino acid sequence of the human tumour necrosis factor
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100.0%; Pred. No. 2.9e-50;
tive 0; Mismatches 0;
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Matches 114; Conservative 0;
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The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA library. This sequence is expressed in cardiovascular and haematopoletic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, dermatopoletic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, dermatological, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic, and ophthalmological, antidiscrement, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease
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                                                                                                                                                           'note" "Potential phosphorylation site"
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140
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/label= Signature_sequence
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157.175
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165..186
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N-PSDB; AAZ49948.
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                                                                   1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                    20 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 79
                                    ;
   Length 235;
                                    Indels
Score 711; DB 21;
Pred. No. 2.9e-50;
Mismatches 0;
100.0%; Silarity 100.0%; P. Conservative 0;
                  Similarity
Query Match
Best Local Sim:
Matches 114;
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CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114

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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoletic cells; lymphoid cell; autoimmune disorders.
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   cttcrhhpcppgggygsggkfsfgfgcidcasgtfsggheghckpwtdctgfgf 133
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                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of the human 312C2 T cell protein.
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Matches 114; Conservative
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Human PRO364 prote Human PRO364 prote Human anglogenesis Polypeptide encode PRO364-related EST

Human immunostimul

TRIISV2 amino acid Human 312C2 protei Human tumour necro

Human tumour necro

TRIISVI amino acid Mouse glucocortico Mouse glucocortico Amino acid sequenc Mouse glucocortico Murine TMF-alpha f Skin cell protein, Mouse type-II memb Mouse type-II memb

Murine 4-1BB polyp Mouse receptor 4-1 Mouse 4-1BB recept Murine CD137 prote

Plasmid pDC406/0X4 OX40/Fc mutein. C

rotal number of

Searched:

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Ox40 protein. U 41bb protein. U 4-1BB receptor p

Human 4-1BB polype Human 4-1BB recept

Isolated 312C2 T cell gene - used to develop products for treating

Zlotnik A;

Gorman DM, Randall TD, (SCHE ) SCHERING CORP.

WPI; 1998-159534/14 N-PSDB; AAV19154.

Human protein PR03 Human PR0364 prote Human tumour necro Human PR0364 prote Human PR0364 prote

Human TNF receptor

Score

Result Š.

Mouse Receptor 4-1 44-1BB receptor pr

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   0;
                                            This is the amino acid sequence of the truncated human 312C2 T cell protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antiger specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
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                                                                                                                                                                                                                                                20 grptggpgggpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 79
  e.g. cancers, auto-immune disorders, transplantation rejection and
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                                                                                                                                                                                                                                                                            61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                                                                                                                                      80 cttcrhhpcppgqgvqsqgkfsfgfqcidcasgtfsggheghckpwtdctqfgf 133
                                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficiency; autoimmune disease; rheumatoid arthritis;
immunosuppressive; antirheumatic; antiarthritic; haemostatic;
dermatological; antiinflammatory; therapy; diagnosis.
                                                                                                                                                                                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                            IR11; human; tumour necrosis factor receptor-like protein;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour necrosis factor receptor-like protein TR11.
                                                                                                                                                                                               Score 711; DB 19;
Pred. No. 2.8e-50;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "conserved domain CD-III"
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ote= "conserved domain CD-IV"
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/label= Intracellular domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-glycosylated"
                             Disclosure; Pages 61-62; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26..234
/label- Mature_protein
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                                                                                                                                                                                                                                                                                                                                                AA.
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100.0%;
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Best Local Similarity 100.
Matches 114; Conservative
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153..16
         other T cell disorders
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                                                                                                                                                                   228 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo saptens
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The present sequence is that of human tumour necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity om murine glucocorticoid induced tumour necrosis actor receptor family-related gene. The sequence was deduced from a cobn clone (see AAA50304) discovered in a Thelper cell library.

TR11 activated NF-kappaB through a TRAF2-mediated mechanism.

Expression is activation-inducible. The TR11 ligand is constitutively expressed in an endothelial cell line. This suggests that TR11 and its ligand may be involved in activated T-cell trafficking. The invention provides TR11, TR15V1 and TR118V2 nucleic acids are AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR118V1 and/or TR15V2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable.immunodeficiency especially common variable.immunodeficiency especially common variable. Immunodeficiency especially common variable. Immunodeficiency especially common variable. TR15V2 cell cells and recombined immunodeficiency activity hyper IgM. TR11, TR118V1 and/or TR118V2 antagonists (e.g. antibodies) are used to treat, prevent, prognose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with
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"conserved domain CD-VII"
                                                         "conserved domain CD-IX"
                                                                                                                                                                                                                                                                                                                                                                                                                     99..107
/note= "epitope-bearing region"
                                                                                                                                                                     "epitope-bearing region"
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                                                                                                               "conserved domain CD-X"
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143..151
^note= "epitope-bearing
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te= "epitope-bearing
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99US-0134172.
99US-0144076.
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                                                                                                                  'note=
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'note=
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13-MAY-1999;
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tumour necrosis factor receptor-like polypeptides used to, e.g.
                                                                                                     treat Digeorge syndrome
                      2000-061922/05
                                         N-PSDB; AAZ37762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor-like protein; TR11; TR11SV1; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV; SCID; Miskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
(SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose
                                                                            arthritis, systemic lupus erythematosus, thrombocytopenia purpura or 1gA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicallular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
inflammatory condition.
                                                                                                                                                                                                                                                  Pred. No. 1.8e-60;
Mismatches
                                                              and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Extracellular domain"
163..179
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100.0%; Pred. No. 1
:ive 0; Mismatches
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/label- TR11
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Matches 137; Conserv
                                                                                                                                                                                                                         234 AA;
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receptor-like protein (TRI) receptor). The invention relates to TRI and two splice variants TRISVI and TRISV2. The invention relates to TRI and two splice variants TRISVI and TRISV2. The nucleotide sequences were determined by sequencing cloned cobasts. TRI receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GTR). TRISVI and TRISV2 polypeptides may be involved in the requiation. TRISVI and TRISV2 polypeptides may be involved in the requiation, and ultimately, cell death. They can be used for screening for agonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating adisease state associated minumodeficiency disorders, bigeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood cagulation disorders, phood platelet disorders or wounds resulting from traume or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, hemmolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.
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                                                                              This is the amino acid sequence of the human tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; molecule associated with cell proliferation; MACP-5;
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Pred. No. 1.8e-60;
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100.0%; Pre-
0;
Claim 14; Fig 1; 167pp; English.
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Best Local Similarity
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Gaps

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0; Mismatches Score 841;

Length 235; Indels

Score 841; DB 21; Pred. No. 1.8e-60;

100.0%; ilarity 100.0%; Conservative 0

Query Match Best Local Similarity Matches 137; Conserv

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61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120 

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Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-flammatory; antipsoriatic; anti-HIV; antiaschmatic; andimatic, antiaschmatic, andimatic; dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell prollferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; crohn's disease; amyloidosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides and polynucleotides useful for treating and detecting ce proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease
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                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US16637.
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N-PSDB; AAZ49948.
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Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antiqen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autolimmune disorders.

/\*tag= a /product= "human 312C2 protein"

WO9806842-A1

19-FEB-1998

97WO-US13931 96US-0027901.

14-AUG-1997; 07-OCT-1996; 16-AUG-1996;

Location/Qualifiers

sapiens

Ношо

Key

Amino acid sequence of the human 312C2 T cell protein.

(first entry)

28-JUL-1998

AAW37839;

AAW37839 standard; Protein; 241

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AAW37839

121 NKTHNAVCVPGSPPAEP 137

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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physicology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells

    used to develop products for treating,
    lisorders, transplantation rejection and

                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. cancers, auto-immune disorders, other T cell disorders
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235 AA;

Sequence

anaemia

Zlotnik A;

Randall TD,

Gorman DM,

cel1

WPI; 1998-159534/14.

N-PSDB; AAV19153

(SCHE ) SCHERING CORP.

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

Human PRO364 prote Human PRO364 prote Human anglogenesis Human 11022 protei Human tumour necro TRIISV2 amino acid

immunostimu]

Polypeptide encode PRO364-related EST Human tumour necro TR11SV1 amino acid

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Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antiqen-specific T cell proliferation; cytokine production by T-cell;
apoptosis; cancer; heamatopoietic cells; lymphoid cell;
autolimmune disorders.
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                                                     AAY95881
AAY52160
AAB47055
                                                                                                                            AAW49016
AAW37838
AAW49017
AAY76013
AAB55952
AAR81881
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AAR76996
AAR70977
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AAW31759
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AAY52159
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AAW49018
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 96US-0027901
96US-0689943
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Gorman DM, Randall TD,
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N-PSDB; AAV19154.
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16-AUG-1996;
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AAW37840;
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RESULT
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Amino acid sequenc
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                                                            ; Search time 126.12 Seconds (without alignments) 65.854 Million cell updates/sec
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                                                                                                                    QRPTGGPGCGPGRLLLGTGT......FPGNKTHNAVCVPGSPPAEP 137
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| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                412676 segs, 60623988 residues
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841
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Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
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AAY52158
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AAW37839
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AAB33431
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Gapop 10.0 , Gapext 0.5
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Match Length
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Score

Result ş 841 841 841 841 841 841

2642978611

Mouse type II memb Mouse Ox40 extrace Plasmid pbc406/0x4 Ox40/Fc mutein. C Deduced sequence e H4-1BB receptor pr Human 4-1BB recept Human CD137 protei Human CD137 protei Human receptor pr

A novel human h4-1 Human h4-1BBSV rec ACT-4 cell surface ACT-4-h-1 receptor

Human 312C2 protein Mouse glucocortico Mouse glucocortico Amino acid sequenc Mouse glucocortico Murine TNF-alpha f Skin cell protein,

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                                                             protein from clone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Bngagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. Iymphoid cells which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                80 cttcrhhpcppgggyqsggkfsfgfgcidcasgtfsggheghckpwtdctqfgfltvfpg 139
                                                                                                                                                                                                                                                                                      CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
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                                                                                                                                                                                                                                                           20 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 79
                                                    This is the amino acid sequence of the truncated human 312C2 T cell
\varepsilon.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
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                                                                                                                                                                                                         Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; dmmunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.
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100.0%; Pred. No. 1.8e-60;
iive 0; Mismatches 0;
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/note= "conserved domain CD-IV"
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26..162
/label- Extracellular_domain
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/label= Transmembrane_domain
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/label- Intracellular domain
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                                Disclosure; Pages 61-62; 71pp; English
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/label- Signal_peptide
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Matches 137; Conservative
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factor receptor family related gene. The sequence was deduced from a CDNA clone (see AAA50304) discovered in a T-helper cell library. TRIL activated NT-Kappab through a TRAF2-mediated mechanism. Expression is activation-inducible. The FRIL ligand is constitutively expressed in an endothelial cell line. This suggests that TRIL and its ligand may be involved in activated T-cell trafficking. The invention provides TRIL, TRIISVI and TRILSVI nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAY56379-81), as well as vectors, host cells and recombinant methods for their production. TRIL, TRIISVI and/or TRIISVI polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency. X-linked agammaglobulinemia, severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of human tumour necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis
                                                                                                                                     "conserved domain CD-VII"
                                                                                 "conserved domain CD-VI"
                                                                                                                                                                                                                                                                                                                                         /note= "epitope-bearing region"
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.134
ce= "conserved domain CD-V"
                                                                                                                                                                                                                                                                                        /note= "epitope-bearing region"
                                                                                                                                                                                                                                       /note= "conserved domain CD-X"
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e= "epitope-bearing
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                                                                                                                                                                                        "conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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                                                                                 /note= "c
176..186
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204..209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA50304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-1999;
13-MAY-1999;
16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
                                                                                                                             AL;
CK;
                                                                                                                                                                                                                                                                                                                                                                                                   The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal diseases (amyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain Barre syndrome, and chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypersensitivity pneumonitis), transplantation associated diseases
                                                                                                                                                                                                                                                       Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                             , Gurney Watanabe (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 85
                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of thirty three novel PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                             ЪЈ,
                                                                                                                                                  Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           including graft rejection and graft-versus-host diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                             Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 841; DB 22;
                                                                                                                           Goddard A, G
Shelton DL,
                                                                                                                             KP, Chan B,
Kabakoff RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB50982 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                    Claim 58; Fig 18; 218pp; English.
                2000WO-US08439.
2000WO-US13705.
2000WO-US07532
                                                      2000WO-US14042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                             N, Baker KP,
Henzel W, Ka
                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                   WPI; 2001-025253/03.
N-PSDB; AAC91469.
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Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AA;
                                                                                                                           Ashkenazi AJ,
21-MAR-2000;
                30-MAR-2000;
17-MAY-2000;
                                                      22-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, amigna, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating
            Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
                          vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; angiogenic disorder; cancer; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seventeen nucleic acids encoding PRO polypeptides which are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mark MR, Marsters SA;
1, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and treatment of cardiovascular, endothelial or angiogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen ME;
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Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 841; DB 22;
Pred. No. 1.9e-60;
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100.0%;
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99WO-US20111.
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99WO-US28409.
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99WO-US30095.
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2000WO-US05004.
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2000WO-US06319.
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99US-0141037
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99US-0145698.
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Best Local Similarity 100.0
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski PJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A, Godowski Daoni NF, Pitti RM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angiogenic disorder.
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                                                                                                                                 WO200073445-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ,
                                                                      wound healing
                                                                                                     Homo sapiens
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30-NOV-1999;
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01-SEP-1999;
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16-DEC-1999;
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23-JUN-1999
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Human PRO364 protein.

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15-MAR-2000; 2000WO-US06884
                     20-JUL-1999;
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Matches
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                                            Gaps
                                                                       85
                                                        1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                0;
                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallargic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "prokaryotic membrane lipoprotein lipid
                           Length 241;
                                                                                                                                                                                                                            PRO364; UNQ319; human; immune disease; autoimmune disease;
                                          Indels
                            ; DB 21;
1.9e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                               'note= "transmembrane domain"
                                          Mismatches
                           Score 841;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment site"
                                                                                                                                                                                                                                                                                            1..25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                         26..241
/label= Mature_protein
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                  AAB20115 standard; Protein; 241 AA.
                                          0;
                            100.0%;
                                                                                                                                                                                                              Human immunostimulant PRO364.
                                   100.0%;
                                                                                                                          121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                               (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          .128
                                                                                                                                                                                                                                                                                                                                                                                                                                         ..162
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25..31
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                                   Best Local Similarity
Matches 137; Conserv
       241 AA;
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                                                                                                                                                                                                                                                                       Homo sapiens
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       Sequence
                                                                                                                                                                                 AAB20115;
                            Query Match
                                                                                                                                                                                                                                                                                           Peptide
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are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune is exponse, or increasing the proliferation of T-lymphocytes in a mammal in response to an artigen. Claimed compositions comprising a PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthric pathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune tromatory chromosycopaenia, thyroiditis, diabetes mellitus, immune-mediated remained disease, demyelinated diseases (such as multiple sclerosis),
                                                                                                                                                       Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CTTCRHHPCPPGOGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and pooriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                         New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is that of novel human immunomodulator PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNQ19), as deduced from cDNA (see AAF30057) isolated from a small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence homology to mouse GITR protein and may be its human counterpart. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC
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100.0%; Pred. No. 1.9e-60;
ive 0; Mismatches 0;
                                                                                                                                                       Goddard A,
Pitti RM,
                                                                                                                                                       s,
SA,
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                                                                                                                                                       KP, Fong
Marsters
99US-0144758
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                                                                                                                                                           Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                              Mark MR,
                                                                                                                                                                                                                                                                                                              2001-103149/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Les 137; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AA;
                                                                                                                                                                                                                                                                                                          WPI; 2001-103149
N-PSDB; AAF30057
                                                                                                                                                           Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using PRO364
                                                                                                                                                                                          ΚЈ,
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146 nkthnavcvpgsppaep 162

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Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                               PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atheroscierosis; hypertension; inflammatory vascularides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor (TWRR) family of polypeptides. The PROJTS cONA sequence was isolated from a library of CDNA fragments derived from human umbilical wein endothelial cells (HUVEC). Administering an effective amount of PRO364 or PROJTS or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of BGF_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PROJTS is useful for inhibiting angiogenesis induced by PRO364 or PROJTS in a human suffering from a tumor or a retinal disorder. PRO364 or PROJTS or their antagonists, are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corticoid-induced tumor necrosis factor receptor (hGTRR). The corresponding ligand (hGTRRL), PR0175, is given in AAB47056. PR0364 and PR0175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a cardiovascular, endothelial, anglogenic or angiostatic disorder. The PR0364 cDMs sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents PRO364 polypeptide, which is a human gluco-
                                                                                                                                                                                                                                                                                                                                                                lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Potential signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                     AAB47054 standard; Protein; 241 AA.
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                                                                                                                       (first entry)
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                                                                                                                   08-MAY-2001
                                                                                                                                                              Human PRO364
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                              AAB47054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                      AAB47054
RESULT
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vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.
                                                                                                                                                                                                                                                                    CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
                                                                                                                                                                           Gaps
                                                                                                                                                                                                   QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                           grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 85
                                                                                                                                                                         0;
                                                                                                                                               Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; antiinflammatory; dermatological; antiarthritic;
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiasthmatic; immune related disorder; disease; autoimmune disease; allergy.
                                                                                                                                            100.0%; Score 841; DB 22;
100.0%; Pred. No. 1.9e-60;
ive 0; Mismatches 0;
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2000WO-US03565.
2000WO-US04341.
2000WO-US04342.
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99WO-US21090.
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2000WO-US00219.
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2000WO-US04914
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2000WO-US07377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                           Best Local Similarity 100.
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO364 protein.
                                                                                                         241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiallergic;
hepatobiliary
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20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001
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                                                                                                          Seguence
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                                                                                                                                                Query Match
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anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, limmune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                             61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                            26 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 85
                                                                                                                                                                                                                                                                                                                           1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour necrosis factor receptor-like protein TR11 mutein.
                                                                                                                                                                                                                                                         Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                         Score 841; DB 21;
Pred. No. 1.9e-60;
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100.0%;
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99US-0134172.
99US-0144076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-2000; 2000WO-US04572.
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                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                         241 AA;
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16-JUL-1999;
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                                                                                                                                                                                                                                                                                          Matches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
          The process sequence is that of a main included included the showing identity to murine glucocorticoid induced tumour necrosis factor receptor family related gene. The invention provides highly conserved TRI1, TRI1SVI and TRI1SV2 proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TRI1, TRI1SVI and/or TRI1SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                                arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 241;
                                                                                                                                                                                                                                                                                 vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 841; DB 21; 100.0%; Pred. No. 1.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                 agonist/antagonist compounds are also provided.
sequence is that of human tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO364 protein sequence SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB24409 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0123957.
99US-0131445.
99US-0134287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0112850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US12252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1998;
12-JAN-1999;
08-MAR-1999;
12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1999;
   present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1999
                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB24409;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenic disorder in mammals by and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosciensis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and associated with decreased PRO expression. AAA77510 to AAA77721 and the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system;
                                                                                                                       Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                            Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or
                                                                                                                     Hillan KJ, Godda
oni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 241;
                                                                                                                       Gerber H, Hillan I
Kuo SS, Paoni NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 841; DB 21;
Pred. No. 1.9e-60;
; Mismatches 0;
                                                                                                                     Ferrara N,
Klein RD, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71467 standard; Protein; 241 AA
                                                                                                                                                                                                                                     Claim 72; Fig 44; 315pp; English.
                                                                                                                                                                                                                  angiogenic disorders in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                               99WO-US21090.
99WO-US21547.
99WO-US23089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                       99WO-US20944.
99US-0144758
         99US-0145698
                   99WO-US20111
                            99WO-US20594
                                                                               99US-0162506
                                                                                                                                 Gurney AL, K
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                       Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO364 protein.
                                                                                                                                                              2000-412154/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               241 AA;
                                                                                                                                                                        N-PSDB; AAA77604
                                                                                                                      Ashkenazi AJ,
                                                                                                                                 Godowski PJ,
Watanabe CK,
       26-JUL-1999;
01-SEP-1999;
                           08-SEP-1999;
13-SEP-1999;
                                               15-SEP-1999;
15-SEP-1999;
                                                                   05-OCT-1999
                                                                               29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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clone, designated as DNA4736-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA41825, relative to the Incyte expressed sequence tag (BST) 3003460. This EST has homology to tumour necrosis factor receptor (INFR) family of polypeptides. PR0364 sequence also shows homology to members of the TNFR family and mouse GITR protein.

This clone is assigned the ATCC deposit No: 209436. PR0364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PR0565, PR0364 and PR0344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the human PRO364 protein, encoded by the CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    composition useful for inhibiting neoplastic cell growth and for ting cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146..150 - .
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                        'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-myristoylation site"
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                                                                                                                                                                                                                        'note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                        /label= Mature_PRO364_protein
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                                                                                                                                                                                                                                                                                               25..31
/note= "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "N-myristoylation
                                                                                                                                                                       /label= Signal_peptide
                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 31; Fig 4; 108pp; English.
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98US-0112850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118..124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-412325/35.
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                                                                         Homo sapiens
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                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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241 AA;
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12-MAR-1999;
02-JUN-1999;
26-JUL-1999;
01-SEP-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-2001
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                                                                                                                                                                                                                                                                                                                                      Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB27651;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                               0;
                                                                                                                                                                                                                                                              61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLIVFPG 120
                                                                                                                               Gaps
                                                                                                                                                                                      26 qrptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc 85
                                                                                                                                                                   1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents human PR0364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the
which affect immunological responses, e.g. autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulating apoptosis and NF-KB activation and proinflammatory or
                                                                                                                                 .
0
                                                                                           Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor homologue - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SA;
                                                                                           Score 841; DB 19;
Pred. No. 1.9e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain"
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mature protein"
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-glycosylated"
162..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TNF receptor homologue PRO364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY06605 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Fig 2A; 104pp; English.
                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US02642.
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                                                                                                                                                                                                                                                                                                                   121 NKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                                                                                                                                                                     146 nkthnavcvpgsppaep 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard A,
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26..241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-494296/41.
N-PSDB; AAX87670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood WI;
                                                                                                            Best Local Similarity
                                    241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9940196-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-1999;
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                                                                                                                             Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pitti RM,
                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY06605;
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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61 CITCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                      are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells (claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin Fc region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic inhibitors.
recombinant production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast host cells, are provided. Claimed polypeptides comperise amino acids 1.241, 1.x, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respdies 157-167 of PRO364. PRO364 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ORPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 841; DB 20;
100.0%; Pred. No. 1.9e-60;
iive 0; Mismatches 0;
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1..25
/label= "Signal peptide"
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99WS-0123957.
99WO-US12252.
99WS-0144768.
99WO-US20111.
99WO-US21090.
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Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein PRO364.
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graft rejection; graft-versus-host-disease.
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                                                                                                                                                                          Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
                                                                                                                                                                                                                                                The present invention relates to methods for stimulating or inhibiting angiogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proceins, PRO179, PRO818, PRO814, PRO816, PRO176, PRO205, PRO311, PRO313, PRO817, PRO819, PRO817, PRO819, PRO819, PRO882 or PRO887. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothalial or angiogenic disorders. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; noctropic; neuroprofective; antianemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; arrcoidosis; didopathic inflammatory myopathy; systemic sclerosis; arrcoidosis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; demyelinating disease; alutoimene disease; immune-mediated skin disease; allergic disease; immune-mediated skin disease; allergic disease; immunelogical disease; transplantation associated disease;
                                                                                                 Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 grptggpgcgpgrlllgtgtdarccrvhttrccrdypgeeccsewdcmcvqpefhcgdpc
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                                                                                     Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 841; DB 21; Length 241; 100.0%; Pred. No. 1.9e-60;
                                                                                                  Paoni NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                     Ferrara N, Gerber H,
llan KJ, Marsters SA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                Hillan KJ, P
PM, Wood WI;
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                                                                                                                                                                                                                            Claim 71; Fig 6; 181pp; English.
30-NOV-1999; 99WO-US28409.
02-DEC-1999; 99WO-US28565
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
                                                                                   Ashkenazi AJ, Baker KP, F
Goddard A, Gurney AL, Hil
Watanabe CK, Williams PM,
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                                                             (GETH ) GENENTECH INC
                                                                                                                                   WPI; 2000-611444/58.
N-PSDB; AAA99903.
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                                                                                                                                                                                                                                                                                                                                                                              241 AA;
                                                                                                 Goddard A, G
Watanabe CK,
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, sosteoarthritis, juvenile chronic arthritis, spoodyloarthropathies, systemic solerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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Yan M;
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D, Shelton E
Wood WI, Yar
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an J, Pennica I
Watanabe CK, V
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                                                                                                                                         99WO-USO5028.
99US-0123618.
99US-0123957.
99US-0125775.
99WS-0128849.
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99US-0144758.
99US-0145698.
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99US-0134287
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2000WO-US04341
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Tumas D,
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N-PSDB; AAC58596.
                                  40200053758-A2.
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Homo sapiens.
                                                                                                         32-MAR-2000;
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18-FEB-2000;
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22-FEB-2000;
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                                                                      14-SEP-2000
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Gaps

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Length 241; Indels

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New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                                                                     Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, M
                                                                                                                                                                                                                                                                Claim 69; Fig 54; 293pp; English.
                                                     99WO-US05028.
99US-0123957.
99US-0134287.
                                                                                                    99WO-US20111.
                                                                                       99US-0144758.
99US-0145698.
                                                                                                                                      99WO-US28313.
99WO-US28409.
                                        2000WO-US00219
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                                                                                 99US-0141037
                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                   Paoni NF, Pitti RM,
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             WO200053753-A2.
Homo sapiens.
                                        05-JAN-2000;
                          14-SEP-2000.
                                                                   14-MAY-1999
02-JUN-1999
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20-JUL-1999
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                                                                                                    01-SEP-1999;
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protein; thymus cell; spleen cell; T cell; cell; cell proliferation; cytckine production by T-cell; haematopoietic cells; lymphoid cell;
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                                                                                                                                                                                                 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                              1 MAOHGAMGAFRALCGLALLCALSLGORPTGGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
   Score 969; DB 22;
Pred. No. 1.3e-69;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Pages 61-62; 71pp; English.
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       100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen-specific T
apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human 312C2 T cell
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV19154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-0CT-1996;
16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-1998.
                                                                                   162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW37840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel human anglogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, agonists or antagonists of a PRO protein, agonists or antagonists of a PRO protein, and comprising a PRO protein, agonists or antagonists of a PRO protein, and comprising a PRO protein, agonists or antagonists of a PRO protein, and additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO anglogenic disorder to a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue, treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO angonist can antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial or angonist or antagonist thereof. PRO nucleic acids, PRO proteins, and methods of inhibiting or stimulating endothelial or angonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat catherosclerosis, osteoporosis, myocardial infarction, hypertension, disease, psoriasis, and issue an ilbraries to isolate constant and acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to scending PRO nucleic acids are additionally useful in the cecombinant production of PRO proteins, to analyse genetic disorders, and in an angonist and pense encoding PRO proteins, to analyse genetic disorders, and in an and in gene therapp. PRO nucleic acids are also be used to produce transgenic animals useful for the development and screening of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KP, Ferrara N, Gerber H, Goddard A;
AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
Watanabe CK, Williams PM, Wood WI;
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protein from crone_A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell axpansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal poliferation, e.g. cancertous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
This is the amino acid sequence of the truncated human 312C2 T cell
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241 AA;

Sequence

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                                                          Gaps
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0
Query Match 96.7%; Score 937; DB 19; Length 228; Best Local Similarity 100.0%; Pred. No. 4.3e-67; Matches 156; Conservative 0; Mismatches 0; Indels C
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PGEEC 66	1111
7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC (	#
CALSLGQRPTGGPGCGPGRL	
7 MGAFRALCGLALLC	

<sup>1</sup> mgafralcglallcals1ggrptggpgcgpgrlllgtgtdarccrvhttrccrdypgeec 60 Óγ g

q οy Search completed: September 4, 2001, 15:56:22 Job time: 339 sec

antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidiabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.

Human; PRO; antiinflammatory; dermatological; antiarthritic;

AA.

AAB50910 standard; Protein; 241

(first entry)

21-MAR-2001

AAB50910;

Human PRO364 protein.

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AAB50910
  RESULT
                                                                     This sequence represents PRO364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGITR). The cortesponding ligand (hGITRL), PRO175, is gluen in AAB47056.

RO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a cardiovascular, endothelial, angiogenic or angiostatic disorder. The RO364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNRR) family of polypeptides. The PRO175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical cells (HUVEC). Administering ne effective amount of RO364 or PRO175 or their antagonists is useful for treating cardiac characterized by the presence of an elevated level of PGE_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Characterized by the presence of an elevated level of PGE_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Characterized by RO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 is useful for inhibiting angiogenesis induced vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaudy andiogenesis arterial restenses; a recention of the protection of a theorypeans and the protection or a retinal vascular-related drug targeting or as therapeutic targets for the thrombothlebities and protection or a retinal angenty angiogenesis and protection or a retinal vascular-related drug targeting or as therapeutic targets for the transfer and protection or a retinal angentic preserved to a retinal angentic protection or a retinal angentic pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.
                                                                   162..180
/note= "Potential transmembrane domain"
/note= "Potential signal peptide"
                                           'note- "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                  11-JUL-2000; 2000WO-US18867
                                                                                                                                                                                                                                                                                99US-0143304
                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; F1g 1; 76pp;
                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-138257/14.
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                                                                                                                                       WO200103720-A2
                     Modified-site
                                                                                                                                                                                                                                                                                12-JUL-1999;
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                                                                     Domain
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99US-0144732. 99US-0144758. 99US-0146222. 99WO-US20111.

28-JUL-1999

15-SEP-1999 .5-SEP-1999

02-JUN-2000; 2000WO-US15264

WO200073452-A2.

07-DEC-2000

Homo sapiens.

99WO-US21547

99WO-US28313 99US-0170262 99WO-US30911

> 01-DEC-1999; 09-DEC-1999;

30-NOV-1999;

99WO-US21090

2000WO-US00376 2000WO-US03565

2000WO-US04341 2000WO-US04342 2000WO-US04414

2000WO-US04914 2000WO-US06884 2000WO-US07377

15-MAR-2000; 20-MAR-2000;

21-MAR-2000;

30-MAR-2000; 17-MAY-2000;

22-FEB-2000; 24-FEB-2000;

2000WO-US08439

2000WO-US13705

2000WO-US00219

05-JAN-2000; 11-FEB-2000;

06-JAN-2000; 18-FEB-2000; 18-FEB-2000;

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odowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                           Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of thirty three novel PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic
                                                                    Godowski PJ,
                                                                Goddard A, G
Shelton DL,
                                                                Baker KP, Chan B,
sel W, Kabakoff RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 58; Fig 18; 218pp; English.
(GETH ) GENENTECH INC
                                                                                                        Henzel W,
                                                                                                                                                                                                      WPI; 2001-025253/03.
N-PSDB; AAC91469.
                                                                    Ashkenazi AJ,
                                                                                                                                     Wood WI;
                                                                                                            Hebert
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Length 241; Indels

100.0%; Score 969; DB 22; 100.0%; Pred. No. 1.3e-69; ive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 162; Conservative

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9 0; Gaps

YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

61 61

121 121

SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162

MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD

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anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sciencosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary bilary cirrhosis, autoimmune chronic active hepatitis, primary bilary cirrhosis, aroundomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, cond phypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary fibrosis contuining graft rejection and graft-versus-host diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 969; DB 22; Length 241; 100.0%; Pred. No. 1.3e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
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2000WO-US04341.
2000WO-US04342.
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99US-0144758
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99WO-US28409
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99WO-US30095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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26-JUL-1999;
28-JUL-1999;
01-SEP-1999;
30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
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18-FEB-2000;
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Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                             SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoprosis; hypertension; mycardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancalianer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                   Seventeen nucleic acids encoding PRO polypeptides which are useful ir diagnosis and treatment of cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                              Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 241;
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                                                                                                                                                                         PJ, Gurney AL, Kuo SS, Mark MR, N
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 969; DB 22; Best Local Similarity 100.0%; Pred. No. 1.3e-69; Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                              Gerber H,
                                                                                                                                                              Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
                                                                                                                                                                                                                                                                                                                                                            Claim 71; Fig 8; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB53090 standard; Protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; transgenic animal
                2000WO-US05841.
                                                15-MAR-2000; 2000WO-US06884.
21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
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                                                                                                                                                                           Goddard A, Godowski PJ,
Paoni NF, Pitti RM, Wa
                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                          disorders in a mammal
                                                                                                                                                                                                                                 2001-025251/03.
                                                                                                                                                                                                                                                    N-PSDB; AAC90566
                                                                                                                                                            Ashkenazi AJ,
                                   10-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB53090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue.
                                      inappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                     9
                                                                                                                                                                                                        1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                      Length 241;
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                                                                                                                                                     Query Match 100.0%; Score 969; DB 21; Best Local Similarity 100.0%; Pred. No. 1.3e-69; Matches 162; Conservative 0; Mismatches 0;
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156..162
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'note= "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..25
/label= Signal_peptide
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO364 protein.
                                                                                                                         241 AA;
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Peptide
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clone, designated as DNA4736-1206. It is isolated from human small intestine tissue CDNA library, identified using probes based on the consensus sequence DNA4736-1206. It is isolated from human small consensus sequence DNA4825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNRR) family of polypeptides. PRO364 sequence also shows homology to members of the TNRR family and mouse GIRR protein.

This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO565, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood WI;
                                                                           /note= "Prokaryotic membrane lipoprotein lipid
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; Pred. No. 1.3e-69;
0; Mismatches 0;
                                                                                                                                                   /note= "Leucine zipper pattern"
                         Transmembrane_domain
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                                                                                                  attachment site"
171..193
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98US-0112850.
98US-0113296.
99US-0144758.
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Best Local Similarity 100.
Matches 162; Conservative
163..183
/label= T
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22-DEC-1998;
20-JUL-1999;
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antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; antialergic; immunostimulant.
                  human; immune disease; autoimmune disease;
     Human immunostimulant PRO364.
                                                                                                                                                                                                                                                                                         15-MAR-2000; 2000WO-US06884
                                                                                                                                                                                        .128
                                                                                                 163..183
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                                                       Homo sapiens
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                 PRO364;
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Gurney AL;
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Tumas D, Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of novel human immunomodulator PRO364 (UND19), as deduced from CDNA (see AAF30057) isolated from a small intestine library. PRO364 (26 kDa, pt 6.34) shows sequence homology to mouse GITR protein and may be its human counterpart. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB70108-20) including PRO364. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "prokaryotic membrane lipoprotein lipid
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Pitti RM,
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re- "N-myristoylation site"
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                                                                                                                                                                                 'note= "transmembrane domain"
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                              1..25
/label= Signal_peptide
                                                                                        26..241
/label- Mature_protein
Location/Qualifiers
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Marsters SA,
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a classic of a manimal, Stimulating of enimatoria of a classic of a mamimal, Stimulating of enimatoria of an antigen. Claimed compositions comprising a PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoria arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, juvenile chronic arthritis, autoimnume haemolytic anaemia, autoimnume chrombocytopaenia, thyroidiis, diabetes mellitus, immune-mediated renal disease, demyellnated diseases (such as multiple sclerosis), autoimnume chronic active hepatitis, primary billary cirrhosis, cartoimnume chronic active hepatitis, primary billary cirrhosis, cartoimnume chronic active hepatitis, primary billary cirrhosis, cartoimnume chronic active hepatitis, primary billary cirrhosis, cartoinnume chronic active hepatitis, solenosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive circh as bullous skin disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermaitits, food hypersensitivity and urticaria), immunologic claimed methods of diagnosing these disorders comprise detecting the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating the proliferation of T lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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  tissue of a mammal, stimulating or enhancing an immune
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100.0%; Pred. No. 1.3e-69;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spendyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; sloqern's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allargic disease; immune-mediated skin disease; allargic disease; immunological disease; transplantation associated disease;
                                                                                                                                    Gaps
                                                                                                                           61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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                                                                                    1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRD 60
                                                                                                                                                                                                                                                                                                              Human; immune related disease; diagnosis; antiinflammatory; cardian; dermatological; antifathritic; antiheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
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0
                                                Length 241;
                                                                  Indels
                                                                                                                                                                 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                           100.0%; Score 969; DB 21;
100.0%; Pred. No. 1.3e-69;
1ve 0; Mismatches 0;
sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          graft rejection; graft-versus-host-disease
                                                                                                                                                                                                                                                                                             Human PRO364 protein UNQ319 SEQ ID NO:92.
                                                                                                                                                                                                                                   AAB33431 standard; Protein; 241 AA
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99US-0131445.
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99US-0123957
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                                               Query Match 100.
Best Local Similarity 100.
Matches 162; Conservative
                   241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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20-APR-1999;
28-APR-1999;
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02-JUN-1999
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be used in the treatment of immune related diseases. The human PRO
proteins, anti-PRO antibodies, agonists and antagonists are useful for
treating and diagnosing immune related diseases. The human PRO
proteins, anti-PRO antibodies, agonists and antagonists are useful for
treating and diagnosing immune related disorders. The disorders are
calcuted from systemic lupus erthritis, rheumatorid arthritis,
systemic sclerosis, idopathic inflammatory myopathies, Sjogren's
systemic sclerosis, idopathic inflammatory myopathies, Sjogren's
systemic sclerosis, idopathic inflammatory myopathies, Sjogren's
systemic vasculitis, sarcoldosis, autoimmune haemolytic
anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
immune-mediated renal disease, demyelinating diseases of inflammatory
bowel disease, gluten-sensitive enteropethy and Whipple's disease,
autoimmune or immune-mediated skin diseases, allergic diseases,
including graft rejection and graft-versus-host-disease.
AACS8379 to AACS8378 represent PCR primers and hybridisation probes used
in the isolation of human PRO sequences, AACS8679 to AACS8642 and
AACS8371 to AACS8678 represent human PRO polynucleotide and protein
sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes sixty four human PRO proteins which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henzel W;
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D, Shelton DL, Smith V;
Wood WI, Yan M;
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100.0%; Pred. No. 1.3e-69;
tive 0; Mismatches 0;
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I, Pennica
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US04341.
2000WO-US04342.
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2000WO-US03565.
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Lu Y, Pan J,
                                                                                                                99WO-US28301
99WO-US28634
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Kabakoff RC, Lu Y, Pa
Stewart TA, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
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N-PSDB; AAC58596.
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                                                                                                                                                                                                                                                                                                                            05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
29-0CT-1999;
29-NOV-1999;
30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
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16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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18-FEB-2000;
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Best Local Simi
Matches 162;
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The present sequence is that of human tumour necrosis factor receptor-like protein TR11 (see also AAY95879), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The invention provides highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, sepecially common variable immunodeficiency, (SCID), Wiskott-Aidrich syndrome or X-linked immunodeficiency deficiency with hyper IgM. TR11SV1 and/or TR11SV1 and/or TR11SV2 and/or diagnose an autoimmune disease especially rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis systemic lupus erythematosus, thrombocytopenia purpura or iga nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the
                                                                                                                                                                                                   Human tumour necrosis factor receptor-like protein TR11 mutein.
                                                                                                                                                                                                                                 TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirhemmatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.
Disclosure; 294-295; 278pp; English.
                                                                                                       A
                                                                                                   AAY95895 standard; Protein; 241
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99US-0134172.
99US-0144076.
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                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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13-MAY-1999;
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                                                                                                                                    AAY95895,
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                                                                                                                                                                                                                                                                                                     mutant.
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                                                                                    AAY95895
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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillan KJ, Goddard A;
oni NF, Smith V;
                                         Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
Gerber H, Hillan
Kuo SS, Paoni NF,
                                                                                               SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP
                                                                                                                                                                                                                            Human PRO364 protein sequence SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Ferrara N,
Gurney AL, Klein RD,
Williams PM, Wood WI;
                                                                                                                                                            AAB24409 standard; Protein; 241 AA
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99WO-US05028
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N-PSDB; AAA77604
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Watanabe CK,
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Query Match 100.0%; Score 969; DB 21; Best Local Similarity 100.0%; Pred. No. 1.3e-69; Matches 162; Conservative 0; Mismatches 0;

Length 241;

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                                                                                                                                                This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRII receptor). The invention relates to TRII and two splice variants TRISVI and TRISVI. The nuclectide sequences were determined by sequencing cloned consa A237765 237766. The TRII receptor induced tumour necrosis factor receptor family related gene (GITR). TRIISVI and TRIISV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately cell death. They can be used for screening for and ultimately cell death. They can be used for screening for sourists and alsease state associated with aberrant cell agonists and sleases state associated with aberrant cell survival. They can be used for treating immunodeficiency disorders, bigeorge syndrome, HIV infection, severe combined immunodeficiency consurvival. They can be used for treating immunodeficiency disorders, blood cagulation disorders, blood platelet disorders or wounds resulting from traume or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, heart attacks, strokes, Addison's disease, and liple sclerosis, mysathenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Gullain-Barre syndrome, insulin dependent disperses maltiple sclerosis, mysathenia gravis, Stiff-Man syndrome, infury, complement-mediated molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion infury, changed to repeti, replace, or protect tissue demaged by congenital chemokine induced lung injury, inflammatory bowel disease, Conditions. They can also be used to repeti, replace, or protect tissue demaged by congenital eryclasses, gravier, intouchas, and some central nervous system disease, amyctrophic lateral eryclasses, emperention, disease, amyctrophic lateral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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                                                                                   tumour necrosis factor receptor-like polypeptides used to, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 969; DB 21;
100.0%; Pred. No. 1.3e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW37839 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and prognosis
                                                                                                                           Claim 14; Fig 1; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 162; Conservative
                                                                                                  treat Digeorge syndrome
                                        WPI; 2000-061922/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AA;
                                                       N-PSDB; AAZ37762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
             N1 J,
                                                                                    300
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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell-expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
antigén-specific T cell prolifération; cytokine production by T-cell;
apoptosis; cancer; heamatopoietic cells; lymphoid cell;
autolimune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 maqhgamgafralcglallcals1gqrptggpgcgpgrll1gtgtdarccrvhttrccrd 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SGGHEGHCKPWIDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 969; DB 19;
100.0%; Pred. No. 1.3e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                /product- "human 312C2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Pages 59-60; 71pp; English.
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06605 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US13931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0689943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorman DM, Randall TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-159534/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV19153
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                   WO9806842-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1998
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ID AAYO
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AC AAYO
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Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or
                               PRO364; tumour necrosis factor receptor; human; apoptosis;
                                                                                                                                                                                                                                   Marsters SA;
                                      inflammation; antiinflammatory; NF-KB activation;
                                                                                                                                162..180
/note= "transmembrane domain"
                                                                                        /note- "signal peptide"
                                                                                                          /note= "mature protein"
                                                                                                                       /note= "N-glycosylated"
                                                                                                                                                                                                                                   Gurney AL,
               Human TNF receptor homologue PRO364.
                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Claim 17; Fig 2A; 104pp; English.
                                                                                                                                                                                      99WO-US02642.
                                              autoimmune disease; therapy
                                                                                                                                                                                                     98US-0024087
(first entry)
                                                                                                                                                                                                                                   Goddard A,
                                                                                                  26..241
                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                               autoimmune responses
                                                                                                                                                                                                                                                         WPI; 1999-494296/41.
N-PSDB; AAX87670.
                                                                                                                                                                                                                                   Ashkenazi AJ, Godd
Pitti RM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
                                                                                                                 Modified-site
26-OCT-1999
                                                              Homo sapiens
                                                                                                                                                       WO9940196-A1
                                                                                                                                                                                      09-FEB-1999;
                                                                                                                                                                                                     09-FEB-1998;
                                                                                                                                                                      12-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                  Peptide
                                                                                                   Protein
                                                                                                                                 Domain
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The present sequence represents human PRO364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO, Escherichia coll or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid respides 175-167 of PRO364. PRO364 polypeptides profile in acid and acid sessions sequence, where X is any one of amino acid respides 157-167 of PRO364. PRO364 polypeptides profile immanian and profine in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin For region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
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÷ Gaps 1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60 ô Indels 100.0%; Score 969; DB 20; 100.0%; Pred. No. 1.3e-69; ö 0; Mismatches 162; Conservative Local Similarity Matches

Length 241;

Query Match

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Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and anglogenic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to methods for stimulating or inhibiting and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PR0179, PR0218, PR0314, PR0844, PR0846, PR01760, PR0205, PR0311, PR0317, PR0817, PR0817, PR0819, PR0819, PR0810, PR0810,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME;
Paoni NF, Pitti RM;
61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                      Cardiovascular; endothelial; angiogenic disorder; PR0179; PR0238; PR0364; PR0844; PR0846; PR01760; PR0205; PR0321; PR0333; PR0840; PR0877; PR0878; PR0879; PR0882; PR0885; PR0887;
                                                                                                                        SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
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Gurney AL, Hillan KJ, Marsters SA,
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..25
/label= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                               AAB27651 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 71; Fig 6; 181pp; English.
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99WO-US12252.
99US-0144758.
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99WO-US28565
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                                                                                                                                                                                                                                                                                                                                                                                                              Human protein PRO364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                 AAB27651;
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Human 312C2 protei
Mouse glucocortico
Mouse glucocortico
Amino acid sequenc
Mouse glucocortico
Muthe TNF-alpha f
Skin cell protein,
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ACT-4 cell surface
ACT-4-h-1 receptor
Human OX40 protein
                                                                                                            Human molecule ass
Human 312C2 protei
Human tumour necro
                                                          Human anglogenesis
Truncated human 31
                                                                                                                                                                                                                                                                             Human tumour necro
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Mouse OX40 extrace
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Human 4-1BB recept
Human CD137 protei
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Human tumour necro
                                                                                                                                                                                         TR11SV2 amino acid
                                                                                                                                                                                                                                                    Polypeptide encode
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OX40/Fc mutein. C
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                                                                                                                                                                                                                        PRO364-related EST
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                                 Human PRO364
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72.81
/note= "conserved domain CD-II"
/note= "conserved domain CD-III"
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26..234
/label- Mature_protein
26..162
/label- Extracellular_domain
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/label- Intracellular domain
146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                     AAW37842
AAY95881
                                                                                                                                                                                         AAY52160
AAY06645
AAB47055
AAY95880
                                                                                                                                                                                                                                                                                                   AAY52159
AAW37841
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AAW37838
AAW49017
AAW49017
AAB55959
AAR81881
AAW48977
AAW48976
AAR74737
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                                                                                      4AW37840
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AAR70977
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                                                                                                                                                                                    4, 2001, 15:56:21; Search time 126.12 Seconds (without alignments) 77.871 Million cell updates/sec
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412676 seqs, 60623988 residues
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Listing first 45 summaries
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AAW37839
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AAB27651
AAB33431
AAY95895
                                                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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and is derived by analysis of
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The present sequence is that of human tumour necrosis factor receptor-like protein TRII, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family related gene. The sequence was deduced from a cDMA clone (see AAA50304) discovered in a T-helper cell library.

TRII activated NF-kappaB through a TRAF2-mediated mechanism. Expressed in activation-inducible. The TRII ligand is constitutively cappressed in an endothelial cell line. This suggests that TRII and its ligand may be involved in activated T-cell trafficking.

The invention provides TRII, TRIISVI and TRIISV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see AAA50304-06) and highly conserved encoded proteins (see CAAY5879-81), as well as vectors, host cells and recombinant methods for their production. TRII, TRIISVI and/or TRIISV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                           203..211
/note= "epitope-bearing region"
222..230
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te= "epitope-bearing region"
             "conserved domain CD-IV"
                                                                  "conserved domain CD-VI"
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tte= "epitope-bearing region"
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/note= "epitope-bearing
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224..23
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156..16
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N-PSDB; AAA50304.
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13-MAY-1999;
16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunodeficiency and solution of the second of the
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 969; DB 21; 100.0%; Pred. No. 1.3e-69;
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/note= "Extracellular domain"
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/label= Signal_peptide
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Matches 162; Conservative
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67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
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                                    CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG
                                                                                                                                                                                                                                                                                                                   APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
ITILE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 937; DB 3; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                         121 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 156
                                                                                                                  HCKPWIDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14 AUG-1997
CLASSIPECATION: 536
PROOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.7%; Scur.
100.0%; Pre
                                                                                                                                                                                                                                       US-08-911-423-8; Sequence 8, Application US/08911423; Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650-496-1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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STREET: 901 C..
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                          61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
                                    Gaps
                                                                                                 1 MAQHGAMGAFRALCGLALLCALSLGORPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 228;
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US/08/911,423
APPLICATION NUMBER: US 60/023,419
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING APPLICATION NUMBER: US 60/027,901
                                                                                                                                                                                                                                                              121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                           121 SCGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 162
            Pred. No. 5.3e-77;
; Mismatches 0;
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Pred. No. 3e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.7%; Scor. 100.0%; Pred. No. c. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlocnik, Albert TITLE OF INVENTION: MAMMALIAN TITLE OF INVENTION: REAGENTS NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: 150-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
              Best Local Similarity 100.
Matches 162; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-911-423-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 90
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US-08-911-423-6
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Gaps

2, Appli 2, Appli 4, Appli 23, Appl 2, Appli 15, Appli

Sequence 7, P Sequence 2, P Patent No. 539

Appl

Sequence 6, Appagnence 6, Appagnence 11, A Sequence 11, A Sequence 12, A Sequence 2, Appagnence 23, Appagnence 23, Appagnence 23, Appagnence 15, A Sequence 15, A Sequence 115, A Sequence 115

Wed

Sequence:

Run on:

Searched:

Database

Result

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; Sequence 4, Application US/08911423
; Patent No. 611090
; GENERAL INFORMATION:
   APPLICANT: Gorman, Daniel M.
   APPLICANT: Randal, Troy D.
   APPLICANT: Albert
   TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
   TITLE OF INVENTION: REAGENTS
   NUMBER OF SEQUENCES: 8
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: DNAX Research Institute
   STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUDNIER: USA

CUDNIER: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423

FILING DATE: 14-AUG-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419

FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901

FILING DATE: 07-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: CANING, EGWIN P.
REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0612K

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-08-995-659-4
US-08-996-6139-6
US-08-995-659-6
US-08-974-022-49
US-09-042-785A-11
US-09-042-785A-12
US-08-996-139-2
US-08-995-659-2
US-09-042-785A-3
US-09-042-785A-3
US-09-042-785A-3
US-08-995-659-15
US-08-995-659-15
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
US-08-996-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 241 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-911-423-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: Californi
COUNTRY: USA
      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-08-911-423-4
  Query Match
    Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 2, Appli
                                                                                                                                                                   (without alignments)
50.647 Million cell updates/sec
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Sequence 7, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               ; Search time 65.86 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 191,
                                                                                                                                                                                                                                                                            .....FPGNKTHNAVCVPGSPPAEP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11,
Sequence 2, A
Sequence 2, A
Sequence 8, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Sequence 13,
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Sequence 8,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                         4.5
Compugen Ltd
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US-08-911-423-8
US-08-911-423-7
US-08-911-423-2
US-08-191-827-7
US-08-097-827-7
US-08-097-827-11
US-08-194-574-1
US-08-195-967-2
US-08-195-967-2
US-08-186-605-9
US-08-816-605-9
US-08-816-605-9
US-08-816-605-8
                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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US-08-236-918A-6
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                                                                                                                                                                                                                                                                                                                                                                              197339 seqs, 20590346 residues
                                                                                                                                               4, 2001, 15:57:34
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                       GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                 US-09-512-363-2_COPY_1_162
                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                          1 MAQHGAMGAFRALCGLALLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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17.2%; Sco
ilarity 28.7%; Pro
Conservative 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-494-574-7
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                                                                                                                                                                                                           73 MCVQPEFHCGDPC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5783665
GENERAL INFORMATION:
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      50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-494-574-7
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          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanalow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Indels
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Selected From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENY APPLICATION NUMBER: US/09/188,930A
CURRENY FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SEC ID NOS: 348
SEC ID NO 191
LENGTH: 89
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SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      b; Score 255; DB 4;
b; Pred. No. 1.2e-15;
17; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : |:|| ||:|||| ||:|||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
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APPLICATION NUMBER: US/08/097,827
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: PERKITGLA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO: 7:
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28.7%;
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Best Local Similarity 46.33
Matches 44; Conservative
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immu
STREET: 51 Univ
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: mouse US-09-188-930-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98101
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                                                                                                                            --CPPGQG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 MCVQPEFHCGDPC------CTTCRHHP------CPPGQG 99
                                           26 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Graslow, William
APPLICANT: Graslow, William
APPLICANT: Graslow, William
TITLE OF INVENTION: No. 578365el Cytokine Which is a Ligand for TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
61;
                                                                                                                                                                                                          100 VOSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                    61;
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51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/097,827 FILING DATE: 23-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08494574 Patent No. 5783665
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Sequence 2, Application US/08911423 Patent No. 6111090 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQCVQSQCK---SWRCLWESTQARGSTRAR 117
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                                                                                                                                                                                APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 605; DB 3; Length 232;
Pred. No. 1.6e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
121 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      Sequence 7, Application US/08911423 Patent No. 6111090
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TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
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78.1%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
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STRANDEDNESS: si
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                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         94304-1104
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                                                                                    RESULT 4
US-08-911-423-7
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RESULT 5 US-08-911-423-2

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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLLASSIFICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, EGWin P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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; Patent No. 6150502
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Best Local Similarity 54.5%
Matches 85; Conservative
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APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-911-423-2
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Apple Power Macintosh
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; Sequence 8, Application US/08236918A
; Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (206) 587-0430
TELEPHONE: (415) 326-2400
TELEFRAX: (415) 326-242
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
                                                 TOPOLOGY: 1:-277 amino acids
TOPOLOGY: 1:-277 amino acids
TOPOLOGY: 1:-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.7%
Matches 51; Conservative
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LENGTH: 255 amino acids
TYPE: amino acid
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                                                                                                                                                 ) MOLECULE TYPE: protein US-08-195-967-2
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Patent No. 6242566
GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Englemen, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GARRIGEGPCAALLILGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Indels 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 277;
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                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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; Pred. No. 3.9e-07;
11; Mismatches 92;
                                                                                                                                            FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
ATGANEY FACENT INFORMATION:
NAME: SMITH, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
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NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-230
TELECOMMUNICATION INFORMATION:
                                                                                                                              APPLICATION NUMBER: US/08/147,784 FILING DATE: 03-NOV-1993 CLASSIFICATION: 424
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FILING DATE: 10-FEB-1994
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 29.79
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-147-784-2
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STATE: California
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STREET: 379
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55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
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                                                                                                                                                                         4 GARRLGRGPCAALLLLGLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                  5 GAMGAFRALCGLALLCALSLG------QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
                                                         92; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                      109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
   Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Washington
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APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
; Score 162; DB 4;
; Pred. No. 3.9e-07;
11; Mismatches 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: Apple 7.5.3
Microsoft Word, Version #6.0.1
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FILING DATE: 06-May-1994
CLASSIFICATION: 435
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APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
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linear
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                  Seattle
                                                                                                                                    STATE: WA
COUNTRY: USA
98101
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STATE:
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                                                                                                                         Sequence 11, Application US/08097827
Patent No. 5457035
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gylle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                  111 PRODSGYKLGVDCVPCPPGHFSPGNNQACKPWINCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: 51 University Street
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Patent No. 578365
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Fanslow, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGIGSTRATION NUMBER: 34,693
REFRENCE/CDCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
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amino acid
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Best Local Similarity 28.79
Matches 50; Conservative
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COUNTRY: US
ZIP: 98101
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                                                                                                           US-08-097-827-11
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59 LC-----HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --CPPGQG 99
Gayle, Richard
FENTION: No. 5783665el Cytokine Which is a Ligand for
FENTION: OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Buck, David
APPLICANT: Buck, David
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CQ4+ T-CELLS: ACT-4
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
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28.7%; Pred. No. 2.4e-07;
tive 12; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILLING DATE: 22-UNN-1995
CLASSIFFCATION: 530
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-147-784-2
; Sequence 2, Application US/08147784
; Patent No. 5821332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
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                                                                                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                    TITLE OF INVENTION: TITLE OF INVENTION:
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: California
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145 GNKTHNAVCVPG--
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STATE: NY
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                                                                                       RESULT 15
PCT-US96-03965-8
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                                                                                                                   48 CPPNSFSSAGG--ORTCDI----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                  34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
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                                                 Indels 41;
              Length 255;
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Vi, Guo-Liang
APPLICANT: Vi, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
                                                 52;
                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
            ; Score 160.5; DB 1; Pred. No. 4.9e-07; 12; Mismatches 52
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30.9%; Pred. No. 4.9e-07;
tive 12; Mismatches 52
                                                                                                                                                                                                                           145 GNKTHNAVCVPG-----SPPA---EP 162
                                                                                                                                                                                                                                                             150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Human Genome Sciences, Inc.: 9410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5874240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF25.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 301-309-001.
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 255 amino acids
            ch 16.6%; 1 Similarity 30.9%; 47; Conservative 1
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Matches 47; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-816-605-9
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MEDIUM TYPE: Floppy
            Query Match
Best Local Similarity
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Monoclonal antibody against human TITLE OF INVENTION: receptor 4-1BB NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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306 East State Street, Suite 220
145 GNKTHNAVCVPG-----SPPA---EP 162
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/03965
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
                                                                                                                                                                                                                                                                                                    Sequence 8, Application PC/TUS9603965 GENERAL INFORMATION:
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IBM PC compatible
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TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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MOLECULE TYPE: protein
PCT-US96-03965-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 47; Conserva
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101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWINCTLAGKHTLQPASN 160
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  28 CSNCPAGVFRTRKECSSTSNAECDC---TPGFHCLGAGCSMC-EQDCKQGQELTKKG---
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                                                                         81 ----CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSP 131
                                             83 FGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 137
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                                                                                                                                                                                                                                                              APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Buck, David
APPLICANT: Buck, David
APPLICANT: Buck, David
TITLE OF INVENTION: ECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: 379 Lytton Avenue
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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APPLICATION NUMBER: US/08/147,784
FILING DATE: 03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
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18.8%; Score 158.5; DB 3
Best Local Similarity 31.6%; Pred. No. 6.2e-07
Matches 42; Conservative 10; Mismatches 70
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Job time: 376 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 05490A-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2400
TELEPAX: (415) 326-2400
TELEPAX: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       RESULT 15
US-08-147-784-2
Sequence 2, Application US/08147784
Patent No. 5821332
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 277 amino acids amino acid
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161 SSDAICEDRDPPA 173
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                                                                                                                                                                                                                                                                                                                                                          60 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 119
                                                                                                                                                                                                                                                                                                                                                                                    98 GCSMC-EQDCKQGQELTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                        9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDP 59
                                                                                                                                                                                                                                                                                                               48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRDYPG-----EECCS----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFS 82
                                                                                                                                                                                   Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 4-IBB Receptor Splicing Variant
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
SOFTWENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                            52;
                                                                                                                                                                                19.1%; Score 160.5; DB 5; 30.9%; Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.8%; Score 158.5; DB 2; 33.0%; Pred. No. 5e-07; Live 11; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GNKTHNAVCVPG-----SPPA---EP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISEE: Human Genome Sciences, Inc.: 9410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-816-605-2; Sequence 2, Application US/08816605; Patent No. 5874240; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/CDCKET NUMBER: PF2!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 219 amino acids TYPE: amino acid
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301-309-8512
                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-03965-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-816-605-2
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 47; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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nes 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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STREET: 94
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Best Local S1
Matches 38;
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CORRESPONDENCE ADDRESS:
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                                                                                         COUNTRY: U
                 ADDRESSEE:
STREET: 5
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                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------CPPGQG 74
                                                                                               APPLICANT: Baum, Peter
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Garslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 VQSQCKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 MCVQPEFHCGDPC------CTTCRHHP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08494574
Patent No. 5783665
GENERAL INFORMATION:
                                                   Sequence 11, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PERLAIDS, PARLICIGA A.
REGISTRATION NUMBER: 34,693
REFERENCE/OOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 438 amino acids
amino acid
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Best Local Similarity 28.77
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-097-827-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 536
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                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                      98101
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                 RESULT 9
US-08-097-827-11
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US-08-494-574-11
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                                                                                                                                                                                                                                                                                              CITY: STATE:
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59 LC-----HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Indels
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STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08236918A
Patent No. 5674704
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
19.8%; Score 166.5; DB 1
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 50; Conservative · 12; Mismatches 51
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
E: Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 438 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
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Floppy disk
                                                        LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                        Query Match
Best Local Similarity 30.9%
Matches 47; Conservative
                                          SEQUENCE CHARACTERISTICS:
301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 607-273-2609 INFORMATION FOR SEQ ID NO:
                      INFORMATION FOR SEQ ID NO:
                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-816-605-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTON: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.1%; Score 160.5; DB 1
Best Local Similarity 30.9%; Pred. No. 3.8e-07;
Matches 47; Conservative 12; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
                    APPLICATION NUMBER: US/08/236,918A FILING DATE: 06-May-1994
                                                                                                                                                                      NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J3-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08816605
Patent No. 5874240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GNKTHNAVCVPG-----
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                            US-08-236-918A-8
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US-08-816-605-9
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                                                                                                             9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCS----EWDCMCVQPEFHCGDP 59
                                                                                                                                                              48 CPPNSFSSAGG--ORTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                            41;
  Length 255;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
19.1%; Score 160.5; DB 2; 30.9%; Pred. No. 3.8e-07; tive 12; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUDRESSEE: Barnard, Brown & Michaels STREET: 306 East State Street, Suite 220 CITY: Ithaca
                                                                                                                                                                                                                                                                                                                          120 GNKTHNAVCVPG------SPPA---EP 137
                                                                                                                                                                                                                                                                                                                                                           | | : || | : || |
|150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: US 07/267,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application PC/TUS9603965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: O'NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: KWO5
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TELEPHONE: 607-273-1711
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34,090
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amino acid
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Best Local Similarity 56.99
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-911-423-2
                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                    STREET: 901 Calife
CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                ZIP: 94304-1104
                                                                                                                  ADDRESSEE:
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US-09-188-930-191
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                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QRPTGGPGCGPGRLLLGTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CTTCRHHPCPPGQGVQSQGKFSFGFQCI----DCASGTFSGGH-EGHCKFWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches 17; Indels
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Pred. No. 2.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
FILING DATE: 16-AUG-1996
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                            E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                Sequence 7, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08911423 Patent No. 6111090
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-490-1200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TRNGTH: 232 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.5%;
74.6%;
140 NKTHNAVCVPGSPPAEP 156
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Best Local Similarity 74.6'
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-911-423-7
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Rese
                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
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67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 PGCGPGRLLLGTGTGARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH·66
APPLICANT: Zlotník, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.4%; Score 465.5; DB 3; Length 56.9%; Pred. No. 1.2e-33; Live 21; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orlust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                    DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 191, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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59 LC-----HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 LC------HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
      ---ALLLLGLTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QQPT-----ALLLLGLTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
                                                                                                                                 75 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                          75 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 166.5; DB 1;
Pred. No. 9.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                ; Sequence 7, Application US/08494574
; Patent No. 5783665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                              48 MCVQPEFHCGDPC----
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                          7 PGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gall, Ray
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 206;
                                                                                                                                                                                                                                         Length 89;
                                                                                                                                                                                                                                    ; Score 219.5; DB 4; Length 8; Pred. No. 1.1e-12; 13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 166.5; DB 1
28.7%; Pred. No. 9.5e-08;
Live 12; Mismatches 51
CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SSOFWARE: FastSEQ for Windows Version 3.0 SSOFWARE: PastSEQ ID NO 191 LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: PERKIAS, PARITOIA A.
REGISTRATION NUMBER: 34.693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 266-587-073
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-normal SOFTWARP.
                                                                                                                                                                                                                                       26.1%;
48.6%;
                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.68
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Best Local Similarity 28.7%
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: protein US-08-097-827-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
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79 YPCQPGQRVE 88
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                                                                                                                                                   ; 'ORGANISM: mouse US-09-188-930-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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Appli Appli Appli Appli Appli Appli Appli Appli

Sequence 4

Sequence 2, Ap Sequence 6, Ap Sequence 4, Ap Sequence 23, A Sequence 23, A Sequence 11, A Sequence 11, A Sequence 115, A Sequence 115, A Sequence 115, A

Sequence 7, Appli Sequence 2, Appli Patent No. 5395760

Run on:

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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Blotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
ADDRESSEE: DAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                               US-08-995-659-4
US-08-996-139-2
US-08-996-139-6
US-08-996-139-6
US-08-995-659-6
US-09-042-7855-4
US-09-042-7855-2
US-08-974-022-49
US-08-974-022-49
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
US-08-996-139-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/911,423
CLASSIFICATION STATE
CLASSIFICATION STATE
CLASSIFICATION STATE
CLASSIFICATION STATE
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AGG-1996
FILING PAPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 6, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-423-6
  US-08-911-423-6
Appl
Appl
                                                                                                                                                                   4, 2001, 15:57:34; Search time 65.86 Seconds (without alignments) 42.831 Million cell updates/sec
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Sequence 191, App
Sequence 7, Appli
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Sequence 4, Appli
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Sequence 7,
                                                                                                                                                                                                                                                                          US-09-512-363-2_COPY_26_162
841
1 QRPTGGPGCGPGRLLLGTGT......FPGNKTHNAVCVPGSPPAEP
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-911-423-2
US-08-188-930-191
US-08-097-827-7
US-08-494-574-7
US-08-494-574-11
US-08-26-918A-8
US-08-816-605-9
PCT-US-06-816-605-8
US-08-816-605-2
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US-08-236-918A-6
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US-08-794-796-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             197339 seqs, 20590346 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                           September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of
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                                                                                                                                                                                                                                                                                                                                 Sequence:
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CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
                                     61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QRPTGGPGCGPGRLLLGTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 841; DB 3;
100.0%; Pred. No. 4.2e-66;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PROOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     E: DNAX Research Institute 901 California Avenue
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US-08-911-423-8
Sequence 8, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090 REFERENCE/DOCKET NUMBER: DX(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                             Daniel M.
                                                                                                                                                                                                                                                                           APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIT
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                311 amino acids
                                                                                           121 NKTHNAVCVPGSPPAEP 137
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Best Local Similarity 100.
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: DNAX Rese
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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                                       Gaps
                                                                                           20 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
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Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 241;
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                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: CALIAG ECANIP.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
 Score 841; DB 3;
Pred. No. 3.2e-66;
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Pred. No. 3.3e-66;
                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08911423 Patent No. 6111090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIR
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                           140 NKTHNAVCVPGSPPAEP 156
                                                                                                                                                                                                                     121 NKTHNAVCVPGSPPAEP 137
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                   Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-911-423-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-911-423-4
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COUNTRY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.7%; Score 140; DB 5; Length 256; 1larity 32.7%; Pred. No. 2.4e-05; Conservative 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFG 113
                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
                       3: Barnard, Brown & Michaels
306 East State Street, Suite 220
                     Brown & Michaels
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DYTA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SE-1993
PRIOR APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UUL-1992
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UUL-1992
PRIOR APPLICATION NUMBER: US 07/927,977
APPLICATION NUMBER: US 07/927,977
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, IGOR
APPLICANT: BELETSKY, IGOR
TITLE OF INVENTION: TWE LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE 3 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390 REFERENCE/DOCKET NUMBER: KWOS TELECOMMUNICATION INFORMATION: TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08477347
Patent No. 6232446
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein
PCT-US96-03965-2
CORRESPONDENCE ADDRESS:
                                                                                                                                    ZIP: 14850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
3Y: linear
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Matches 36; Conserve
                                                                                                                   USA
                                                                      Ithaca
                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-347-17
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTEDTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139; DB 4; Length 140;
Pred. No. 1.8e-05;
7; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 RCCRD-YPGEECCSEWD-----CMCVQPEFHCG----DPC--CTTCRHH--
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 4, 2001, 15:57:35 Job time: 377 sec
                                                                                                                                                                                                                                                                                                                                                                                                    WALLACH-10
                                                                                                                                                                                                                       APPLICALL.

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATYONEEY/ABENT INCOMATION:
NAME: TOWNSEND, G. KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/115,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.1%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                        JECUMNO: 202-02
TELEPHONE: 202-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-477-347-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                           FILING DATE:
CLASSIFICATION:
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1 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 PRQDSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                      Score 147.5; DB 1
Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UL-193
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PALTICIA A.
REGISTRATION NUMBER: 34,693
REPERBNE/POCKET NUMBER: 2806
TELECOMBUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
UNMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/974,022 FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                      20.7%;
28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTONARY, WINTER, ROBERT B.
NAME: WINTER, ROBERT B.
INFORMATION FOR ESQ ID NO: 5
SEQUENCE CHARACTERIZICS:
LENGTH: 205 amino acids
                                                                                                                                                                                                                         438 amino acids
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 28.3
Matches 45, Conservative
                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-494-574-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amgen Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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STATE: California
                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 QOPT-----ALLLIGITIGVIARRINCVKHIYPSGHKCCRECQPGHGMVNRCDHIRDI 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08494574
Patent No. 578365
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Fanslow, William
APPLICANT: Goodwin, Ray
APPLICANT: Goolwin, Ray
APPLICANT: Goolwin, No. 5783665el Cytokine Which is a Ligand for TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for TITLE OF ENVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------CTTCRHHP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 PRQDSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.7%; Score 147.5; DB 1
28.3%; Pred. No. 8.8e-06;
tive 9; Mismatches 44
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APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: PERKINA, PALTICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 MCVQPEFHCGDPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   : 438 amino acids
amino acid
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Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein US-08-097-827-11
                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                          USA
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                                                                                                                                                                                                                         FILING DATE:
                                           98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-494-574-11
                          COUNTRY:
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65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFG 113
                                                                                            RESULT 13
US-08-236-918A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-03965-2
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                    qq
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6
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                                                                                                                                                                                                                                            -- PCPPGQGVQSQGKFSF 83
                                                                                                                                                                                             6 QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC
                                                                                                                                 44;
                                                                                                                                                                    1 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT----RCCRD-YPGEECCSEWD---
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                                                                                         Score 141; DB 3; Length 205;
Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Indels
                                                                                                                               9; Mismatches. 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.7%; Score 140; DB 3; 32.7%; Pred. No. 1.9e-05;
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                                                                                                                                                                                                                                                                                                                                           84 GFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52, Application US/08974022;
Patent No. 6015938;
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TILLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                            47 CMCVQPEFHCG----DPC--CTTCRHH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Winter, Robert B.
REPERBENCE/POCKET NUMBER: A
INFORMATION FOR SCO ID NO. 52:
SEQUENCE CHARACTERISTICS:
                                                                                          19.8%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 amino acids
                                                                                                                               44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-022-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-974-022-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserva
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                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-974-022-52
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                                                                                            Query Match
                                                                                                                               Matches
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9 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW----DCMCVQPEFHCGDPCCTTC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels 18;
               -----CKTCSLGTFNDONGTGVCRPWTNCSLDG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Score 140; DB 1; Length 256; illarity 32.7%; Pred. No. 2.4e-05; Conservative 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDG 143
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
                                                                                                                                                                                                              APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsoft Word, Version #6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 06-May-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor 4-1BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Versic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9603965 GENERAL INFORMATION:
                                                                                                                                        Sequence 6, Application US/08236918A Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-236-918A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
| || : ||
102 -EKDCRPGQELTKQG-
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                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                  Patent No. 5674704
GENERAL INFORMATION:
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1 QRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CTTCRHHPCPPGQGVQSQGKFSFGFQCI --- - DCASGTFSGGH - EGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
71.6%; Score 509; DB 3; Length 232;
Best Local Similarity 74.6%; Pred. No. 4.8e-37;
Matches 88; Conservative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                            SCETWARE STATEM: TO USE STATEM: SCETWARE STATEM: SCETWARE STATEM: PAGE STATEM: SCETWARE STATEM: SCETWARE STATEM: US/08/911,423
FILING DATE: 14-AUG-11997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTON NUMBER: US 60/027,901
FILING DATE: TARGEMATION:
                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 Callfornia Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08911423 ; Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 232 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-911-423-7
                                                                                                                                           CITY: Palo Alto
STATE: California
    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 PGCGPGKVQNGSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 PGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 373.5; DB 3; Leus-Pred. No. 2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 HPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: MISON, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US,09/188,930A
CURRENT FILING DATE: 1998-11-09
       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FITTING COMPANIES: US/08/911,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.9%; Score 219.5; DB 4 48.6%; Pred. No. 1.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 348
SOFWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 191
LENGTH: 89
                                                                                                                                                                                         US-09-188-930-191

. Sequence 191, Application US/09188930A

. Patent No. 6150502

. GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 48.6%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-911-423-2
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-188-930-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: Lottik, Albert
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palo Alto
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08097827
Patent No. 5457035
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for TITLE OF INVENTION: 0.3457035el Cytokine Which is a Ligand for NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
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9; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATGORNEY/AGENT INFORMATION:
NAME: PERKINS, PALLICIA A.
RECISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELECHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08494574 Patent No. 5783665 GENERAL INFORMATION:
26 PGCGPGKVQNGSGNNTRCCSLYA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.3
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-097-827-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                        67 HPCPPGQGVQ 76
                                                                                  :11 ||| |:
79 YPCQPGQRVE 88
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US-08-494-574-7
                                                                                                                                                      RESULT 7
US-08-097-827-7
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APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Immnoc C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 LC------HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ORPIGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 47
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APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Garbe, Richard
TITLE OF INVENTION: 0x. 5457035el Cytokine Which is a Ligand for
TITLE OF INVENTION: 0x40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
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Pred. No. 4.6e-06;
9; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-097-827-11
; Sequence 11, Application US/08097827
; Betten No. 5457035
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 280 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-587-0730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%;
ilarity 28.3%;
Conservative
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 MCVQPEFHCGDPC----
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 45; Conserva
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STREET: 51 .
Tmv: Seattle
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ZIP: 98101
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September 4, 2001, 15:57:34; Search time 65.86 Seconds (without alignments) 35.641 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Sequence:
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/cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/pcTUS\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued\_Patents\_AA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	US-08-911-423-6 Sequence 6, Appli	-423-4 Sequence 4,	-911-423-8 Sequence 8,	-911-423-7 Sequence 7,	-423-2 Sequence 2,	-191 Sequence 191	7 Seguence 7,	-7 Sequence 7,	-11 Sequence 11,	-11 Sequence 1	51,	52 Sequence 52,	6, 4	7		8 Sequence 8,	Sequence 9,	-8 Sequence 8,	-8	7	-784-2 Sequence 2,	Sequence 2,	-796-2 Sequence 2,	49,	-785A-11 Sequence 11,	
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Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 15, Appli Sequence 15, Appli Sequence 23, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 15, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli
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Sequence 6, Application US/08911423
Sequence 6, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: RAMMAIIAN CELL SURFACE ANTIGENS; RELATED TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-AUG.1997
CLASSIFICATION: 4536
                                                                                                                                                                                                                                       ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 60/023,419

FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/027,901

FILING DATE: 07-0CT-1996

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
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TELEPHONE: 650-496-1200
TOTAL TO NO:
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MOLECULE TYPE: peptide US-08-911-423-6
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                                            Gaps
                                                                                1 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
                                                                                                      20 QRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
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                                                                                                                                                                                    0 CTTCRHHPCPPGQGGVGSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 133
                                                                                                                                                                 61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
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                                            Indels 0;
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
  Score 711; DB 3;
Pred. No. 2.2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 711; DB 3;
100.0%; Pred. No. 2.3e-54;
Live 0; Mismatches 0;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REFERENCE/DOCKET NUMBER: DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DNAX Research Institute
STREET: 901 Callifornia Avenue
CITY: Palo Alto
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    US-08-911-423-4; Sequence 4, Application US/08911423; Patent No. 6111090
100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100. Matches 114; Conservative
                                          Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-911-423-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS ADDRESSE: DNAX Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304-1104
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGF 114
                                                              APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
ATILE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,023,419 FILING DATE: 16-AUG-1996 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,027,901 APPLICATION NUMBER: US 60,027,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 711; DB 3;
Pred. No. 2.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US.60/027,901
FILING DATE: 07-0CT-1996
ATTONNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DX0612K
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 8, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
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100.0%;
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Randall, Troy D.
Zlotnik, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                         STREET: 901 Califor
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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APPLICANT:
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                                                                                                                                                                          85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                98 GCSMC-EQDCKQGQELTKKG------CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 CCTICRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 41; Gaps
                                                                                            34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EWDCMCVQPEFHCGDP 84
                                                                                                                                   48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                       41;
                  Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 4-IBB Receptor Splicing Variant
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRIE 20850

ZIF: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FTITING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.4%; Score 160.5; DB 2; 30.9%; Pred. No. 4.8e-07; tive 12; Mismatches 52;
                                    4.8e-07
              16.4%; Score 160.5;
30.9%; Pred. No. 4.8e
tive 12; Mismatches
                                                                                                                                                                                                                                                       145 GNKTHNAVCVPG-----SPPA---EP 162
                                                                                                                                                                                                                                                                                            150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08816605 Patent No. 5874240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECISTRATION NUMBER: 36,373
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ni, Jan
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 30.9
Matches 47; Conservative
                                                     Conservative
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                                Local Similarity
nes 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ROCK
STATE: MD
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US-08-816-605-9
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              Query Match
                                    Best Loc
Matches
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85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
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                                                                                                                                                                                                                      APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 4.8e-07; 12; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                    3: Barnard, Brown & Michaels
306 East State Street, Suite 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GNKTHNAVCVPG------SPPA---EP 162
145 GNKTHNAVCVPG-----SPPA---EP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                               150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-70L-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: MICHAELS, Christopher A
REGISTRATION NUMBER: 34,390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US96/03965
                                                                                                                                                                    Sequence 8, Application PC/TUS9603965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 255 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 30.9
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607-273-2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 14850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Ithaca
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US96-03965-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE
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Search completed: September 4, 2001, 15:57:37 Job time: 379 sec

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59 LC------HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QOPT-----ALLLGLTLGVTARRINCVKHTYPSGHKCCRECOPGHGMVNRCDHTRDT 58
   Gayle, Richard
FENTION: No. 5783665el Cytokine Which is a Ligand for
FENTION: OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-147-784-2

Sequence 2, Application US/08147784

Fabrian LNO 5821312

GENERAL INFORMATION:

APPLICANT: Godfrey, Wayne

APPLICANT: Buck, David

APPLICANT: Engleman, Edgar G.

TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED

TITLE OF INVENTION: CD4+ T-CELLS: ACT-4

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND Khourie and Crew

STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 166.5; DB 1
llarity 28.7%; Pred. No. 2.4e-07;
Conservative 12; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 MCVQPEFHCGDPC------CTTCRHHP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PARTICLA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            TITLE OF INVENTION: NO. 5783665e1
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 438 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 50; Conserva
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                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                               ZIP: 98101
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                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-494-574-11
                                                                                                                                                                                                                                            CITY: S
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 MCVQPEFHCGDPC-----CPTCRHHP-----CPPGQG 99
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodlin, Ray
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                     111 PRQDSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 VOSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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28.7%; Pred. No. 2.4e-07;
tive 12; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PERFAINS, PARITICIA A.
RECISTRATION UNBER: 34.693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08494574
Patent No. 5783665
GENERAL INPORMATION:
PAPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
                                                                                                                                                                                                                                         Sequence 11, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
TOTAL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 438 amino acids
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Best Local Similarity 28.7%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-097-827-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
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                                                                                                                                                                                                                                                                                                                                                                                 4 GARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                                                                                                                                                                                                                                          5 GAMGAFRALCGLALLCALSLG-----QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
                                                                                                                                                                                                                                                   ; Score 162; DB 4; Length 277;
; Pred. No. 3.8e-07;
11; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
UNMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236.918A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-May-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION INMERS: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/08236918A; Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 4.2.
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 28
                                           TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
                                                                                                          LENGTH: 277 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 29.7%
Matches 51; Conservative
                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-195-967-2
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MOLECULE TYPE: protein
US-08-236-918A-8
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                       TELEPHONE:
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US-08-236-918A-8
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Patent No. 6242566

GENERAL INFORMATION

GADICANT: Godfrey, Wayne

APPLICANT: Engleman, Edgar G.

TITLE OF INVENTION: CD4+ T-CELLS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GARRIGRGPCAALLILGIGISTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GAMGAFRALCGLALLCALSLG-----QRPTGGPGCGPGRLLLGTGTDDARCCRVHT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 277;
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
ATTORNEX/ACENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 162; DB 2;
; Pred. No. 3.8e-07;
11; Mismatches 92
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION UNBER: 30,233
REFERENCE/DOCKET NUMBER: 05490A-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2420
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05490A-230
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10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.7%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-147-784-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-195-967-2
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US-09-188-930-191
Sequence 191, Application US/09188930A
Fetent No. 6150502
GENERAL INFORMATION:
Sequence 2, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.1%
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-911-423-2
                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI----DCASGTFSG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQCVQSQGK---SWRCLWESTQARGSTRAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEEC 66
                                                                                                                                                                                         APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
121 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 605; DB 3;
Pred. No. 1.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            Sequence 7, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 232 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.1%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GH-EGHCKPWTDCTQFG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 GRARGHRCPARTCGVWG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650-496-1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-911-423-7
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1104
                                                                                                                                                                           GENERAL INFORMATION:
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US-08-911-423-2
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66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Blotnik, Albert
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
GORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 228;
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                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PROR APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
ATPONENTY NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATPONEY/AGENT INPOMBER: US 60/027,901
FILING DATE: O7-OCT-1996
ATPONEY/AGENT INPOMBATION:
NAME: Ching Fadit DE CANTON NAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 GHCRLWINCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.1%; Score 510; DB 3; 54.1%; Pred. No. 2.3e-37; iive 25; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene
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Gaps

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LC-----HPCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQ 110
                                                              QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 QRPTGGPGCGPGRLLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 MCVQPEFHCGDPC-----CPPGQG 99
                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08494574
Sequence 7, Application US/08494574
Patent No. 5783665
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              100 VQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                    51; Indels
  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2e-07;
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
ETLING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.7%;
Matches 50; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-494-574-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC COMP
                                                                                                                  73 MCVQPEFHCGDPC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE
  50;
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                                                                                                                                                                                                                                                                                             RESULT 8
US-08-494-574-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                          56
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           1 GAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKED 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 166.5; DB 1; Length 206; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                             Length 89;
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
OPERATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                           Score 255; DB 4;
Pred. No. 1.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : |:|| ||:||||| | :|:|| ||| ||:
CPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVE 88
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                  CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 191
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFRENCE/CDOCKET NUMBER: 2801
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%;
28.7%;
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46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 amino acids
                                                          FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                           Query Match 26.0
Best Local Similarity 46.3
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 206 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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STREET: DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-097-827-7
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Gaps

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Length 206;

Appli Appli

Sequence (Sequence (Sequen

Sequence 12, psequence 11, psequence 2, psequence 2, psequence 2, psequence 4, psequence 2, psequence 15, psequence 11, psequenc

Sequence 7, Appli Patent No. 5395760

Total number of

Database

Searched:

Perfect score:

Run on:

Sednence:

Scoring table:

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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: Albert
TITLE OF INVENTION: MAMAALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG.1997
CLASSIFICATION: 536
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US-08-94-022-49
US-08-94-135A-11
US-08-996-139-2
US-08-995-659-2
US-09-042-785A-4
US-08-95-382-2
US-08-95-382-2
US-08-95-15
US-08-95-59-15
US-08-95-659-15
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                              US-08-996-139-6
US-08-995-659-6
US-08-974-022-6
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US-09-042-785A-7
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APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-A0C-1996
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REFERENCE/DCOKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECHOME: 650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5395760-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Sequence 6, Appli
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Sequence 2, App
Sequence 191, App
Sequence 7, App
Sequence 11, App
Sequence 11, App
Sequence 11, App
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Sequence 8,
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-188-930-191
US-08-09-7827-7
US-08-097-827-11
US-08-494-574-7
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US-08-195-967-2
US-08-236-918A-8
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PCT-US96-03965-8
US-08-816-605-2
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US-08-794-796-2
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US-08-911-423-8
US-08-911-423-7
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Maximum Match 100%
Listing first 45 summaries
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Result

141.5 139.5 139.5 139.5

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67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG 126
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                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 947; DB 3; Length 311;
Pred. No. 4.3e-75;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
PRIOR APPLICATION: 536
                                                                                                                               121 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 158
                                                                                              127 HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
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                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/023,419 FILING DATE: 16-AGG-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/027,901 FILING DATE: 07-0CT-1996 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DX0612K
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100.08; Fi
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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Best Local Similarity 100.(
Matches 158; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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California
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COUNTRY:
                                                                                                                                                                                       RESULT 3
US-08-911-423-8
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                                                                                                                               61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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                                                                         0; Gaps
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                                                      1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 228;
                     Indels
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                                                                                                                                                                                                                            SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                     121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 164
5.7e-78;
thes 0;
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100.0%; Pred. No. 3.2e-75;
iive 0; Mismatches 0;
100.0%; Pred. No. 5.7 tive 0; Mismatches
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FILING DATE: 14-AUG-1997
CLASSIETCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-007-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DX0612K
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                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-911-423-6
'Sequence 6, Application US/08911423
'Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Inst: 901 California Avenue CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: DI
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 amino acids
                   164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.7
Best Local Similarity 100.
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650-496-1200
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Best Local Similarity
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                                                                                                                                                                                                                                            121
                   Matches
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APPLICATION NUMBER:
FILING DATE: 03-NOV
CLASSIFICATION: 424
Palo Alto
California
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              STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 -CTTCRHHP------CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGH 82
                                                                    APPLICANT: Gayle, Richard
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
STREET: 51 University Street
CITY: Seatile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.4%; Score 158; DB 1; Length 438; 27.4%; Pred. No. 5.1e-07; Live 11; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08147784
Patent No. 5821332
GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-----
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                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 CKPWTDCTQFGFLTVFPGNKTHNAVC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 CKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Particia A.
REGISTRATION NUMBER: 34,693
REFERENCE/POCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
                                 APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.45
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS LENGTH: 438 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                  : Baum, Peter
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                  CITY: Seatt
STATE: WA
COUNTRY: US
ZIP: 98101
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STREET 239 Lytcon Avenue

STATE: California

COMPUTE READALE FORM:

ZIP: 94301

ZOMPUTER: LBM PC COMPATIBLE

COMPUTER: LBM PC COMPATIBLE

CLASSIFICATION NUMBER: 05.047.7.784

FTLING DATE: 03.040-1993

ATTORNEY/AGEN TUNDRAFTION:

NAME: SEALLY NUMBER: 05.400

FTELECOMMUTCATION NUMBER: 05.400

FTELECOMMUTCATION NUMBER: 05.400

FTELECOMMUTCATION NUMBER: 05.422

INTORNATION FOR SEO ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 277 and no and a compatible of the compatible
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13 CRDYPG-----EECCS----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Gayle, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 FGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 ----CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.5%; Score 158.5; DB 2; Best Local Similarity 33.0%; Pred. No. 2.4e-07; Matches 38; Conservative 11; Mismatches 45;
                    APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                    NAME: Brookes, A. Anders
REGIETRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF25.
TELECOMMUNICATION INFORMATION:
TELEFAN: 301-309-8504
'TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-097-827-7; Sequence 7, Application US/08097827; Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTOREY/AGENT INFORMATION:
NAME: PETKINS, PALTICIA A.
RECISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO: 7;
                                                                                                                                                                                                                                                                                                                    LENGTH: 219 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 206 amino acids TYPE: amino acid
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-816-605-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 GVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG-- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RCCRVHTTRCCRDYPG----EECCS----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: N1, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC Compatible
OPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.6%; Score 159.5; DB 5; Best Local Similarity 31.9%; Pred. No. 2.3e-07; Matches 44; Conservative 12; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-5EP-1993
PRIOR APPLICATION NUMBER: US 08/122,796
FILING DATE: 01-FEB-1993
FILING DATE: 01-FEB-1993
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-011-1992
PRIOR APPLICATION NUMBER: US 07/267,577
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-198
ATTORNEY AGENT INFORMATION:
NAME: MICHAELS, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: 34,390
REFERENCE/DOCKET NUMBER: MOS
TELECOMMUNICATION INFORMATION:
MARINGATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                      APPLICATION NUMBER: PCT/US96/03965
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 -----SPPA---EP 117
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164 DLSPGASSVTPPAPAREP 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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COUNTRY: US
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US96-03965-8
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83 CKPWTDCTQFGFLTVFPGNKTHNAVC 108
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                                                                                                                                                                                                                                                                                                                                                                                            E: Immunex Corporation 51 University Street
                                                                                                                                                                                                      Sequence 11, Application US/08097827 Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/08494574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 amino acids
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Best Local Similarity 27.4%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-097-827-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                 41 -CTTCRHHP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98101
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-494-574-11
                                                                                                                                                                        RESULT 13
US-08-097-827-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                     ----CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGH 82
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, Walliam
APPLICANT: Fayle, Ribard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                 ; Score 158; DB 1; Length 206;
; Pred. No. 2.5e-07;
11; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 158; DB 1; Length 206; Pred. No. 2.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC----
                                                                                                                     5 CRVHT --- - TRCCRD - YPG --- - EECCSEWDCMCVQPEFHCGDPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         83 CKPWIDCIQFGFLTVFPGNKTHNAVC 108
                                                                                                                                                                                                                                                                           139 CKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 51 University Street CTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia A.
REGISTRATION UNUBER: 34,693
REPERENCE/DOCKET UNMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08494574
Patent No. 5783665
                                                 21.48; 27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.48;
27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 amino acids
                                             Query Match
Best Local Similarity 27.4°
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                        41 -CTTCRHHP------
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-08-494-574-7
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                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-494-574-7
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US-08-097-827-7
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79 OCTOCNHRSGSELKONCTPTODIVCRCRPGTOPRODSGYKLGVDCVPCPPGHFSPGNNOA 138
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-----CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 CVKHTYPSGHKCCRECOPGHGMVNRCDHTRDTLC-----HPCETGFYNEAVNYDTCK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 -CTTCRHHP-------CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGH 82
                                                                                                                                                                                                                                                                                                        APPLICANT: Baum, Peter

APPLICANT: Goodwin, Ray

APPLICANT: Goodwin, Ray

APPLICANT: Fanslow, William

APPLICANT: Gayle, Richard

TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.4%; Score 158; DB 1; Length 438; 27.4%; Pred. No. 5.1e-07; ive 11; Mismatches 45; Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQQQQQGK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION UNBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOUTHWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 395; DB 3;
Pred. No. 2.6e-28;
5; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 175.5; DB 4
Pred. No. 3.3e-09;
8; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSFGFQCI ---- DCASGTFSGGH-EGHCKPWTDCTQFG 93
                                                                                                                                                   FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION 1536
PRIOR APPLICATION DATE: 16-AUG-1996
PRIOR APPLICATION DATE: 16-AUG-1996
PRIOR APPLICATION DATA: 60-027, 901
APPLICATION NUMBER: US 60/027, 901
FILING DATE: 07-CCT-1996
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 191, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.68;
69.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.8%;
56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.69
Best Local Similarity 69.49
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-911-423-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches '28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: mou
US-09-188-930-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 HTTRCCRDY - PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 CIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
ADDRESSE: BOAN Research Institute
STREET: 901 Callfornia Avenue
CITY: Palo Alto
STATE: Callfornia
MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION UNBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                             NUMBER OF SEQUENCES: 8
CORRESONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 Callfornia Avenue
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
                                                                                                                                STREET: 901 Calife
CITY: Palo Alto
STATE: California
                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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54 GVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG-- 111
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                                           Human 4-IBB Receptor Splicing Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence S. Application PC/TUS9603965
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/816,605 FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.6%; Score 159.5; DB 2
Best Local Similarity 31.9%; Pred. No. 2.3e-07;
Matches 44; Conservative 12; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
                                                                                                       E: Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ----SPPA---EP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 DLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I: 255 amino acids amino acids
    Yu, Guo-Liang
                        APPLICANT: Gentz, Reiner TITLE OF INVENTION: Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-816-605-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                               NUMBER OF SEQUENCES: 9
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                                                                                                                            STREET: 9410 key
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                                              USA
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                                                                                                         ADDRESSEE:
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39 NNTRCCSLYAPGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVE 88
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                                                                                                                                                                                                                                                                                                                       E: Kathryn A. Anderson, Immunex Corporation
51 University Street
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Sonth, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.6%; Score 159.5; DB 1
31.9%; Pred. No. 2.3e-07;
Live 12; Mismatches 43
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COMPOTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 75.3
SOFTWARE: Microsoft Word, Version #6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/236,918A FILING DATE: 06-May-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Anderson, Kathryn A.
RECISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (226) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                          Sequence 8, Application US/08236918A Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-816-605-9; Sequence 9, Application US/08816605; Patent No. 5874440; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 31.9%
Matches 44; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Washington
COUNTRY: US
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Appli Appli Appl App1: App.

Sequence Seq

Sequence 7 Sequence 4 Patent No.

Sequence

US-09-042-785A-7 US-08-650-000-4

5395760-4

ALIGNMENTS

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Sequence 6, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Gorman, Daniel M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-ANG-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-ANG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: CALING, EGAID P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET UNBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                   US-08-996-139-2
US-08-995-659-2
US-08-995-659-6
US-08-974-022-2
US-09-042-7858-4
US-09-042-7858-23
US-08-974-022-49
US-08-974-022-49
US-08-995-158-11
US-08-995-158-11
US-08-995-659-15
US-08-995-659-15
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901 California Avenue
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Palo Alto
STATE: California
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US-08-911-423-6
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; Search time 65.86 Seconds
(without alignments)
37.204 Million cell updates/sec
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Sequence 7, A
Sequence 7, A
Sequence 11,
Sequence 2, A
Sequence 2, A
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Sequence 8, A
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Sequence 7,
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Sequence 6
Sequence 1
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/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-911-423-7
US-09-188-930-191
US-08-236-918A-8
US-08-816-605-9
PCT-US96-03965-8
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US-08-097-827-11
US-08-494-574-11
US-08-147-784-2
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3-08-911-423-2
3-08-911-423-7
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US-08-236-918A-6
PCT-US96-03965-2
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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length: 2000000000
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Maximum DB
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                                             Gaps
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                                                                                                             40 DARCCRVHTTRCCRDYPGEECCSEMDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGK 99
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Length 228;
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                                           Indels
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100.0%; Score 737; DB 3; 100.0%; Pred. No. 1.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 737; DB 3; 100.0%; Pred. No. 1.2e-58;
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                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERUCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08911423 Patent No. 6111090
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVEWION: MEMMALIA.
TITLE OF INVEWION: REAGENTS
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amino acid
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Matches 119; Conservative
                                           Matches 119; Conservative
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
Query Match
Best Local Similarity
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US-08-911-423-4
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COMPUTER TEACH TILD
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-ANG-1997
CLASSIFICATION 536
PROOF APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-ANG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATPLICATION NUMBER: US 60/027,901
FILING DATE: UT-OKENATION:
APPLICATION NUMBER: US 60/027,901
FILING DATE: UT-OKENATION:
APPLICATION NUMBER: US 60/027,901
FILING DATE: UT-OKT-1996
ATPLICATION NUMBER: US 60/027,901
FILING DATE: UT-OKENATION:
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100.0%; Pred. No. 1.5e-58;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                     ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
US-08-911-423-8; Sequence 8, Application US/08911423; Patent No. 6111090; GENERAL INFORMATION:
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Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
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TELEPHONE: 650-852-9196
                                                                                               APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotnik, Albert
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Randall, Troy D.
Zlotnik, Albert
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STATE: California
                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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ZIP: 94304-1104
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US-08-911-423-2
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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Blotnik, Albert
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
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APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-ANG-1997
CLASSIFICATION DATA:
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-ANG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 10-ANG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CAING, EGANIN P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET UNBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0612K
TELECOMMUNICATION:
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ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
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; MOLECULE TYPE: peptide
US-08-911-423-6
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STATE: California
                                                                                                                                                       September 4, 2001, 15:57:35; Search time 65.86 Seconds (without alignments) 38.142 Million cell updates/sec
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1 GCGPGRLLLGTGTDARCCRV......TQFGFLTVFPGNKTHNAVCV 122
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/RB_COMB.pep:*
/cgn2_6/ptodata/2/laa/RB_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-097-827-7
US-08-094-574-7
US-08-494-574-11
US-08-494-574-11
US-08-28-918A-8
US-08-18-605-9
PCT-US96-03965-8
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PCT-US96-03965-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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152.5
152.5
149.5
149
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                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                             OM protein
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                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                     Run on:
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Appl	Appli	23, Appl	, Appli	Appl	Appl	Appl1	App11	App11	Appli	Appli	e 6, Appli	Appl	.5, Appl	, Appl1	Appl	Appl	Appl
12,	4,	23,	~	4	11,	4	4	7	7	9	9	15,	15,	'n	C	10,	48,
Sequence 12, Appl	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-042-785A-12	US-09-042-785A-4	US-09-042-785A-23	US-08-959-382-2	US-08-974-022-49	US-09-042-785A-11	US-08-996-139-4	US-08-995-659-4	US-08-996-139-2	US-08-995-659-2	US-08-996-139-6	US-08-995-659-6	US-08-996-139-15	US-08-995-659-15	US-09-042-785A-2	US-09-041-886-27	US-09-042-785A-10	US-08-974-022-48
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401	253	605	655	197	289	451	451	591	591	616	919	625	625	573	276	277	227
17.7	17.1	17.1	17.1	16.9	16.9	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	15.5	15.2	15.2	15.0
133	128.5	128.5	128.5	127.5	127.5	121	121	121	121	121	121	121	121	117	114.5	114.5	113
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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                                        Gaps
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                                                                             1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gorman, Daniel M.
APPLICANT: Rondall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Record
                                        ó
 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 241;
                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 6.3e-60;
ive 0; Mismatches 0;
 100.0%; Score 753; DB 3; 100.0%; Pred. No. 6e-60;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08911423 Patent No. 6111090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 122; Conservative
                                      Matches 122; Conservative
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California
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14
CLASSIFICATION:
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                                                                                                                                                                                                                               121 CV 122
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|147 CV 148
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US-08-911-423-4
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61 PCPPGQGVQSQGKFSFGFQCLDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
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                                                                                                                                                                                                                                                                             MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
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PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 7.9e-60;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                    ; Sequence 8, Application US/08911423
; Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                 APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIA
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                       Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 amino acids
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Best Local Similarity 100.
Matches 122; Conservative
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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APPLICANT: Gorman,
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ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino a STRANDEDNESS:
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| CV | 154
                                                                  121 CV 122
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US-08-911-423-8
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0; Indels

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72 NYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFS 131
      12 LILGESEGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAV 71
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                                                            ------PCPPGQGVQSQGKFSFGFQCIDCASGTFS 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%; Score 149; DB 4; 28.9%; Pred. No. 1.1e-06;
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                                                                                                                                                                90 GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
                                                                                                                                                                                                                                                                            Sequence 17, Application US/08477347 Patent No. 6232446
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BELETSKY, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34,033
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,03:
REFERENCE/DOCKET NUMBER: W.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. KEVIN:
                                                                                                                                                                                                                                                                                                                                     WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-628-5197
202-737-3528
                                                            51 --DPC--CTTCRHH-----
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Best Local Similarity 28.99
Matches 37; Conservative
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20004
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US-08-477-347-17
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                                                                                                                                                                                                                                                                                                                 53 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 112
                                                                                                                                                                                                                                                                                                                                       98 GCSMC-EQDCKQGQELTKKG------CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149
                                                                                                                                                                                                                                      2 CGPGRLLLCTGTGTDARCCRVHTTRCCRDYPG----EECCS----EWDCMCVQPEFHCGDP 52
                                                                                                                                                                                                                                                                          48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                              27;
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                                                                                                                                                            Length 255;
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                                                                                                                                                                                                Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/O?'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.9%; Score 149.5; DB 3; Best Local Similarity 28.9%; Pred. No. 1.5e-06; Matches 44; Conservative 11; Mismatches 60;
                                                                                                                                                        Ouery Match 20.3%; Score 152.5; DB 5; Best Local Similarity 31.8%; Pred. No. 9.6e-07; Matches 41; Conservative 11; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BOJE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
UNDER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPBILIBLE
OPERATING SYSTEM: PC-DOS/MS-DK
SOFTWARE: PATENTIN Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
                                                                            ; MOLECULE TYPE: protein
PCT-US96-03965-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-974-022-51
                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                            TOPOLOGY:
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7 LLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD-----CMCVQPEFHCG-- 50

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72 PTEDTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPA 131 . අ

114 NKTHNAVC 121 ; : ! | 132 SNSLDTVC 139 οχ

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Search completed: September 4, 2001, 15:57:35 Job time: 377 sec

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CORRESPONDENCE ADDRESS:
                                                          Seattle
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                                                                                                                   ZIP: 98101
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                                                                                                  COUNTRY:
                                                          CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC 53
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                                                                                                              APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Gayle, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.8%; Score 164; DB 1; Length 438; 29.2%; Pred. No. 1.5e-07; tive 11; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 IDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                      Sequence 11, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08494574 Patent No. 5783665 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: PGEKINS, PATICIA A.
REGISTRATION UNUBER: 34.693
REFRENCE/DOCKET NUBBER: 2806
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ.547-0730
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 438 amino acids
amino acid
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Best Local Similarity
Matches 47; Conservi
                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   USA
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64 ETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDC 123
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Patent No. 5674704
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TILE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 IDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
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;; Pred. No. 1.5e-07;
11; Mismatches 49
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Microsoft Word, Version #6.0.1
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PARTICLA A.
REGISTRATION NUMBER: 34,693
REFERNEK/COCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CTASSIFICATION: 530
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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E: Immunex Corporatic
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%; 29.2%;
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amino acid
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Best Local Similarity 29.2'
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11
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MEDIUM TYPE: Floppy
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E: Floppy disk
IBM PC compatible
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                                                                                                                                                                       20.3%;
31.8%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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                                                   255 amino acids
                                                                                                                                                                     Query Match
Best Local Similarity 31.8%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
    TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                single
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-816-605-9
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                amino acid
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                                                                             STRANDEDNESS:
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                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 GCSMC-EQDCKQGQELTKKG------CKDCCFGTFNDQKRGICRPWINCSLDGKSVLVN 149
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 52
                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08816605
Patent No. 5874240
BAPPLICANT: NI, Jian
APPLICANT: Yu, Go. C.Lang
APPLICANT: Gents. Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                     ; Score 152.5; DB 1
; Pred. No. 9.6e-07;
11; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Human Genome Sciences, Inc
9410 Key West Avenue
                               US/08/236,918A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                        20.3%;
31.8%;
                            06-May-1994
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Best Local Similarity 31.88
Matches 41; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 GTKERDVVC 158
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                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE:
US-08-236-918A-8
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US-08-816-605-9
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53 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 112
                                                                                                               2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 52
                                                                                                                                                                  48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                       Indels 27;
        Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
; Score 152.5; DB 2;
; Pred. No. 9.6e-07;
11; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Barnard, Brown & Michaels
306 East State Street, Suite 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/267,577 FILING DATE: 07-NOV-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390
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61 PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 GCGPGKVQNGSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKHY 80
                                            MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.2%; Score 445.5; DB 3; Length 57.4%; Pred. No. 1e-32; Live 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stracthen, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,423
FILING DATE: US/08/911,423
FILING DATE: US/08/911,423
FLICATION NUMBER: US/08/911,423
FLICASIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-027-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 191, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DX0612K
                                                                                                                                                                                                                                                                                S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                              REAGENTS
    Randall, Troy D.
                        Zlotnik, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 228 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-911-423-2
                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Rese
                                                                                                                                                                                                                                    ZIP: 94304-1104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTIC
                                                                                                                                                                        CITY: Palo Alto
STATE: California
COUNTRY: USA
                        APPLICANT: Zlotnik,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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141 CI 142
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                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: RAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PCPPGQGVQSQGKFSFGFQCI----DCASGTFSGGH-EGHCKPWTDCTQFG 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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Pred. No. 1e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIPTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY AGENT INFORMATION:
NAME: CALL
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            Sequence 7, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08911423 Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 650-852-9196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-1200
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
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Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
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STRANDEDNESS: sli
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147 CV 148
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US-08-911-423-2
                                                                                    RESULT 4
US-08-911-423-7
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Length 228;

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12 LLLGLTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-
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Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                             RESULT 8
US-08-494-574-7
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                                                                                                                                                                                                                                                                                                           1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Baum, Peter
APPLICANT: Govern, Ray
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                           Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 164; DB 1; Length 206;
; Pred. No. 7.6e-08;
11; Mismatches 49; Indels
                                                                                                                                                                                                                         b; Score 212.5; DB 4; Length
b; Pred. No. 1.8e-12;
13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/097,827
CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 191 LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFRENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08097827 Patent No. 5457035
                                                                                                                                                                                                                           Query Match 28.2%;
Best Local Similarity 47.8%;
Matches 33; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-097-827-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 47; Conserva
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                                                                                                                                          ) ORGANISM: mouse US-09-188-930-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98101
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64 ETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDC 123
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-----CPPGQGVQSQGKFSFGFQC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLLG--TGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LLLGLTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC------HPC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CPPGQGVQSQGKFSFGFQC 80
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
APPLICANT: Gayle, Richard
TITLE OF INVENTION: 0x. 5783665el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 206;
                                                                                                                          IDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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Pred. No. 7.6e-08;
1; Mismatches 49
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FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Immunex Corporation
: 51 University Street
Seattle
                                                                                                                                                                                                                                                              Sequence 7, Application US/08494574; Patent No. 5783665; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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REGISTRATION NUMBER: 34,69
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29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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Gorman, Daniel M.

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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                       MAMMALIAN CELL SURFACE ANTIGENS; RELATED
REAGENTS
   Length 228;
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                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                            27 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 67
                                                                        1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 GCGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 67
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 100.0%; Score 255; DB 3; 100.0%; Pred. No. 3.6e-21;
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                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAMME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                  3: DNAX Research Institute
901 California Avenue
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FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
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Patent No. 6111090
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                  APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert.
TITLE OF INVENTION: MAMMALLI
TITLE OF INVENTION: REAGENTS
                                                                                                                                                                                                                                                          Daniel M.
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TYPE: amino acid
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Matches 41; Conservative
                                      Conservative
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STATE: California
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Ouery Match
Best Local Similarity
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US-08-911-423-4
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US-08-911-423-7
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TTUE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TTTLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 255; DB 3;
100.0%; Pred. No. 3.8e-21;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
                                                                                                         E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
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US-08-911-423-8
Sequence 8, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
                                                                                                                                                                                              ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 650-852-9196
                                                      REAGENTS
Randall, Troy D.
Zlotnik, Albert
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MEDIUM TYPE: Floppy disk.
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Matches 41; Conservative
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                                                                     NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                          STREET: 901 Califo
CITY: Palo Alto
STATE: California
                                 TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-249-472-44 US-08-809-455-44

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PCT-US95-06613-67 US-08-346-455B-69 US-08-977-221-69 PCT-US95-06613-69 US-08-977-221-38 PCT-US95-06613-38 US-08-977-767-3 US-08-977-767-3 US-08-86-165-4 US-08-465-397-44 US-08-461-965-44 US-08-461-965-44 US-08-461-965-44 US-08-461-965-44 US-08-461-965-44 US-08-461-965-44 US-08-641-965-44

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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Blotnik, Albert
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tab PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-ANG-1997
FILING DATE: 16-ANG-1996
PRIOR APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-ANG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATPONENTY/AGRAT INFORMATION:
WANNEY TABLE OF TA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
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Patent No. 6111090
GENERAL INFORMATION:
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amino acid
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-423-6
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STATE: Californi
COUNTRY: USA
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TELEFAX: 6
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US-08-911-423-6
LENGTH:
Sequence 4, Appli
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Sequence 191, App
Sequence 2, Appli
Sequence 4, Appli
                                                                                                        ; Search time 65.86 Seconds (without alignments) 12.818 Million cell updates/sec
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Sequence 7, Appli
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Sequence 334, App
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Sequence 65,
Sequence 6, A
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Sequence 3,
Sequence 8,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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            4.5
Compugen Ltd
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S-08-482-847-8

S-08-881-843A-215

S-08-974-549A-334

S-08-878-474-7

S-08-469-486-52

S-08-469-686-52
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-08-346-455B-67
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US-09-188-930-191
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S-08-815-718-3
S-08-884-072-6
S-08-997-897-2
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US-08-918-914-4
US-08-527-044-2
US-09-013-780-2
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-07-927-071-2
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                      US-09-512-363-2_COPY_33_73
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Gapop 10.0 , Gapext 0.5
            GenCore
Copyright (c) 1993
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Query
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Maximum DB
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Gaps

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DB 2; Length 109
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ZIP: Z08550-4373
CMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/013,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BUMSTEAD, Janene Marilyn J.M.
APPLICANT: TOMLEY, Flona Margaret F.
APPLICANT: DUNN, Patrick Paul James P.
APPLICANT: VERMEULEN, Arnoldus Nicolaas A.N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 3;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                25.1%; Score 64; DB 42.9%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 TDARCCRVHTTRCCRDYPGEECCSEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TNACCCLRYTNSCCSKY----CCSKCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 6001363el N.V
STREET: 1300 PICCARD DRIVE #206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TNACCCLRYTNSCCSKY----CCSKCCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 TDARCCRVHTTRCCRDYPGEECCSEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/527,044
FILING DATE: 12-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: GORMLEY, MARY E.
REGISTRATION NUMBER: 34,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.509-013-780-2
; Sequence 2, Application US/09013780
; Patent No. 6001363
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.1%;
Best Local Similarity 42.9%;
Matches 12; Conservative 3
                                                                                                                           TOPOLOGY: lines OLECTION OF A TOPOLOGY: Lines OLECTION OF A TOPOLOGY: Lines OLECTION OLECTION
   ATTORNEY/AGENT INFORMATION:
NAME: GORMLEY, MARY E.
          NAME: GONLEY, MARY E.
REGISTRATION NUMBER: 34,
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino actac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 109 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-527-044-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-013-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-08-821-994-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CGPG-----RLLLG-TGTDARCCR---VHTTRCCRDYPGEECC--SEW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08527044
Patent No. 588558
GENERAL INFORMATION:
APPLICANT: BUNSTEAD, Janene Marilyn J.M.
APPLICANT: TOMLEY, Fiona Margaret F.
APPLICANT: DUNN, Patrick Paul James P.
APPLICANT: VERMEUJEN, Arnoldus Nicolaas A.N.
TILLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPEWARE: FastERC for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Akzo No. 5885568el N.V STREET: 1300 PICCARD DRIVE #206 CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94202667.6
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/918,914
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/527,044
FILING DATE: 12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0369
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1070094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.3
Best Local Similarity 39.6
Matches 19; Conservative
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COMPUTER READABLE FORM:
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Palo Alto
                                                                      USA
                                                                                                  94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-527-044-2
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Gaps

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Sequence 2, Application US/08911423 Patent No. 6111090 GENERAL INFORMATION:
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  US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-918-914-4
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Fatent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ontust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 87.5; DB 4; Length 89;
Pred. No. 0.0034;
9; Mismatches 10; Indels
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                                  SOFTWARE PATENTIN STATEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-40G-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-40G-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 255; DB 3; Best Local Similarity 100.0%; Pred. No. 4.7e-21; Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 348
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 191
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                     DX0612K
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET UNMBER: DXC
TELECOMMUNICATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.3%;
Best Local Similarity 36.6%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mouse US-09-188-930-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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RESULT

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Gaps
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APPLICANT: Gorman, Daniel M.
APPLICANT: Standall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 87.5; DB 3; Length 228;
Pred. No. 0.0078;
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mitchell, Peter
APPLICANT: Hutchinson, Nancy
APPLICANT: Hutchinson, Michael
APPLICANT: Lawton, Michael
APPLICANT: Yocum, Sue
APPLICANT: Murry, Lynn E.
APPLICANT: Murry, Lynn E.
APPLICANT: MURSENO: SUE
APPLICANT: MURSENO: CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 GCGPGKVQNGSGNNTRCCSLYA-----PGKEDCPKERCI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/911,423
FILING DATE: 14 AUG-1997
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16 AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                               ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DX0612K
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08918914; Patent No. 5876963; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.3%;
36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 228 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 36.6
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-2
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                             CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                 ZIP: 94304-1104
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UNSURE
(119)
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(129)
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(259)
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(349)
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(185)
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(219)
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Patent No. 6114514

GENERAL INFORMATION:
FAPLICANT: SRIVASTAVA, RANJANA

APPLICANT: SRIVASTAVA, RANJANA

APPLICANT: SRIVASTAVA, BRAHM SHANKER

APPLICANT: SRIVASTAVA, BRAHM SHANKER

APPLICANT: SRIVASTAVA, BRAHM SHANKER

APPLICANT: SRIVASTAVA, BRAHM SHANKER

APPLICANT: SIVASTAVA, BRAHM SHANKER

APPLICANT: OF INVENTION: WYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT

FILE REFERENCE: U011469-7

CURRENT APPLICATION NUMBER: US/08/997,897C

CURRENT FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 7

SECTWARR: PALENTIN Ver. 2.0

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 559;
NUMBER OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                    COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPUTER: TBM COMPATION
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
COMPATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGPGRLLLGTGTDARCCRVHTTRCCR-DYPGEECCSE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.1%; Score 61.5; I Best Local Similarity 37.8%; Pred. No. 12; Matches 14; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-O
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: (E SEQUENCE CHARACTERISTICS: LENGTH: 559 amino acida TYPE: amino acid STRANDEDNESS: 81ngle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: Genbank
CLONE: 496120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
LOCATION: (4)
FEATURE:
NAME/KEY: UNSURE
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US-08-997-897-2
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                                                                  DB 1; Length 801;
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG
APPLICANT: FENG
APPLICANT: GENTZ, REINER
TITLE OF INVENTION: EPIDERMAL DIFFERENTIATION FACTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: AREMARY & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,718
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                                                               Score 64; DB 1
Pred. No. 8.8;
1; Mismatches
                                                                                                                                                                                                 326 CACGICTIGIGGIGGCCGGGICACCCIGIGACCCI 360
                                                                                                                                                      2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCS 36
                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/08815718
; Patent No. 5981220
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Patent No. 5872234
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.1%;
Best Local Similarity 37.8%;
Matches 14; Conservative
                                                                  Query Match 25.1%;
Best Local Similarity 37.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corley, Neil C.
Guegler, Karl J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07069
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                     RESULT 12
US-08-815-718-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-884-072-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AN
TITLE OF INVENTION: TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ĥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/07/906,349A
FILING DATE: 30-JUN-1992
CLASSIFICATION: 434
PRIOR APPLICATION:
                                                        APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Johns, Didier RP
TILE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION UNMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1997-03-18
SAPLIER PILING DATE: 1997-03-18
SOFTWARE: PALENTING DATE: 1996-03-22
NUMBER OF SEQ ID.NOS: 89
SOFTWARE: PALENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 4
Pred. No. 5.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3228
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 801 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 16
CORRESSONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
65, Application US/08821994A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-906-349A-6
Sequence 6, Application US/07906349A
Patent No. 5434064
GENERAL INFORMATION:
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ilarity 35.3%;
Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Brassica napus US-08-821-994-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 12; Conserv
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                                           GENERAL INFORMATION:
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STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
    Sequence
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NAME/KEY: UNSURE LOCATION: (349)
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                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6245585
GENERAL INFORMATION:
APPLICANT: Srivastava, Ranjana
APPLICANT: Srivastava, Brahm Shanker
APPLICANT: Srivastava, Brahm Shanker
ITILE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT;
FILE REFERENCE: U 011876-4
CURRENT APPLICATION NUMBER: US/09/156,836B
CURRENT FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 08/997,897
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SSET DE NO 2.
                                                                                                                                                                              7;
                                                                                                                                    DB 3; Length 430;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (20)
OTHER INFORMATION: amino acid has not been identified
NAME/KEY: UNSURE
LOCATION: (29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: amino acid has not been identified NAME/KEY: UNSURE LOCATION: (54)
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OTHER INFORMATION: amino acid has not been identified
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OTHER INFORMATION: amino acid has not been identified
NAME/KEY: UNSURE
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OTHER INFORMATION: amino acid has not been identified
NAME/KEY: UNSURE
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NAME/KEY: UNSURE
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OTHER INFORMATION: amino acid has not been identified
NAME/KEY: UNSURE
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                                                                                                                                  Query Match 22.9%; Score 58.5; E
Best Local Similarity 40.0%; Pred. No. 20;
Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                        200 CCRCWRTRCC-----CCRCWQSL 217
                                                                                                                                                                                                                          17 CCRVHTTRCCRDYPGEECCSEWDCM 41
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09156836B Patent No. 6242585
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OTHER INFORMATION:
NAME/KEY: UNSURE
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                ; NAME/KEY: UNSURE
; LOCATION: (421)
US-08-997-897-2
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                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-156-836B-2
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FEATURE:
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Gaps
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                                                                                                                            LOCATION: (182)
OTHER INFORMATION: amino acid has not been identified NAME/KEY: UNSURE
LOCATION: (185)
OTHER INFORMATION: amino acid has not been identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: amino acid has not been identified NAME/KKEY: UNSURE
LOCATION: (410)
OTHER INFORMATION: amino acid has not been identified
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: amino acid has not been identified NAME/KEY: UNSURE LOCATION: (259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (291)
OTHER INFORMATION: amino acid has not been identified
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (323)
OTHER INFORMATION: amino acid has not been identified
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OTHER INFORMATION: amino acid has not been identified
                                                                          amino acid has not been identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid has not been identified
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Job time: 378 sec
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Best Local Similarity 40.0
Matches 10; Conservative
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LOCATION: (356)
OTHER INFORMATION: a
NAME/KEY: UNSURE
LOCATION: (366)
                                                       LOCATION: (169)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE LOCATION: (269) OTHER INFORMATION:
                                                                                                                                                                                                                                                           NAME/KEY: UNSURE LOCATION: (219)
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; MOLECULE TYPE: peptide US-08-911-423-8
                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             STREET: 901 Califo
CITY: Palo Alto
STATE: California
                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
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                      APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                   Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 241;
                                                                                       Indels
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ZIP: 94304-1104

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDTUM TYPE: FILDOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION
                                                                                                                                                                               68 CVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCI 107
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                                                                                                                                                  1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
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100.0%; Pred. No. 2.5e-20;
tive 0; Mismatches 0;
                                                                                 Mismatches
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FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DX0612K
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08911423; Patent No. 6111090; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %5-08-911-423-8
Sequence 8, Application US/08911423
Patent No. 6111090
GERERAL INFORMATION:
APPLICANT: GOTMAN, Daniel M.
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TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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amino acid
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REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
Query Match
Best Local Similarity 100.
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STATE: California
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Best Local Similarity
Matches 40; Conserv
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US-08-911-423-4
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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: BOLOTH, Albert
TITLE OF INVENTION: MAWMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
Albert
MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 311;
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                                                                                                                                                                                                                                      ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14 AUG-1997
CLASSIFICATION: 536
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100.0%; Pred. No. 3.1e-20;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFLACATION: 230.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-A0C-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
RECISTRATION NUMBER: DX0612K
TELECOMMUNICATION:
TELEPHONE: 650-852-9196
                                                                                                                     ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAX Research Institute
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; Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 California Avenue
Palo Alto
California
                                                REAGENTS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
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Sequence 6, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: RAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPTAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG.1997
CLASSIFICATION: 536
                   US-09-029-348-3
US-09-029-348-3
US-08-972-008-5
US-08-972-008-5
US-08-772-008-5
US-09-381-586-20
US-08-479-7528-2
PCT-US95-0251-18
US-08-470-7528-2
US-08-470-758-2
US-08-470-758-2
US-08-470-758-2
US-08-470-758-2
US-08-476-559A-5
US-08-746-559A-4
US-08-249-687C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-COT-1996
ATONNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-652-9196
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 228 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
single
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                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 901 Califor
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
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228
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Sequence 52, Appl
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Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51
Sequence 49
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Sequence 7,
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Sequence 7,
Sequence 4,
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Sequence 5,
Sequence 17
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                                                                                                                  US-09-512-363-2_COPY_74_113
252
1 CVQPEFHCGDPCCTTCRHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                       197339
                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-327-832-5
US-08-828-584-5
US-08-477-347-17
US-08-974-022-51
US-08-974-022-49
US-09-042-785A-11
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5-09-041-886-27
5-09-042-785A-10
5-08-147-784-2
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-188-930-191
US-08-974-022-52
US-08-236-918A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-050-319B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US96-03965-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-12374-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-336-708A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-465-982-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-219-237B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-911-423-8
US-08-911-423-7
US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-911-423-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-484-438-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-475-035-4
                                                                                                                                                                                               197339 segs, 20590346 residues
                                                                          4, 2001, 15:57:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                                            length: 0
length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  September
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                                                                                                                              Perfect score:
                                                                                                                                                                Scoring table:
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Maximum DB
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                                                                                                                                            Sequence:
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                                                                           Run on:
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Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 306 East State Street, Suite 220 CITY: Ithaca
                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                  87 CIE-GFHCLGPQCTRC-EKDCRPGQELTKQG 115
                                                                                                                                                                                                                                                                         1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnard, Brown & Michaels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-70L-1992
PRIOR APPLICATION DATA: WORD APPLICATION DATA: NOW-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9603965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.6%;
                                                                                                                                                                                     Query Match
Best Local Similarity 45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                      LENGTH: 256 amino acids TYPE: amino acid
                                                                                                                                                                                                                                14; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607-273-2609
                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-236-918A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
PCT-US96-03965-2
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Kathryn A. Anderson, Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08236918A
Patent No. 5674704
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: MICROSOFT WORD, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION 1935
FILING DATE: 07-May-1993
CLASSIFICATION: 435
FILING DATE: 07-May-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
FILING DATE: 07-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQG 31
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NAME: ANGERON, KRILIYN A.
REGISTRATION NUMBER: 32,172
REFERRUCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 587-0430
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REPERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 55
SEQUENCE CHARACTERISTICS:
                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 45.2
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-022-52
                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                   91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 51 Uni
CITY: Seattle
                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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US-08-236-918A-6
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Gaps

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Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Strachan, Lorna

APPLICANT: Steeman, Matthew

APPLICANT: Onrust, Rena

APPLICANT: Onrust, Rena

APPLICANT: Onrust, Rena

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: Compositions Isolated From Skin Cells

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 49.6%; Score 125; DB 4; Length 89; Best Local Similarity 64.3%; Pred. No. 4.4e-07; Matches 18; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                              Score 168; DB 3;
Pred. No. 2.5e-11;
6; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cs-u8-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: BOYle, Willaim J.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Debestions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CVTPEYHCGDPQCKICKHYPCQPGQRVE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 191, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
                                             DX0612K
                    REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                              66.7%;
ilarity 62.5%;
Conservative
                                                                                                                                                                       LENGTH: 228 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                   TELEPHONE: 650-852-919
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-188-930-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
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Patent No. 6111090
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Randall, Troy D.
APPLICANT: 210tnlk, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILLING DATE: 14-AUG-1997
                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.3%; Score 207.5;
nilarity 82.5%; Pred. No. 1.46
Conservative 3; Mismatches
                                                                                                                     CLASSIECCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 550-822-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 232 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 901 Califo
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-911-423-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Gaps

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APPLICANT: Ono, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retroviral Expression Contructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Onc. Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
    ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Banner, Birch, McKie & Beckett
1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: POSOTSKe, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.46362
TELECOMMUNICATION:
TELEPHONE: 20-2 508-9153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 5, Application US/08828584
; Patent No. 5908762
; GENERAL INFORMATION:
                                                                                                                             ; Sequence 5, Application US/08327832
; Patent No. 5840832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840 CTTPRADCGHPCMAPCHTSSPCP 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVQPEFHCGDPCCTTCR-HHPCP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington, D.C.
District of Columbia
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington, D.C.
STATE: District of Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 508-9153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-327-832-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                      RESULT 14
US-08-327-832-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: KING, C. R.
APPLICANT: KRAUS, WATTHIAS H.
APPLICANT: AARONSON, STUART A.
TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM TITLE OF INVENTION: EGF RECEPTOR GENE
                                                                                                                                                                                                                                                                                                                                     Score 60; DB 2; Length 1210;
Pred. No. 45;
5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 EFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 EFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: NEEDLE & ROSENBERG, P.C.
Suite 1200, 127 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB
Pred. No. 45;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPLICATION NUMBER: US/08/475,035
FILING DATE: 7 Jun 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PETEYMAN, DAVIG G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.656
TELECHMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
REGISTRATION NUMBER: 18,872
REPERBENGE/ZDOCKET NUMBER: 5624-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELES: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08475035 Patent No. 5985553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%;
33.3%;
                                                                                                                                                                                                                                                                                                                                       Query Match
23.8%;
Best Local Similarity 33.3%;
Matches 12; Conservative :
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1210 amino acids
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 404/688-9880 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                 TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-484-438-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-475-035-4
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US-08-475-035-4
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ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                           US-08-336-708A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-484-438-7
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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------HPCPPGQGVQSQGKFSFGFQC 39
 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 5; Length 283;
 Indels
                                                                                                                                                                                                                                                                                ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd. STREET: 180 N. Stetson, Suite 4700
 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                Sequence 2, Application PC/TUS9612374
GENERAL INFORMATION:
APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Pacifict, Robert E.
APPLICANT: Thomason, Arlen R.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Hybrid Receptor Molecules
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.7;
3; Mismatches
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFCATION:
ATTORNES/FACATION:
NAME: Northrup, Thomas E.
REGISTRATION NUMBER: 33.268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
                                                         1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQG 31
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08336708A Patent No. 5521295
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25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 283 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVQPEFHCGDPCCTTCRH--
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Matches 14; Conservative
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein
PCT-US96-12374-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 91320-1789
                                                                                                                             RESULT 10
PCT-US96-12374-2
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 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HER4 HUMAN RECEPTOR TYROSINE KINASE
                                                            SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,708A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy
REFERENCE/COKET NUMBER: A-241A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 EATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 EFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CILOUSCOU, Jean-Michel APPLICANT: Shoyab, Mohammed APPLICANT: Siegall, Clay B. APPLICANT: Hellstr m, Ingegerd APPLICANT: Hellstr m, Karl E. TITLE OF INVENTION: HER4 HUMAN RECENUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/981,165 FILING DATE: 24-NOV-1992 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/150,704 FILING DATE: 10-NOV-1993
                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plowman, Gregory D
                                                                                                                                                                                                                                                                                               LENGTH: 644 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 33.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                            OPERATING SYSTEM:
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COMPUTER READABLE FORM:

MEDIUM TYPER: Floppy disk
MEDIUM TYPER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,584
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POSOTSK6, Laurence H.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: 1107.46362
RELEPAX: 202 508-9299
INFORMATION POSS SI
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: anino acid
TYPE: anino acid
TOPOLOGY: linear
MOLECULE TYPE: proteain
US-08-828-584-5

OUGETY MATCh
BEST LOCAL SIMILATITY 43.5%; Pred No. 46;
MALCHES 10; CORBERVALIVE 0; Mismatches 12; Indels 1; Gaps 1;
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Search completed: September 4, 2001, 15:57:36 Job time: 378 sec

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1 CVQPEFHCGDPCCTTCR-HHPCP 22

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STATE:
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                                       Gaps
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0
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APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 241;
Length 228;
                                       Indels
                                                                                             100 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                           1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
100.0%; Score 246; DB 3; 100.0%; Pred. No. 1.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 246; DB 3;
Pred. No. 1.3e-23;
; Mismatches 0;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTCRNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          Sequence 4, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
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US-08-911-423-8
Sequence 8, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
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REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
TELECOMMUNICATION: TELEPHONE: 650-852-9196
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INFORMATION FOR SEC ID NO: 4:
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                                     Conservative
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STATE: California
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Best Local Similarity
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Query Match
Best Local Similarity
Matches 41; Conserv
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ZIP: 94304-1104
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US-08-911-423-4
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                                    MAMMALIAN CELL SURFACE ANTIGENS; RELATED
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                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NURBER: US/08/911,423
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
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APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-MG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                   1: DNAX Research Institute
901 California Avenue
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-652-9196
                                                             REAGENTS
Randall, Troy D.
Zlotnik, Albert
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                    TITLE OF INVENTION: MA
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
STATE: California
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Matches 41; Conserv
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-423-6
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Sequence 11,
Sequence 2, P
Sequence 8, P
Sequence 9, P
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Sequence 4,
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1 DCASGTFSGGHEGHCKPWTD.....TQFGFLTVFPGNKTHNAVCV
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-147-784-2
US-08-147-784-2
US-08-097-827-7
US-08-097-827-1
US-08-097-827-11
US-08-097-827-11
US-08-16-605-2
US-08-16-605-9
PCT-US6-08-16-05-9
PCT-US6-03965-8
US-08-050-3198-44
US-08-050-3198-44
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US-08-477-347-17
US-08-974-022-51
US-08-974-022-2
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US-08-996-139-15
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 6, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Slotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-007-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                      E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DX0612K
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 228 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650-496-1200
                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                               94304-1104
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2 CASGIFSGGHEGHCKPWIDCIQFGFLIVFPGNKIHNAVC 40
                                                       US/08/097,827
                                                                                                           NAME: PEFKINS, PATLICIA A.
REGIZTRATION NUMBER: 34,693
REFRENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              38.6%;
                                                                      FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
22-JUN-1995
                                                                                                                                                                                                                                                        : 206 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 amino acids
amino acid
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Best Local Similarity 46.2 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-7
                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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US-08-097-827-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-097-827-11
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            APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: 00.5457035el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Gayle, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
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                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentun Release #1.0, Version #1.25
SURRINY APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95; DB 1; 1
Pred. No. 7.9e-05;
5; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CASGTESGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08494574 Patent No. 5783665
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PERKING, PARLICIGA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 206 amino acids amino acids
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Best Local Similarity 46.2'
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein us-08-097-827-7
                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                              Seattle
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                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                    ZIP: 98101
                                                                                                                                                                                                                                     COUNTRY:
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Length 206;

Score 95; DB 1; ue.... Pred. No. 7.9e-05; '---+rhes 16; Indels

5; Mismatches

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APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Goodwin, Ray
APPLICANT: Gayle, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
NUMBER OF SEQUENES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                 Sequence 11, Application US/08097827
Patent No. 5457035
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Particia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Gaps

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APPLICANT: Godfrey, Wayne
APPLICANT: Engleman, Edgar G.
TITLE OF INVEWTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED TITLE OF INVENTION: CD4+ T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                .;
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"~~d. No. 8.1e-05;
L^a 16; Indels
                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-FEB-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                     128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAIC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAIC 166
                                                                                                                                                                                Score 96; DB 2; Dred. No. 8.1e-05; 6; Mismatches 16
                                                                                                                                                                                                                                                                       2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 05490A-230
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-195-967-2
; Sequence 2, Application US/08195967
; Parent No. 624256
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/08097827; Patent No. 5457035
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.0%;
43.6%;
                                                                                                                                                                             Query Match 39.0%;
Best Local Similarity 43.6%;
Matches 17; Conservative
  ; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-147-784-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 277 amino acids amino acid
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Best Local Similarity 43.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-195-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abu...
STREET: 3/2 L.
CITY: Palo Alto
Cmarg: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inear
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US-08-097-827-7
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APPLICANT: Buck, David
APPLICANT: Corp. ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                             OPERATING SYSTEM: rc_rous/marlus
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
ATTORNEY-AGENT INFORMATION:
NAME: Ching. Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SACONMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 CAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 192; DB 3;
Pred. No. 6.8e-17;
6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/147,784
03-NOV-1993
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OBERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08147784 Patent No. 5821332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 228 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.0%;
Best Local Similarity 75.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         650-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-911-423-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 0: CLASSIFICATION:
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Sequence 8, Application PC/TUS9603965 GENERAL INFORMATION:
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COUNTRY:
                                            RESULT
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                                                                                                                                                                                                                                                                               Length 255;
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                                                                                                                                                                                                                                                                                                                   18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVC 158
                                                                                                                                                                                                                                                                                                                                                         1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                          Score 93; DB 1; 1
Pred. No. 0.00018;
6; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08816605
Patent No. S874240
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF/
TELECOMMUNICATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.8%;
                                                                                                                                                                                                                                                                          Query Match 37.8%;
Best Local Similarity 40.0%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: N1, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.8
Best Local Similarity 40.0
Matches 16; Conservative
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                                                                                                                                                                           TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-918A-8
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-816-605-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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119 DCCFGTFNDQKRGICRPWINCSLDGKSVLVNGTKERDVVC 158

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APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Moddfied human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Pactor alpha) Receptor
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
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Pred. No. 0.00018;
                                                                                                                                                         ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16.5EP-1993
PRIOR APPLICATION NUMBER: US 08/012,269
FILING DATE: 01.FEB-1993
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30.010.1992
PRIOR APPLICATION NUMBER: US 07/267,577
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07.NOV-1988
ATTORNEY AGENT INFORMATION:
NAME: MIChaels, Christopher A
REGISTRATION NUMBER: 34,390
REGISTRATION NUMBER: 34,390
REGISTRATION NUMBER: 44,390
REGISTRATION NUMBER: KWO5
TELECOMMUNICATION:
TELEPHONE: 607-273-1711
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40.0%;
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Best Local Similarity 40.03
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein
PCT-US96-03965-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Kathryn A. Anderson, Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
RECISTRATION NUMBER: 36,373
RECISTRATION NUMBER: 36,373
RECISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word, Version #6.0.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/236,918A FILING DATE: 06-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                         E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/060,843 FILING DATE: 07 May-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08236918A Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P: TELECOMMUNICATION INFORMATION TELEPHONE: 301-309-8512 TELEFAX: 301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson, Kathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.8 Best Local Similarity 40.0 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-816-605-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRECT: 51 C.
CITY: Seattle
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                     Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                  USA
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                         ADDRESSEE:
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US-08-236-918A-8
                                                                                                                  COUNTRY:
                                                                                          STATE:
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                                                                                                                                                                                                                                                                                    APPLICANT: Coodwin, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanalow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 578365sel Cytokine Which is a Ligand for NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human 4-IBB Receptor Splicing Variant
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
Best Local Similarity 46.2%; Pred. No. 0.00017;
Matches 18; Conservative 5; Mismatches 16;
                                                                                               126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                   2 CASGIFSGGHEGHCKPWIDCIQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CASGTFSGGHEGHCKPWTDCTOFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/WS-DOS
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                          Sequence 11, Application US/08494574
Patent No. 5783665
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PERKINS, PATTICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08816605 Patent No. 5874240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 438 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.2 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-494-574-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: N1, J1
                                                                                                                                                                                                   US-08-494-574-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-816-605-2
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NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alio
STATE: California
COUNTRY: USA
IP: 94301
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenin Release #1.0, version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-050-319B-44
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Gaps

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Query Match
34.1%; Score 84; DB 1; Length 41;
Best Local Similarity 41.0%; Pred. No. 0.00035;
Matches 16; Conservative 4; Mismatches 19; Indels

8 6

Search completed: September 4, 2001, 15:57:36 Job time: 378 sec

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C; Accession: T13954

R; Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
Genomics 51, 27-34, 1998
A; Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A; Reference number: Z14126; MUID: 98360089
A; Reference number: Z14126; MUID: 98360089
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T13054
A; Residues: 1-1574 < NAK>
A; Residues: 1-1574 < NAK>
A; Residues: 1-1574 < NAK>
A; Experimental source: strain Sprague-Dawley; brain
C; Genetics:
A; Gene: MEGF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 PGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 GS----PPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRKTQLLLEVPPS---TED 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 GSYLCECKPGFRLHTDGRTCLAISSCTLGNGGCQ--HQCVQLTVTQHRCQCRPQYQLQED 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 TDARCCRVHTTRCCRDY---PGEE-CCSEWDCMCVQPEFHCGDPCCTT----CRHHPCP 95
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1574;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.9%; Score 119; DB 2; Length 157
Best Local Similarity 28.3%; Pred. No. 0.092;
Matches 52; Conservative 10; Mismatches 68; Indels
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Search completed: September 4, 2001, 16:12:10 Job time: 1107 sec

208 ARSC 211 | 1 | 242 GRRC 245

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A.Map position: 20q12-20q13.2

C.Superfamily: CD27 antiqen; NGF receptor repeat homology

C.Superfamily: CD27 antiqen; NGF receptor repeat signal sequence #status predicted <SIG>
F.12-27/Product: B-cell activation protein CD40 #status experimental <MAT>
F.21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
F.31-37/Product: Exansmembrane #status predicted <TMM>
F.316-277/Domain: transmembrane #status predicted <CYT>
F.316-277/Domain: intracellular #status predicted <CYT>
F.316-277/Domain: antique carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Homo sapiens (man)
C; Species: O3-Jun-1993 #sequence_revision O3-Feb-1994 #text_change 21-Jul-2000
C; Date: O3-Jun-1993 #sequence_revision O3-Feb-1994 #text_change 21-Jul-2000
C; Accession: S04460; A60771
R; Stamenkovic, I; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A; Title: A B-lymphocyte activation molecule related to the nerve growth factor recept A; Reference number: S04460; MUID:89356608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S04460
A; Molecule type: mRNA
A; Residues: 1-77 <STA>
A; Cross-references: EMBL: X60592; NID: 929850; PIDN: CAA43045.1; PID: 929851
A; Cross-references: EMBL: X60592; NID: 929850; PIDN: CAA43045.1; PID: 929851
B; Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J: Immunol. 142, 562-567, 189
A; Tille: Biochemical characteristics and partial amino acid sequence of the receptor-A; Reference number: A60771; MUID: 89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene murine tumour necrosis factor receptor 2 protein . mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999 C;Accession: 148854
                                                                             944 TSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDPGAC 1003
       --- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 NKTHNAVCVPGSPPAEPLGWLTV--VLLAVAACVLLLTSAQLGLHIWQLRKTQLLLEVPP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CGESEFLDTWNRETHC -- - HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES
                                                                                                                                                                                                    1004 DPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTCNLLGTDP 1050
                                                                                                                                                      121 ------SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 126.5; DB 2; Length Best Local Similarity 24.0%; Pred. No. 0.0069; Matches 48; Conservative 27; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                 B-cell activation protein CD40 precursor - human N;Alternate names: B-cell surface antigen Bp50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 STEDARSCOFPEEERGERSA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 PKQEPQEINFPDDLPGSNTA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB:CD40
       108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Accession: 30339
R.Hunter 30-201-3199 | sequence_revision 30-uun-1991 | *text_change 10-Dec-1999
C.Accession: 30339
R.Hunter 30-201-319, 18291 | *sequence_revision 30-uun-1991 | *text_change 10-Dec-1999
C.Accession: 30339
NATILE: A Laminin-like adhesive protein concentrated in the synaptic cleft of the neurc
A.Recession: 303539 | MUID: 89159410
A.Accession: 203539 | MUID: 89159410
A.Accession: 303539 | MUID: 89159410
A.Accession: 303599 | MUID: 801599 | M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
HTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQGKFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840 GALSALCEGTSGOCLCRTGAFGLRCDHCQRGQWGFPNCRPCVCNGR------ADECDA
                                                                                                            ---SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG------WLTVVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1801;
                                                                                                                                                                                                                                                                                                         172 AVAACVLLITSAQLGLHIWQ-----LRKTQLLLEVPPSTE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134.5; DB 1;
Pred. No. 0.0063;
6; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laminin beta-2 chain precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.9%;
Matches 63; Conservative
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tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S5481
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-284, 1991
A;Title: Cloning and expression of conNas for two distinct murine tumor necrosis facto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A) Residues: 1-474 <-GOODA A) Residues: 1-474 <-GOODA A) Residues: 1-674 <-GOODA A) Residues: 1-674 <-GOODA A) Residues: 1-674 <-GOODA A) References: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:g199828 R) Kitissonerghis: N. F. Fellowes: R. F. Fellowes: N. F. Fellowes: R. Fellowes: R. Fellowes: R. Fellowes: R. Fellowes: A) Residue A: R. Fellowes: R. Fell
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C,Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C,Seywords: Cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;24.74/A/Product: tumor necrosis factor receptor type 2 #status predicted <NAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                        939 FATSCHQDEYSQQIVCHCRAGYTGLRCEACAPGHFGDPSRPGGRCQLCECSGNIDPMDPD 998
                                                                                                            -CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQ-- 101
                                                                                                                                                                       885 ECNTHTGACLGCRDHTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPGSQRH 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQG 104
              ---CVCNGHAD 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 EIRACTKOONRVCACEAGRYCAL-----KTHSGS--CROCMRLSKCGPGFGVASSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             999 ACDPHTGQCLRCLHHTEGPHCAHCKP-----GFHGQAARQSCHRCTCNLLGTNPQQ 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 -----SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPPAE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 474;
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                   837 GALSSLCEKTSGQCLCRTGAFGLRCDRCQRGQWGFPSCRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%; Score 119; DB 2
llarity 31.0%; Pred. No. 0.039;
Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                   ----SQGKFS------FGFQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Reference number: A38634; MUID: 91187885
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-474 <LEW>
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A; Molecule type: DNA
A; Residues: 1-22 <KIS>
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C; Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
C; Accession: 853869
R; Ilvanainen, A.; Vuolteenaho, R.; Sainlo, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Trygg
Abarix Balol. 14, 489-497, 1994
A; Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss
A; Reference number: 853869
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: 148854; MUID:95178848
A;Reference number: 148854; MUID:95178848
A;Reference receptor gene.
A;Rocession: 148854
A;Rolecule type: mRNA
A;Residues: 1-459 <RES>
A;Rocess-EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 RTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGS--CRQCMRLSKCGPGF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCCRVHTTRCCRDYPGEECCSEWD --- CMCVQPEF ---- HCGDPCCTTC - RHHPCPPGQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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F;347-407/Domain: laminin-type EGF-like homology <LE02>
F;347-407/Domain: laminin-type EGF-like homology <LE02>
F;410-467/Domain: laminin-type EGF-like homology <LE04>
F;420-519/Domain: laminin-type EGF-like homology <LE04>
F;522-552/Domain: laminin-type EGF-like homology <LE06>
F;783-828/Domain: laminin-type EGF-like homology <LE06>
F;341-674/Domain: laminin-type EGF-like homology <LE06>
F;947-983/Domain: laminin-type EGF-like homology <LE08>
F;927-983/Domain: laminin-type EGF-like homology <LE08>
F;966-1035/Domain: laminin-type EGF-like homology <LE09>
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C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAFRALC ---- GLALLCALSLGQR -----PTGGPGCGPGRLLLGTGTDARC ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%; Score 120.5; DB 2;
30.3%; Pred. No. 0.029;
Live 11; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
253869
Laminin beta-2 chain precursor (version 2) - human
N;Alternate names: s-laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:132363; OMIM:150325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.0%
Best Local Similarity 30.3%
Matches 37; Conservative
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A; Residues: 1-1798 <IIV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||
SP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP 158
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A; Residues: 23-461 CDEMA
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Note: sequence extrected from NCB1 backbone (NCBIN:63368, NCBIP:63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons A; Reference number: A36007; MUD:90349572
A; Status: preliminary
                                   A; Residues: 1-195, R7, 197-461 <KOH>
A; Residues: 1-195, R7, 197-461 <KOH>
A; Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
B; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A; Reference number: A48416; MUID:91370690
A; Accession: A48416
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A; Residues: 23-40;56-56;136-141;300-306 <LOE>
A; Residues: 23-40;65-66;131-1536, 1990
J. Biol. Chem. 265, 1531-1536, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden A; Reference number: A35010; MUID: 90110215
A; Accession: B35010
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A; Residues: 116-140, 'P',142-195,'R',197-362,'T',364-461 <HEL>
A; Residues: 116-140, 'P',142-195,'R',197-362,'T',364-461 <HEL>
A; Cross-references: GB: M35897; NID: 9339751; PIDN: AAA63262.1; PID: 9339752
B; Loctscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Blol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Reference number: A23666; MUID: 91056048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X80021; NID: 9666044; PIDN: CAA56324.1; PID: 9825701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 461;
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C; Superfamily: tumor necrosis factor receptor type 2; NGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;262-279/Domain: transmembrane #status predicted <TMN> F;280-461/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 10.4%; Score 139.5; DB 1; Local Similarity 23.0%; Pred. No. 0.00097; les 64; Conservative 26; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;120-162/Domain: NGF receptor repeat homology <NG3> F;164-201/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;40-76/Domain: NGF receptor repeat homology <NG1> F;78-119/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: GDB:125914; OMIM:191191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule Lype: protein
A; Residues: 27-31 < ENGS
R; Khnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial
A; Reference number: I38094; MUID:95121934
A; Accession: I38094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 CGPG---RLLLGTGTDARC----
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1p36.2-1p36.2
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A; Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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Best Local S.
Matches 64
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SKENDLY

OX40 antigen precursor - rat

OX40 antigen precursor - rat

OX40 antigen precursor - rat

NiAlternate names: nerve growth factor receptor homolog

C; Species: Rattus norvedtous (Norway rat)

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C; Accession: S12783; Secondary, A.N.

A; Reference number: S12783; MUID:90214614

A; Reference number: S12783; MUID:90214614

A; Recession: S1278

A; Nolecule type: mRNA

A; Residues: 1-271 < MAL>

A; Cooss-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831

C; Superfamily: CD27 antigen: NGF receptor repeat homology

C; Keywords: growth factor receptor; transmembrane protein

F; 1-19/Domain: signal sequence #status predicted < MAT>

F; 21-231/Product: OX40 antigen #status predicted < TMM>
F; 211-235/Domain: transmembrane #status predicted < TMM>
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N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Specias: Homo saplans (man)
C;Specias: Homo saplans (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A;Reference number: A35356; MUID:90260639
A;Reference number: A35356; MUID:90260639
A;Reture: prelliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>A;Residues: 1-461 <SMI>A;Residues: 1-461 <SMI>A;Residues: 1-461 <SMI>A;Residues: 1-461 <SMI
A;Residues: 1-461 <MI
A;Residues: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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182 PPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.0%; Score 160.5; DB 2 26.0%; Pred. No. 1.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Conservative
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Matches 59; Conserva
                                                                                                                                                                                   194 KTQLLLEVPP 203
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11;

Gaps

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A;Status: pre-liminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-28/, LV/ <GRI>
A;Cross-references: GB:MM3312; NID:g1553059; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A;Experimental source: BALB/C, liver
A;Mote: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46515.
C;Superfamily: CD27 antigon; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
J. Immunol. 149, 3921-3926, 1992
A,Tilte: Genomic structure and chromosomal mapping of the murine CD40 gene. A;Reference number: A46515; MUID:93094586
A;Accession: A46515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 CHPCDSGEFSAQWNREIRCHOHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 NKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRK------ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
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A,Molecule type: mRNA
A,Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --------RVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
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A;Accession: 154182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: 154182
R; Beans, M; Chaffante, M.; Cassiman, J.J.; Van den Berghe,
Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a hncDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              necrosis factor receptor 2-related protein - human
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A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 0.00079; 23; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 134.5; DB 2; 26.4%; Pred. No. 0.0023; tive 17; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 ARRODPOEMEDYPGHNTAAPVOETLHGCOPVTOEDGKES 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), DB 2;
0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LCGL--ALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.4%;
Best Local Similarity 23.3%;
Matches 65; Conservative 23
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les 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: JC5559
R; Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A; Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phyto A; Reference number: JC5559; MUID: 97290889
A; Accession: JC5559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: root (Comment: This protein is a lectin specific for N-acetylgucosamine-containing saccharid (Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0 Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 17-Mar-2000
                      -CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 122
                                                     -----SPPAE----PLGW-----LTVVLLAVAACVLLLTSAQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 CGVDFGNRTCPNDLCCSEWGWCGITEGYCGEGCQSQC---NHQRCGKDFAGRTCLNDLCC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ-C---IDCASGTFSGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Cross-references: GB:M83312; NID:g1553058
A;Cross-references: GB:M83312; NID:g1553058
A;Vote: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, rel.
B;Gtimaldi, J.C.; Torres, R.; Rozak, C.A.; Chanq, R.; Clark, B.A.; Howard
                                                                                                                                                               |:| | : | | | STDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP
                                                                                                                                                                                                                                                                            230 TPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: This protein is a section special continuation of C;Superfamily: lection-related plant chitinase; hevein chitin-binding dc;Keywords: glycoprotein C;Keywords: glycoprotein predicted P;96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                      185 LGLHIWQLRKTQLLLE----VPPSTED-ARSCOFPEEE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Phytolacca americana (Virginian pokeweed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.4%; Score 139; DB Best Local Similarity 28.8%; Pred. No. 0.00 Matches 36; Conservative 18; Mismatches
                                                                                                                                GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lectin-B - Virginian pokeweed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-295 <YAM>
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NDAHC 243
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Gaps

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GenCore version 4.5
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OM protein - protein search, using sw model

September 4, 2001, 15:53:43 ; Search time 80.15 Seconds (without alignments) 222.394 Million cell updates/sec Run on:

US-09-512-363-2 1340 1 MAQHGAMGAFRALCGLALLC......EEERGERSAEEKGRLGDLWV 234 Title: Perfect score: Sequence:

Scoring table:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES ery tch Length DB ID	To the first	256	4.7 255 2	2.6 272 2	2.3 277 2	2.0 271 2	0.4 461 1	0.4 295 2 JC5559	0.4 305 2	0.0 435 2	0.0 1801 1	1 277 2	0 459 2	9 1798 2	9 474	9 1574 2	5 1371 2	5 1687 2	329	1 1797 2	152 2	2318 2	3 1111 2	2 2907 2	2 164 2 T2427	2 2531 2	1 3635 2	1 3566
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Result No. Score		20						7 139									115.5										109	

thrombospondin 2 p MEGF2 protein - hu	Doc4 protein, stre	MEGF8 protein - hu	thrombospondin 3 -	fibrillin I - bovi	agglutinin isolect	integrin beta-3 ch	insulin-like growt	latent transformin	hypothetical prote	alpha-2-macroglobu	integrin beta-5 ch	notch protein homo	fibrillin 1 precur	agglutinin isolect
TSHUP2 T00250	T14271	T00209	A46016	A55567	A28401	PN0510	IGHUR1	A55494	T25061	A53102	JC2005	S18188	A47221	AEWT2
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1172	2825	1737	926	2871	186	680	1367	1820	788	4543	959	2531	3002	213
7.8	7.8	7.7	7.6	7.6	7.6	7.6	7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.5
105	104.5	103.5	102.5	102.5	102	102	101.5	101.5	101	101	100.5	100.5	100.5	100
	35	m	4	S.	9	7	۵	6	0		~	m	4	ß

## ALIGNMENTS

RESULT 1  BA2333 T-Call antigen 4-1BB precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Musculus (house mouse) C; Accession: B32333; 148879 R; Kwon, B.S.; Weissman, S.M. A; Reference number: A32393; MUID:89184547 A; Reference number: A32393; MUID:89184547 A; Residues: 1-256 KWO A; Residues: 1-256 KWO A; Residues: 1-256 KWO A; Residues: 1-256 KWO A; Reference number: A3256-252, 1994 A; Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B A; Reference number: 148879; MUID:94179805 A; Cross-references: EMBL:U02567; NID:91117783; PIDN:AA493113.1; PID:9409178 A; Retain: preliminary; translated from GB/EMBL/DDBJ A; Retaidues: 1-256 CRES A; Cross-references: EMBL:U02567; NID:91117783; PIDN:AA493113.1; PID:9409178 A; Retaidues: 1-256 CRES A; Cross-references: EMBL:U02567; NID:91117783; PIDN:AA493113.1; PID:9409178 A; Residues: 1-256 CRES A; Cross-references: EMBL:U02567; NID:9411783; PIDN:AA493113.1; PID:9409178 A; Residues: 1-256 CRES A; Cross-references: EMBL:U02567; NID:9411783; PIDN:AA493113.1; PID:9409178 A; Residues: 1-256 CRES A; Cross-references: EMBL:U02567; NID:9411783; PIDN:AA493113.1; PID:9409178 A; Residues: 1-256 CRES A; Cross-references: Status predicted CMAT> E; 24-256/Product: 4-1BB protein #status predicted CMAT>	Query Match  Query Match  Query Match  Best Local Similarity 28.7%; Pred. No. 9:8e-09;  Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;  Qy 34 CGPGRL-LLGTGTDARCCRVTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC 89
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A; Title: The human OX40 homolog: CDNA structure, expression and chromosomal assignmen
A;Title: Gene structure and chromosomal localization of the mouse homologue of A;Reference number: 148334; MUID:95255413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
                                 A:Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------CPPGQGVQSQGKFSFGFQCID 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GEYNEAVNYDICKOCIOCNHRSGSELKONCIPIODIVCRCRPGIOPRODSGYKLGVDCVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VPGSPP--AEPLGWLTVVLLAVAACVLLLTSAQLGLHI----WQLRK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 TVQSTTVWPRTSELP-SPPTLVTPEGPAFAVLLGLGLGLGAPLTVLLALYLLRKAWRLPN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID:9472957; PIDN:CAA53576.1; PID:9472958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LALTIGVTARRINCVKHTYPSGHKCCRECOPGHGMVSRCDHTRDTLC------HPCET 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GAMGAFRALCGLALLCALSLG------QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 272;
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                                                                                                                                                                                                                                                                                            A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                         12.6%; Score 168.5; DB 2; 24.9%; Pred. No. 3.7e-06; iive 18; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: 137552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling,
Eur. J. Immunol. 24, 677-683, 1994
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A; Accession: 137552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:X75962;
C; Superfamily: CD27 antigen; NGF
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Matches 60; Conserv
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A; Residues: 1-277 <RES>
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OX40 homolog
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A.Residues: 1-106, KR., 108-255 <SCH>
C.Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neord C.Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix C.Superfamily: CD27 antigen: NGF receptor repeat homology
C.Superfamily: CD27 antigen: NGF receptor repeat homology
C.Reywords: glycoprotein; phosphorotein; receptor; transmembrane protein
F.1-17/Domain: signal sequence #status predicted <SIG>
F.18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <WAT>
F.18-13/Domain: transmembrane #status predicted <TMM>
F.187-13/Domain: carbohydrate (Asn) (covalent) #status predicted
F.242/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted F.242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794
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N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: 148700; 148334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: 148700; MUID:94044750
A;Accession: 148700
                                                                                                                                                                                                      В.
                                                                                         C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #text_change 01-Dec-2000
C;Date: 29-May-1998 #text_change 01-Dec-2000
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C;Accession: I38426; JT0752
C;Accession: M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.
A;Reference number: I38426; MUID:94374434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U03397; NID:9571320; PIDN:AAA53133.1; PID:9571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
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                                                              lymphocyte activation-induced receptor ILA precursor - human
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                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
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A; Residues: 1-272 <RES>
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PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.
PROSITE; PSO0139; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PSO011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; 1 ATP-binding; Phosphorylation; Repeat; Signal.
SIGNAL 31 741 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
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8.6%; Score 115.5; DB 1; Length 1370;
Best Local Similarity 27.1%; Pred. No. 0.021;
Matches 57; Conservative 22; Mismatches 52; Indels 79;
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EXTRACELLULAR (POTENTIAL)
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                            62 CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
                                                                                    C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                         146 NKTHNAVCVPGSPPAEPLGWLTV - VLLAVAACVLLLTSAQLGLHIWQLRKTQLLLEVPP 203
                                                                                                                                                                                                                 179 TNKTDVVC----GPQDRLRALVVIPIIFGILFAILLVL----VFIKKVAK-KPTNKAPH 228
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STRAIN=VDB; TISSUB-Lung;
MEDLINE=96072804; Pubmed=7594541;
FORCE W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
Browning J.L., Ware C.F.;
Mouse lymphoto.in-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping."; Genomics 30:312-319(1995).
CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT
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-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
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HSSP; P25942; 1CDF.
A MGD; MGI:104875; Ltbr.
JR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00050; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
$1 30 POTENTIAL.
$1 415 LYMHOTOXIN-BETA RECEPTOR.
$1 223 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-07T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                415 AA
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EMBL; L38423; AAB00846.1; -.
EMBL; U30798; AAA81334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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P50284;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- PGTEAEVTDEIMDTDVNCVPCKPGHFONTSSPRARCOPHTRCEIOGLVEAAPGTSYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  necrosis factor receptors demonstrate one receptor is species specific.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDILINE-9118785; Pubmed-1849278; MEDILINE-91187885; Pubmed-1849278; Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Coeddel D.V.; "Cloning and expression of cDNAs for two distinct murine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Mismatches 103; Indels
                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.2%; Score 123; DB 1; 25.3%; Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-91246168; Pubmed-1645445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWR2_MOUSE STANDARD; PR. P25119; P97893; 01-MAY-1992 (Rel. 22, Last seque 15-JUL-1999 (Rel. 38, Last annot TUMOR NECROSIS FACTOR RECEPTOR 2 TNFRSFIB OR TWFR2 OR TWFR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44956 MW;
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415 AA;
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82
171
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receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 EIRACTKOONRVCACEAGRYCAL-----KTHSGS--CROCMRLSKCGPGFGVASSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGGGVQSQG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 119; DB 1; Length 474; Pred. No. 0.0047;
                                                                           Feldmann M., Chernajovsky Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Indels
                           Jacob C.O., Liu J., Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                    Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (P
462EAE398C4D6563 CRC64;
                                                                                                                                                                                                                                                                                                                 Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
N-LINKED (GLCNAC...
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                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                                    PFam; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                           Kissonerghis M., Fellowes R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50319 MW;
                                                                                                                                                                                                          EMBL; M60469; AAA39752.1; -. EMBL; M59378; AAA40463.1; -. EMBL; U39488; AAA85021.1; -. EMBL; X87128; CAA60618.1; -.
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                                                                                                                                                                                                                                                                  MGD; MGI:1314883; Infrsflb.
InterPro; IPR001368; -.
[3]
SEQUENCE OF 1-26 FROM N.A.
                                                        SEQUENCE OF 1-22 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                         HSSP; P19438; INCF
                                                                  rissur-Liver;
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: TETRAME NOT 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA RALNS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 187:934-939(1992).

-!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
TYROSINE-PROTEIN KINASE ACTIVITY.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Du J., Delafontaine P.; "Inhibition of vascular smooth muscle cell growth through antisense "Inhibition of a rat insulin-like growth factor I receptor cDNA."; Circ. Res. 76:963-972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental regulation of the rat insulin-like growth factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                                                      01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
1NOULOR-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 913-1017 FROM N.A.
MEDLINE-92412145; PubMed-1530648;
Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
"A new member of the insulin receptor family, insulin receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natí. Acad. Sci. U.S.A. 86:7451-7455(1989)
PRT; 1370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
MEDLINE-95277910; PubMed-7758167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90017496; Pubmed-2477843;
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Pfam; PF01030; Recep_L_domain;
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN TYROSINE PHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-364 FROM N.A.
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STANDARD;
                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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InterPro; IPR000494;
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Pfam; PF00069; pkinz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95191650; PubMed=7885444;
MEDLINE=95191650; PubMed=7885444;
Moakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
"Aberrant differentiation of neuromuscular junctions in mice lacking s-laminin/laminin beta 2.";
Nature 374:258-262(1995).
-I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ -I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-I- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR NERVE TERMINALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBGULIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANES (MAJOR COMPONENT).
TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMIN CHAINS TO FORM A COLLED COLL STRUCTURE.
DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
SIMILARITY: CONTAINS 12 LAMININ BGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 12 LAMININ DOMAIN IV.
                                                  1003
892 HTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SQRHFA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.-G., Ortonne J.P., Meneguzzi G.; band of mouse chromosome 9.";
                                                                                                                                                                                                                                                                                                                                                                                "Structural organization of the human and mouse laminin beta2 chain genes, and alternative splicing at the 5' end of the human transcript.";
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                  944 TSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDPGAC
                                                                                                   1004 DPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTCNLLGTDP 1050
                                                                           -----SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 159
                                                                                                                                                                                                                                                                                                                                                            Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
Albrechtsen R., Wewer U.M.;
                                                                                                                                                                         061292; 062182; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1999 (Rel. 38, Last annotation update) LAMININ BETA-2 CHAIN PRECURSOR. LAMB2 OR S-LAM OR LAMS.
                                                                                                                                                                 PRT; 1799 AA
                          ----FGFQCIDCASGTF----
                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 271:13407-13416(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94319092; Pubmed-8043959;
Aberdam D., Galllano M.F., Mattel
"S-laminin gene (Lams) maps to Fl
Mamm. Genome 5:393-334(1994).
                                                                                                                                                                                                                                                                                                                                    STRAIN-129/J;
MEDLINE-96278760; PubMed-8662701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 348-428 FROM N.A.
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                         PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TFE_EGF; 12.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCOMPLETE).
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COLLED COLL (POTENTIAL).
BY SIMILARITY.
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EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
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EMBL; 045624; AAC53535.1; JOINED.
EMBL; X75928; CAA53532.1; -.
HSSP; P02468; 1KLO.
                                                                                                                                                                                                                            Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                            MGD; MGI:99916; Lamb2.
InterPro; IPR000561; -.
InterPro; IPR001886; -.
InterPro; IPR002049; -.
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3D-STRUCTURE MODELING OF 24-144.
MEDLINE=97189482; PubMed=9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";
                  MEDLINE-69356608; PubMed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
"A B-lymphocyte activation molecule related to the nerve growth
factor receptor and induced by cytokines in carcinomas.";.
EMBO J. 8:1403-1410(1989).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
BC8776EC2C4A5680 CRC64;
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InterPro; IRPO01368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
PROSITE; PS50050; TNFR_NGFR_2; 4.
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TNER-CYS 3.
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Matches 48; Conserv
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01-MAY-1992 (Rel. 22, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAOL RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
(TUMOR NECROSIS FACTOR RECEPTOR 5).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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Pred. No. 0.0026;
8; Mismatches 63; Indels 115;
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W; 1F28967A67AEDE33 CRC64;
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N-LINKED (GLCNAC...) (
                                        SIMILARITY
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Best Local Similarity 24.7%;
Matches 61; Conservative
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[1]
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                                                                                               MIM;
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                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                            | : | | | | | | : | : | | | | | | | CAQHTPCIPGFGVMEMATETIDIVCHPCPVGFFSNQSSLFEKCYPWISCEDKNLEVLQKG 178
                                                                                                                                                                                                                                                                                                                        179 TSQTNVICGLKSR------MRALLVIPVVMGILITIFGVFLYIKKVVKKPKDNEMLPPA 231
                                                                                                                                                                                                                                                                                                          146 NKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRK------ 194
                                                                                                                                                           Gaps
                                                                                                                                                                                                   58
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                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR)
LIBBR OR INFECR OR INFRSF3.
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                                                                                                                                                                                                7 LCALWGCLLTAVHLGQCVT----CSDKQYL----HDGQCCDLCQPGSRLTSHCTALEKTQ
                                                                                                                                                                                                                        C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ware C.F., Hession C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith C.A.;
                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL). C791CB6D2FEA574E CRC64;
                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
                                                                                                                                      Length 289
                                                                                                                                    10.4%; Score 139; DB 1; Length 28
23.3%; Pred. No. 6.6e-05;
.ive 23; Mismatches 107; Indels
          EXTRACELLULAR (POTENTIAL).
                    POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F.,
Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G.,
"A lymphotoxin beta-specific receptor.";
Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNE DEVELOPMENT.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                   ----TOLLEVP-----PSTEDARSCOFPEERGERS 222
                                                                                                                                                                                                                                                                                                                                                                       232 ARRODPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKES 270
                                                                                                                                                                              LCGL--ALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCC--
                                                                                                                                                                                                                                                                                                                                                                                                                          435 AA
 CD40L RECEPTOR
                                        4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                       32111
                                                                                                                                                        65; Conservative
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                    215
289
187
60
103
144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                        AA;
                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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153
289
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          DOMAIN
TRANSMEM
                                                                                           CARBOHYD
SEQUENCE
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Best Local
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TNRC_HUMAN
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the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 CPP----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICOLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG------WLTVVLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --CRDYPGEE---C 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .) (POTENTIAL) . .) (POTENTIAL)
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 435;
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                                                                                                                                                                                                                           PROSITE; PS00620; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
624626E6022F656F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AVAACVLLITSAQLGLHIWQ-----LRKTQLLLEVPPSTE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 PLAFFLLLATVFSC---IWKSHPSLCRKLGSLLKRRPQGE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134.5; DB 1
Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                    LYMPHOTOXIN-BETA
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                   the European Bioinformatics Institute. Thuse by non-profit institutions as long
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TNFR-CYS
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26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          211
81
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                                                                                                                                                                                            -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
                                                                                                   Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
"A laminin-like adhesive protein concentrated in the synaptic cleft
of the neuromuscular junction.";
Nature 338:229-234(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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8 X LAMININ EGF-LIKE REPEATS (DOMAIN
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N BGF-LIKE 2.
N BGF-LIKE 3.
N GGF-LIKE 4.
N BGF-LIKE 5 (INCOMPLETE).
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EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 10.
EGF-LIKE 112.
EGF-LIKE 112.
EGF-LIKE 113.
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                                                              TISSUE=Liver;
MEDLINE=89159410; PubMed=2922051;
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InterPro; IPR001886; -.
InterPro; IPR002049; -.
Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X16563; CAA34561.1; -
PIR; S03539; MMRTS.
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                                       SEQUENCE FROM N.A.
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DOMAIN II.  DOMAIN ALPHA.  COLLED COIL (POTENTIAL).  COLLED COIL (POTENTIAL).  COLLED COIL (POTENTIAL).  BY SIMILARITY.  BY SHAMILARITY.  BY SIMILARITY.  BY S	LINNED (GLCNAC ) ( -LINKED (GLCNAC ) ( -LINKED (GLCNAC ) ( ; 97AEF3ZF8F31FA75 CRC  core 134.5; DB 1; Len red. No. 0.00068; Mismatches 60; Ind	GAERALC-GLALLCALSLGORPTGG-PGCGPGRLLLGTGTDARCCRV 52
11100 1100 1100 1100 1100 1100 1100 11	1351 1502 ; 196473 M 10.0%; 26.9%; vative 6	-GLALLCALSLG
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PDB;
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- I- FUNCTION: RECEPPOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

- I- PUNCTION: RECEPPOR FOR TNF-BETA.

- I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEAVELOW THESEJUES.

- I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW WETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID PORTION OF THERE CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF THERE CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF THE TALKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO THE ALCHARA AND BLOCKS ITS INVERACTIONS WITH RECEPPORS.

--- SIMILARITY: CONTRAINS A LA-NGFR/TNER-TYPE CYSTEINE-RICH REGION.

--- DATABASE: NAME-ENDY-E1, NOTE-CLINICAL INFORMATION ON ENDY-E1;

--- DATABASE: NAME-ENDY-E1, NOTE-CLINICAL INFORMATION ON ENDY-E1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.; "Blochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90110215; PubMed-2153136;
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human
"The Evidence for immunological cross-reactivity with cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                               "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                        "Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX. MEDIINE-9221409; bubmed-10206649; PARK Y.C., Burkitt, V., Villa A.R., Tong L., Wu H.; Structural basis for self-association and receptor recognition of
                                                                                                                          SEQUENCE FROM N.A.

BEDLINE-SGOS99748, PubMed-8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
MEDLINE-91056048; PubMed-2173696;
Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
A second tumor necrosis factor receptor gene product can shed naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
Ringold G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation.";
J. Biol. Chem. 267:21172-21178(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990)
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MEDLINE-93016040; PubMed-1328224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | | | : | | | STDICRPHQICN----VVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 -CMCVQPEFHC-----GDPCCTTCRHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 122
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BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 CSPGQHAKVECTKTSDIVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR
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                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00552; TRER_NGFR_1; 2.
PROSITE: PS50050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
Phosphorylation; Pharmaceutical; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> T (IN REF. 4).
603B580ECD67636F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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               or send an email to license@isb-s1b.ch)
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AAA36755.1;
                                           EMBL; M32315; AAA59929.1;
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TNFR_C6; 4
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, A23666; A23666.
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MIM; 191191; -.
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196
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461 AA;
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96
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                                                     230 TPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMT---- 285
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HSSP; P25942; ICDr.
HSSP; P25942; ICDr.
i InterPor; IPR00158; -.
A Pfam; PF00020; TNFR_C6; 4.
A PROSITE; P500652; TNFR_NGFR_1; 1.
DR PROSITE; P550050; TNFR_NGFR_2; 1.
A Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
TGNAL 1 19 CD40L RECEPTOR.
20 >269 CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunology 90:294-300(1997).
-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirano A., Brown W.C., Estes D.M.; "Cloning, expression and biological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. .) (POTENTIAL) (GLCNAC. .) (POTENTIAL)
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                                                                                                           185 LGLHIWQLRKTQLLLE----VPPSTED-ARSCQFPEEE 217
                                                                                                                                               -----QVKKKPLCLQREAKVPHLPADKARGTQGPEQQ 317
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TNFR-CYS 1.
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TNER-CYS 3.
TNER-CYS 4.
N-LINKED (GL
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MEDLINE-97281252; PubMed-9135560;
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Best Local Similarity 27.00
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DT 01-NOV
DT 01-NOV
DT 15-JUL
DE CD40L
GN HIRRSP
OC BUKALY
OC BUKALY
OC BUXALY
OC COLORI
RT COLORI
DR ENCST
CC COLORI
DR FROST
DR FROST
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT REPEAT
FT REPEAT
FT CARBOH
FT CARBO
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                                                                                                                                                                                                                                                                                        01-707-1992 (Rel. 23, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
                         118 SCTPHSLCLPGFGVKGIATGLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKGLVEQHV 177
                                                                  145 GNKTHNAVC------VPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLR 193
88 TCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Torres R.M., Clark E.A.; "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."; J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00652; TWFR_NGFR_1; 1.
PROSITE; PS50050; TWFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                          289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=92105763; Pubmed=1370315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-Liver; MEDLINE-93094586; PubMed=1281194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M94128; AAA37404.1; JOINED. M94127; AAA37404.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M83312; AAB08705.1; -. EMBL; M94126; AAA37404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00020; TNFR_c6; 4
                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:88336; Infrsf5
InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A46476; A46476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
                                                                                                                                    194 KTQLLLE 200
                                                                                                                                                                      226 PCTLWLK 232
                                                                                                                                                                                                                                                                                                                                                            INFRSF5 OR CD40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torres R.M.;
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CD40_MOUSE
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                                                                                                                                                                                                                 Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                               "Gene structure and chromosomal localization of the mouse homologue
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Immunol. 25:926-930(1995).

- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

- I- SUBGELLUIAR LOCATAINS: THE OX40L/GP34 CYTOKINE.

- SIMILARITY: CONTAINS A LA-NGFR/TWRR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 4.
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> G (IN REF. 2).
W, 06F7BE4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:104512; Thfrsf4.
InterPro: IPR001368; -.
Pfam; PF00020; TNRR_C6; 3.
PROSITE; PS00652; TNRR_NGF_1; 3.
PROSITE; PS50050; TNRR_NGFR_1; 3.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                      Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A., Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                              update)
                           272 AA
                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                   MEDLINE-94044750; PubMed-822823;
                                                                                                                                                                                                                                                                                                         MEDLINE-95255413; PubMed-7737295;
                                                                                                                                                                                                                                                                   Immunol. 151:5261-5271(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z21674; CAA79772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAA59476.1; -.
                                                                                                    INFRSF4 OR TXGP1 OR OX40.
                           STANDARD;
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272
272
236
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165
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124
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                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                            rat 0X40 protein.
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15
272 AA;
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HSSP; P25942; 1CDF.
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                                                                                                                                                                            SEQUENCE FROM N.A.
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20
212
237
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                        OX40_MOUSE
P47741;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                                      186 TVQSTTVWPRTSELP-SPPTLVTPEGPAFAVLLGLGLGLGAPLTVLLALYLLRKAWRLPN 244
                                                -----CPPGQGVQSQGKFSFGFQCID 114
                                                                                                                                                                                 154 -----VPGSPP--AEPLGWLTVVLLAVAACVLLLTSAQLGLHI----WQLRK 194
               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94170844; PubMed=7510240;
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
Hummel M., Fonatsch C., Stein H.;
"The human OX40 homolog: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLATLLWETQRPTFRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoml;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001368; -.
Pfam: PF00120; TNFR_c6; 3.
PROSITE: PS00652; TNFR_NGFR_1; 3.
PROSITE: PS500650; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (ACT35 ANTICEN) (TAX-TRANSCRIPTIONALLY
ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
                                                                                                                  CASGIFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC----
                                                                                                                                                                                                                                                                                                                                                                     277 AA
                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
01-OCT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X75962; CAA53576.1;
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P25942; 1CDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFRSF4 OR TXGP1L
                                                                                                                                                                                                                                                                                                                                                                   OX40_HUMAN S'
P43489; Q13663;
01-NOV-1995 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S76792;
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11;

Gaps

93;

70; Indels

DB 1; Length 272;

12.6%; Score 168.5; DB 1 24.9%; Pred. No. 2.1e-07; iive 18; Mismatches 70

Conservative

60;

Matches

Similarity

Query Match Best Local S

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SEQUENCE FROM N.A.
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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                Signal.
                                                                                                                                          SIGNAL
                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                  55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                            ....-----PLGWLTVVLLAVAACVLLLTSAQLGLHIWQLR 193
                                                                                                                                                                                                                                                                                                                                                                                           182 PPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLLR 241
                                                                                                                                                                                                                                                                                                         62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-90214614; PubMed-2157591;
Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive T
lymphocytes - a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                   4 GARRIGRGPCAALLILGIGISTVTGIHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN
                                                                                                                                                                                                                                     5 GAMGAFRALCGLALLCALSLG-----QRPTGGPGCGPGRLLLGTGTDARCCRVHT
                                                                                                                                                                                                                                                                                                                                109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAE----
                                                                                         TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
TNFR-CYS (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
49F15525941550BF CRC64;
                                                                                                                                                                                      12.3%; Score 165; DB 1; Length 277; 25.2%; Pred. No. 4.2e-07; ive 18; Mismatches 113; Indels
                       OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC 0X40).
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                                                                   4 X TNFR-CYS.
TNFR-CYS 1.
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                                                                                                                                                     29340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFRSF4 OR TXGP1L OR OX40.
                                                                                                                                                                                                  Best Local Similarity 25.23
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
         28
277
214
235
277
169
65
107
1126
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242 RDORL---PP 248
                                                                                                                                                                                                                                                                                                                                                                                                                          194 KTQLLLEVPP 203
                                                                                                                                                    277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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P15725;
                                           TRANSMEM
DOMAIN
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REPEAT
REPEAT
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CARBOHYD
CARBOHYD
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01-AUG-1991 (Rel. 19, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
1-GT-2000 (Rel. 40, Last annotatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90260639; PubMed=2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PCPPGQGVQSQGKFSF 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL) C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
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MEDLINE-91045991; PubMed-2172983;
Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
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POTENTIAL.
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TWER-CYS 3 (INCOMPLETE).
TWER-CYS 4.
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TNFR-CYS 1.
send an email to license@isb-sib.ch).
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## ALIGNMENTS

RESULT	JLT 1						
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666	01-FEB-1991 01-FEB-1991 15-JUL-1999	(Rel. 17, (Rel. 17, (Rel. 38,	Created) Last seq Last ann	sed) sequence update) annotation update)	pdat upd	.e) Jate)	
GN	4-1BB LIGAND RECEPTOR F TNFRSF9 OR ILA OR LY63	RECEPTOR	OR C	R (T-CE 7 OR CD	LL A	(T-CELL ANTIGEN 4-1BB). OR CD157.	
SO	Mus musculus (Mouse)	(Mouse)		•		•	
88	Eukaryota; Metazoa; Mammalla; Eutheria;	., .,	Chordata; Rodentia;	Craniat Sciurog	a; V nath	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.	
X O	NCBI_TaxID=10090;	:0600;					
r gr	SEQUENCE FROM N.A.	N. N. N.					
RX.	MEDLINE-89184547; PubMed-2784565	14547; Pub	4ed-27845	65;			
RA	Kwon B.S., W	B.S., Weissman S.M.;	. M.;	E	-	. = ()	
RL		sequences of two inductions 1-cert genes.; Natl Acad Sci H.S.A. 86:1963-1967/1989)	I.S.A.	86.1963	-196	57 (1989)	
RN	[2]				ì		
RP	SEQUENCE FROM N.A	M N.A.					
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XX o	MEDLINE=941/9805; PubMed=8133039;	19805; Publ	4ed-81330	39;	3	E	
RT	"Genomic ord	Janization	and chro	nosomal	100	nwon b.s., notan c.a., nim n.n., Fichald n.i.,	
R	antigen 4-1B	B. ":		1000	1	;	
RL	J. Immunol.	Immunol. 152:2256-2262(1994)	2262(1994				
RN	[3]						
RP	CHARACTERIZATION, AND	TION, AND	SEQUENCE	OF 25-29	29.		
XX :	MEDLINE-9313	19510; Pubh	led=7678	21;			
RA		Kim YJ.		Z., Hurtado		J., Kin K.K., Pickard R.T.,	:
KA E	Kwon B.S.;	1001	4.10		,	0,000	
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Z.	J. Immupol. 150:771-781(1993).	150:771-78	31(1993).				
႘	- 1 - FUNCTION	1: RECEPTOR	R FOR THE	PUTATI	VEC	SYTOKINE 4-1BBL. POSSIBLY	
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ဗ္ဗ		SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN	ION: TYPE	I MEMB	RANE	S PROTEIN.	
3 5	N HOSSIT - I -	TISSUE SPECIFICITY: EXPRESSED INDUCTION: OPETANT BY DAY AND	C EXPRES	SED ON	ON THE	SURFACE OF ACTIVATED T-CELLS	. 277
3 8		INDUCTION: OFTIMAL BI FMA AND IONOMICIN.	L BI FMA	AND LON		INDUCTION: OFTIMAL BI FMA AND LONOMICIN.	
3 5	STEET C	TI CONTA	WT W CNT	NGF R/ 1 N	1 1 1	ALII: CONIMINS A LA-MGEN/INETIFE CISIELNETALCH REGION.	
88	This SWISS-F	ROT entry	is copyr	ight. I	t is	SWISS-PROT entry is copyright. It is produced through a collaboratio	poratio
ပ္ပ	between the	Swiss Ins	stitute o	f Bioin	form	the Swiss Institute of Bioinformatics and the EMBL outstation	cation
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3 5	or send an email to license	an email to licenseelsb-sib.cn)	censeels	e18D-S1D.Cn).	:		
3 2	EMBL: ,104492	J04492: AAA40167	7.1:				
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 KDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKW 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J. Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G., "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94085794; PubMed=8262389; Schwarz H., Tuckwell J., Lotz M.; "A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE
                                                                                                                                                                                                                                     Ther-cys 1.
Ther-cys 2.
Ther-cys 3.
Ther-cys 4.
N-Linked (GLChAC. . .) (POTENTIAL).
N-LINKED (GLCHAC. . .) (POTENTIAL).
W, 93A10D03C60813C4 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
4-1BE LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
(T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 201.5; DB 1; Length 256; 28.7%; Pred. No. 3.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Indels
                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                  Pfam; PF00020; TNFR_C6; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL). 4 X INFR-CYS.
                                                                                                                                      4-1BB LIGAND RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 QLRKTQLLLEVP-----PSTEDARSCQFPEEERG 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Immunol. 24:2219-2227(1994)
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27598
  Tnfrsf9
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256
187
208
256
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MGD; MGI:1101059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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Q07011;
                    InterPro;
                                                                                                                                                         DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                  SIGNAL
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ilenserice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GNKTHNAVCVPG-----SPPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
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-LINKED (GLCNAC. . .) (POTENTIAL)
F3A563FE5EF00460 CRC64;
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                                                                                                                                                                                                                                                                                                                            Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
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| HSSF; ...
| MIM: 602250; ...
| InterPro; IPR001368; ...
| R Pfam: PP00020; TNFR_C6; 2. |
| PROSITE; PS00052; TNFR_NGFR_1; 1. |
| DANSITE; PS0050; TNFR_NGFR_2; 1. |
| DANSITE; PS0050; TNFR_NGFR_2; 1. |
| FT CHAIN 18 255 4-1BB LIGAND RECEPTOR. |
| FT CHAIN 18 255 4-1BB LIGAND RECEPTOR. |
| FT TRANSMEM 187 213 POTENTIAL. |
| FT DOMAIN 47 213 POTENTIAL. |
| FT TREPEAT 47 86 TNFR-CYS 1. |
| FT REPEAT 47 86 TNFR-CYS 1. |
| TNFR-CYS 1. 
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                                                                                                  to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVE DURING T CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                           MEDLINE-95347766; PubMed-7622190;
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                                                                                                  Submitted (MAR-1999)
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REVISION TO 107
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Best Local Similar
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168 IValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL 185
                                                                                                                                                                                                                                                                                                 sGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysGlyA 228
                                                                                                                                                                                                                                                                                                                 663 CCAGTTCCCTGAGGAGGAACGCGGGGACCAGACA...GAAGAAAAGTGTC 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGTTTGGATTTCTCACCATGTTCCCTGGGAACAAGACCCACAATGCT 462
                                                                                                                                                                                                                                195 ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSerCy 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reagents
                                                      613 ACCCAGCCATTCGCGGAGGTGCTGTCAGCTGAGGATGCTTGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AGGAGAAGCACTATGGGGGCATGGCCATGCTGTATGGAGTCTCGATGCT
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                                                                                                                                                               euGlyLeuHisIleTrpGlnLeuArgLys........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
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Gaps: 4
Percent Identity: 53.975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1073)
Gorman,D.M., Randall,T.D. and Zlotnik,A.
Mammalian cell surface antigens; related
Patent: US 6111090-A 1 29-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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LOCUS AR108737 1073 bp DNA
LOCUS Sequence 1 from patent US 6111090.
ACCESSION AR108737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
283 c 310 g
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3.847
76.569
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US-09-512-363-2 x AR108737
                                                                                                                                                                                                                                                                                                                                                                   228 rgLeuGlyAspLeuTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pat1:AR108737
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JOURNAL
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KEYWORDS
SOURCE
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413
                                152
                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                 211
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                                                             CSLYAPGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVA
CAMGTFSAGROGHCRUWTNCSQFGFLTMFPGNKTHNAVCIPBPLDTBQYGHLYVIFLV
MAAOIFFLTTYVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTE
EKCHLGGRWP"
                                              /translation="MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRC
                                                                                                                                                            /note="type I transmembrane protein"
/product="glucocorticoid induced TNFR family related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 AGTGCAAGATCTGCAAGCACTACCCCTGCCAACCAGGCCAGAGGGTGGAG 312
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14-FEB-2001

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TPASPCYSMetCysValGinProGluPheHisCysGlyAspProCysCys	103 103 16204 CCCCTGACGCCTGACGCCTCCTCATCCATCCCAGCAACTCCACCAG 16253
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15754 TCCTGTCTGGGGCCTGGGGCTGCTCTGGAAGGAGCAGCTCAAG 15803	######################################
103 103	188 SITETIPGIBLEUATG
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LOCUS MMU82534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 ysCysThrThrCysArgHisHisProCysProFroGlyGlnGlyValGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 TCTCAAGGGGATATTGTGTTTGGCTTCCGGTGTGTTGCCTGTGCCATGGG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 yThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysT 135
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                                                               1 (bases 1 to 1020)
Riccardi, C.
RECEPTOR BELONGING TO THE TNE/NGF RECEPTOR FAMILY
                                                                                                                     Patent: WO 9824895-A 1 11-JUN-1998;
RICCARDI CARLO (IT); PHARMACIA & UPJOHN SPA (IT)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG
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Percent Identity: 53,975
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                                unidentified
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KEYWORDS
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                  SOURCE
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/note="type I transmembrane protein; belongs to the tumor
necrosis factor receptor/nerve growth factor receptor
family"
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Nocentini, G., Giunchi, L., Ronchetti, S., Krausz, L.T., Bartoli, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nocentini, G., Ronchetti, S., Bartoli, A., Spinicelli, S., Delfino, D., Migliorati, G. and Riccardi, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nocentini,G., Bartoli,A., Ronchetti,S., Giunchi,L., Cupelli,A.,
Dellino,D., Migliacrati,G. and Riccardi,C.
Gene structure and chromosomal assignment of mouse GITR, a member
of the tumor necrosis factor/nerve growth factor receptor family
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Mus musculus glucocorticoid induced TNFR family related protein
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/product="glucocorticoid induced TNFR family related
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Cell Death Differ. (2000) In press
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463 GTGTGCATCCCGGAGCCACTGCCCACTGAGCAATACGGCCATTTGACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="thymocytes" 46. .732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Cell Biol. (2000) In press
4 (bases 1 to 1020)
Riccardi, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                         euGlyLeuHisIleTrpGlnLeuArgLys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C3H/HeN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U82534.1 GI:2228583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgLeuGlyAspLeuTrp 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    710 ATCTGGGGGGTCGGTGG 726
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COMMENT

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121564 121653: gap of 100 bp 124321 124420: gap of 100 bp 124421 124539: contig of 2657 bp in length 124321 1245420: gap of 100 bp 124421 124583: contig of 4163 bp in length 128684 128683: gap of 100 bp 131528 131527: contig of 2844 bp in length 131528 131627: contig of 3046 bp in length 131628 134673: contig of 3046 bp in length 134674 134773: gap of 100 bp 100 bp 139104 139203: gap of 100 bp 110 gap of 139504 145549: contig of 6346 bp in length 145550 145649: gap of 100 bp 110 bp 145550 145649: gap of 100 bp 169504 145549: contig of 6346 bp in length 145550 145649: gap of 100 bp 169504 145549: contig of 6346 bp in length 145550 145649: gap of 100 bp 169504 145549: contig of 6346 bp in length 145550 146047: contig of 6346 bp in length 145550 146047: contig of 6346 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1703.3 1704.2: Cont.y of 100 bp
1703.3 1704.2: gap of 100 bp
1703.3 181011: contig of 10469 bp in length
1809.1 181011: gap of 100 bp
181012 184184: contig of 3173 bp in length.
Location/Qualifiers
                           20: gap of 100 bp
97596: contig of 13876 bp in length
                                                                       97696: gap of 100 bp
104680: contig of 6984 bp in length
                                                                                                                     104780: gap of 100 bp 10764: contig of 2384 bp in length 107264: gap of 100 bp 113440: contig of 6176 bp in length 113540: gap of 100 bp 121563: contig of 8023 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148008 148107: gap of 100 bp
148108 151671: contig of 3564 bp in length
151672 151771: gap of 100 bp
151772 157223: contig of 5452 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157224 157333: gap of 100 bp

157324 161601: contig of 4278 bp in length

161602 161701: gap of 100 bp

161702 170342: contig of 8641 bp in length
       83620: contig of 3982 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29867 . .33002
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48363 . .52129
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                                                                                                                                                                                                                113441 113540; gap of
113541 121563; contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-465B22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment_cha1
11115. .23404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:T7
                                                                                                                     104681 104780:
104781 10716
107165 107264:
107265 11344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184184)
                                                                                                                                                                                                                                                        Mclay, K.
Direct Submission
Submitted (21-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquirites: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13396610.
  DNA HTG 22-MAR-2001
1 clone RP11-465B22, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads Chemistry:
Dye-terminator Big Dye; 96% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 180984; sum-of-contigs
Insert size: 227650; 6.6% error; agarose-fp
Quality coverage: 4.53x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.2.
8110 11014: contig of 25...
11015 11114: gap of 100 bp
11115 23404: contig of 12290 bp in length
23405 23504: gap of 100 bp
23405 23504: gap of 100 bp
23405 23504: contig of 2635 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102: gap of 100 bp 48262: contig of 15160 bp in length 162: gap of 100 bp 52129: contig of 3767 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11115 23404: contig of 12290 bp in length 23505 25139: contig of 2635 bp in length 26140 2639: gap of 100 bp 100 bp 29766: contig of 3527 bp in length 29767 29866: gap of 100 bp 2966: contig of 3537 bp in length 2967 29866: gap of 100 bp 2966: contig of 3136 bp in length 29867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5628 5727: gap of 100 bp 5728 88009: contig of 2282 bp in length 8810 8109; gap of 100 bp 11014: contig of 2905 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp
4799 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p of 100 bp
contig of 9225 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54: gap of 100 bp
63812: contig of 2258 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oof 100 bp contig of 4191 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp
6436 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5627: contig of 5627 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 172641 bases at least 040 Consensus quality: 176408 bases at least 030 Consensus quality: 178512 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
AL390719 184184 bp DNA
Homo sapiens chromosome 1 clone RI
PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenter code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73103 79538: contig of 79539 79638: gap of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of
                                                                                             AL390719.15 GI:13445418
HTG; HTGS_PHASE1; HTGS_DRAFT
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68103: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52229: gap of 61454: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73102: gap of
79538: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
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                                                                                                                                                                    Homo sapiens
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61555
63813
63913
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  LOCUS
DEFINITION
                                                                                                                                                                    ORGANISM
                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                         REFERENCE
                                                                                                                   KEYWORDS
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34	ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys	50 14353
51	rgValHisThrThrArgCysCys	61
14354	GETTCACACGACGCGCTGCTGCCGC	14403
. 61		61
14404	GTTTACTTAACGCGGACCGGCCAAGGCGTCCCGCGGAAGCCGGGATGGGT	14453
61		61
14454	GGGCGCCCCCTTCCCGTGCTCAGACCGGCGTTGCTGAGGTCTAAGGAGG	14503
. 61		61
14504	GTGGGCACAGAGCCGCCAGCAGCGGGAGCCTTCCGGAGGGAG	14553
61		61
14554	GCGGAGGTGTGCCAGCTCCAGTGGC	14603
61		61
14604	GCCAGGTGGGAGCGCCCTCAA	14653
61		61
14654	GGCTGTTCCAGGTCCTGCTGGGCGGGTCGTG	14703
61		61
14704	AGCCCCCTCCTGCCCAGTT	14753
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14754	CTGGCCTGCTGCTGTGACCTGCACCTGGGGATGAGGGTTCAGCTG	14803
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14804	ACACGGCTGGTCTGGAGGAAGCTGGCAGGGAAGTCACCCCAGAGCTTC	14853
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14854	TTCCTCCAGGGCCTGTGGGTTGGGAAGGGAGGCTCTGTCCGGAGGCCCCAG	14903
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14904	TGTGGCTGGTGGGGGGGGACAGCGCCCAGACACCAGGCAGG	14953
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14954	TGAGGTGTCGACGGGCCTCCAGGGGACTGTGGCACTGTTGGGGGGCCACCCC	15003
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15004	TGGGTCCTGCAGGGCAGCTCCTGGTTGCATATGGAGTTAGCACCTGGGC	15053
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15054	AGGGCCAGCTGTGGGGCGCAAAGGGGGAGTAGCCAGGCCCACATGGCCCCA	15103
61		61
15104	GGAGAAAGAGACAGGTAAAACCCAAGGGTCCAGACTCCCAGCCAG	15153
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15154	CCCTCTGCTCCCTGGAGCCAACTGTGGGTGGAGAACGGACAACCTCACTC	15203
61		61

Φ

alignment\_scores:
Quality: 905.50 Length: 910
Ratio: 3.870 Gaps: 7
Percent Similarity: 25.714 Percent Identity: 25.385

Align seg 1/1 to reverse of: AL162741 from: 1 to: 110195

alignment\_block: US-09-512-363-2 x AL162741/rev

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61		61
16003	GGGGCAGCTCCTGGTTGCATATGGAGTTAG	16052
61		61
16053	TGAGGTGTCGACGGGCCTCCAGGGGACTGTGCACTGTTGGGGGCCACCCC	16102
61		61
16103	TGTGGCTGGTGGTGGGGACAGCGCCCCAGACACCAGGCAGG	16152
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16153	TTCCTCCAGGGCCTGTGGGTTGGGAAGGGAGGCTCTGTCCGGAGGCCCAG	16202
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16203	ACACGGCTGGTCTGGAGGAAGCTGGCAGGGAAGTCACCCCAGAGCTTC	16252
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16253	CTGGCCTGCTGCCTCTGACCTGCGGGATGAGGGTTCAGCTG	16302
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16303	CCATCGCCCAGCCCCTCCTGCCCAGTTGAGGGCCCCCCTGCACCACCGT	16352
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16353	AGGACGGCTGTTCCAGGTCCTGCTGGGCGGGTCG	16402
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16453	GGGAGGCGGAGGTGTGCCAGCTCCAGCCAGTGGCCC	16502
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16553	CCCCCTTCCCGTGCTCAGACCGGCGTTGCTGAGGTC	16602
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16603	TAACGCGGACCGGCCAAGGCGTCCCGGCGGAAGCCGGG	16652
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50 16703	ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys	34
16753	GCTGCTGTGCGCGCTCAGCCTGGGTCAGCGCCCCACCGGGGGTCCCGGGT	16802
34	LeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGl	17

C3031 JHJKJHJJKKJKJJJKKJKJJHJHJKKJJJKJJHJHJJJHJHJJJHJHJJJJ CV03	15002 TGCGCACCTCCCCCAG
	103
61	14952 CTGGGACGGCAGACA
5852 CCCIGGAGGCCCGAGGGAGGCCTGGGAGGGGGGCCCTCAGCCCAGCT 15803	
62Pro.GlyGluGluCysCysSerGluT 70	14902 GAATGGATGATGGGG
rpaenCvsWetCvsValGlnDrnGlnDheHisCvsGlvAenDrnCvsCvs 86	103
GGGACTGCATGTGTGTGTTTTTTTTTTTTTTTTTTTTTT	14852 CCCTGCACTGGCCTG
87 ThrThrCysArgHisHisProCysProProGlyGlnGlyValGlnSer.G 103	14802 CCTCCCTCCTCCTC
	109 lyPheGlnCysIleAs
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103 103	126 GlyHisCysLysProT
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103 103	a.

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ć	Co. Latter Biographic Teacher Co. of Teacher Co.	
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194 194	101
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Align seg 1/1 to: AR108739 from: 1 to: 723	
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17 aLeuLeuCysAlaLeuSerLeuGlyGlnargProThrGlyGlyProGlyC 34	ACCURNAL REFERENCE AUTHORS TITLE
34 ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys	JOURNAL FEATURES SOUR
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67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84  :::	SOD

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                                                                                                                                                                                                                                                                                                                                                                       12-APR-2000
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                                                                                                                                                                               IntendlyLeuHisIleTrpGlnLeu.....hrg 193
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CON Homo sapiens GITR-D mRNA, complete cds.
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Mclay, K.
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| 511 TG
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                                                                                                              217
                                   411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 GGGGACCTTCTCCGGGGGCCACGAAGGCCACTGCAAACCTTGGACAGACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 ValProProSerThrGluAspAlaArgSerCysGlnPheProGluGluGl 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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Percent Identity: 72.650
GenBank Accession Number AF229434"
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ç
                                                                   /product="GITR-D"
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US-09-512-363-2 x AF241229
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Euteleostomi;
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Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L0872; 100% of reads
Chemistry: Dye-terminator ET-amersham; 23% of reads
Consensus quality: 10531 bases at least Q40

Consensus quality: 107393 bases at least Q30

Consensus quality: 107393 bases at least Q30

Consensus quality: 107393 bases at least Q30

Insert size: 108995; sum-of-contigs

Insert size: 160899; 6.7% error; agarose-fp

Quality coverage: 6.7% error; agarose-fp

Quality coverage: 6.79x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequesf@sanger.ac.uk on Mar 11, 2001 this sequence version replaced g1:13234857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reads Chemistry:
                                                                                                                                                                                                                                                                                                                                              *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                 234
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22302 35252: contig of 12951 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42169: COLLEGE 100 bp 100 bp 62318: contig of 20149 bp in length 67218: aso of 100 bp
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3673 7177: contig of 3505 bp in length
7178 7277: gap of 100 bp
7278 11454: contig of 4177 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35253 35352: gap of 100 bp
35353 42069: contig of 6717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3572: contig of 3572 bp in length
                                                 uArgGlyGluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpV
                                                                                GTGCCGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTCCCCGAGGAAGA
                                                                                                                                                                                                                                                                                                                                              DNA
1 clone RP5-902P8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ***, 13 unordered pieces.
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Eukaryote; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 110195)
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HTG; HTGS_PHASE1; HTGS_DRAFT
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PROGRESS ***, 13 unordocen
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42070 42169: gap of
42170 62318: conti
62319 62418: gap of
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167 621 184

194 721 210 771

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostom1;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,
Tumas,D., Watanabe,C. K. and Wood,W.I.
Compositions and methods for the treatment of immune related
                                                                                                                                                                                                                                                                                                                                                                                                                     184 InLeuGlyLeuHisIleTrpGlnLeu......arg 193 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
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                                                                                                                                                                                                                                                                                                             rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC
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Genentech, Inc. (US)
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WO0105972
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/db_xref="taxon:9606"
335 c 354 g 17:
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Location/Qualifiers
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KEYWORDS
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1 (bases 1 to 1008)
Williams, P.M. and Gerritsen, M.E.
Promotion or inhibition of angiogenesis and cardiovascularization by tumor necrosis factor ligand/receptor homologs
Patent: WO 0103720-A 1 18-JAN-2001;
Genentech, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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GAGACCCAGCTGCTGGTGGTGCCGCCGTCGACCGAAGACGCCAGAAG
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Percent Identity: 96.680
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 335 c 354 g 17
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LOCUS AX074381 1008 bp DNA
DEFINITION Sequence 1 from Patent WO0103720.
AX074381 GI:12710522
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Ratio: 5.652
Mlarity: 97.095
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alignment\_scores:

source

FEATURES

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

BASE COUNT ORIGIN

alignment\_block

Align seg 1/1

17

21

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AX074384
AX074384.1 GI:12710524
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                             source
                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                             REFERENCE
AUTHORS
                                                                                                                          JOURNAL
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                                                                                                                                                FEATURES
                                                                                                    TITLE
                                                                                                   AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
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                                                                                                                                    17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
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  Percent Identity: 96.680
                                                                  to: 1008
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5.652
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                                                                 to: AX077027
                                alignment_block:
US-09-512-363-2 x AX077027
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           Percent Similarity:
                                                                  Align seg 1/1
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91)
Williams, P.M. and Gerritsen, M.E.
Promotion or inhibition of anglogenesis and cardiovascularization
by tumor necrosis factor ligand/receptor homologs
Patent: WO 0103720-A 4 18-JAN-2001;
Genentech, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                            uLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyCysG
                                                                                                                                                                                                                                                                                                                                                                                     Length: 263
Gaps: 3
Percent Identity: 88.213
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                                                                                                                                                                                                                                                                                                                                             to: 951
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 317 c 336 g 16.
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                Quality: 1246.00
Ratio: 5.348
Harity: 88.593
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                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-512-363-2 x AX074384
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human
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06-FEB-2001

PAT

Wed

LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

TITLE

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14-FEB-2001
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                                                                                                                                                                                 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrH1sAsn 150
                                                                                                                                                                                                                                                                                                                                                                                                          GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
                                                                                                                                                                                                                                                                                                             rGlyThrPheSerGlyGlyH1sGluGlyH1sCysLysProTrpThrAspC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reagents
                                                                                                          301 CAGTCCCAGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTGCCTC
                                                                                     sSerGluTrpAspCysMetCysValGlnProGluPheH1sCysGlyAspP
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Gorman, D.M., Randall, T.D. and Zlotnik, A.
Mammalian cell surface antigens; related
Patent: US 6111090-A 3 29-AdG-2000;
Location/Qualifiers
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LOCUS AR108738 1006 bp DNA
DEFINITION Sequence 3 from patent US 6111090.
AR108738 GI:12824225
VERSION AR108738.1 GI:12824225
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Quality: 1322.50
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Unclassified.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                           Gurney, A.L., Marsters, S.A., Huang, A., Pitti, R.M., Mark, M.,
Baldwin, D.T., Gray, A.M., Dowd, P., Brush, J., Heldens, S., Schow, P.,
Goddard, A.D., Wood, W.I., Baker, K.P., Goddowski, P.J. and Ashkenazi, A.
Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR
Curr. Blol. (1999) In press
2 (bases I to 726)
Gurney, A.L., Marsters, S.A., Huang, A., Pitti, R.M., Mark, M.,
Baldwin, D.T., Gray, A.M., Dowd, P., Brush, J., Heldens, S., Schow, P.,
Goddard, A.D., Wood, W.I., Baker, K.P., Godowski, P.J. and Ashkenazi, A.
AF125304 726 bp mRNA PRI 02-APR-1999
Homo sapiens glucocorticoid-induced TNFR-related protein (TNFRSF18)
MENNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDARCCRVHTTRCCRDYPGEBCCSENDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVOS
QGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLFVFPGNKTHNAVCVPGSPPA
EPLGWLTVVLLAVAACVLLITSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 726)
                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-FEB-1999) Molecular Oncology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
Location/Qualifiers
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/protein_id="AAD22635.1"
/db_xref="GI:4558503"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GCTGCTGTGCGCGCTCAGCCTGGGTCAGCGCCCCACCGGGGGTCCCGGGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="TNFRSF18"
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                                                                                                    AF125304.1 GI:4558502
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Ratio: 5.652
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US-09-512-363-2 x AF125304
             seq_documentation_block:
LOCUS AF125304
                                                                                                                                                              Homo sapiens
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source

FEATURES

gene

CDS

JOURNAL

TITLE

alignment\_scores:

BASE COUNT

ORIGIN

Align seg 1/1

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AX055408
AX055408.1 GI:12228687
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Ratio: 5.652
Marity: 97.095
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ACCESSION
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SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                        TITLE
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                                                                                                             MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCySGlyLeuAl
                                                                                                                                                                    aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
                                                                                                                                                                                                                           34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys
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    1.680
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             Percent Identity: 96
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Sequence 38 from Patent W00073452.
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5.652
97.095
                                                                                 to: AR108738
                                        alignment_block:
US-09-512-363-2 x AR108738
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LOCUS AX055408 ·
Ratio:
Percent Similarity:
                                                                               Align seg 1/1
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251 101

29

17

LOCUS DEFINITION

210

194

184

151

167

134

227

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Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                    Goddard, A., Godowski, P.J.
abakoff, R.C., Shelton, D.L.
                                               Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A. Godowski, P. J. Gurney, A.L., Hebert, C., Henzell, W., Kabakoff, R.C., Shelton, D. I. Tunas, D., Watanabe, C. K. and Wood, W.I. Compositions and methods for the treatment of immune related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170
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Gaps: 1
Percent Identity: 96.680
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Genentech, Inc. (US)
Location/Qualifiers
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148 a 335 c 354 g 171 t
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US-09-512-363-2
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1 (bases 1 to 723)
Williams, P. M. and Gerritsen, M.E.
Promotion or inhibition of angiogenesis and cardiovascularization by tumor necrosis factor ligand/receptor homologs
Patent: WO 0103720-A 2 18-JAN-2001;
Genentech, Inc. (US)
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                                                  67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP
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/db_xref="taxon:9606"
236 c 254 q 127
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Sequence 2 from Patent W00103720.
AX074382 GI:12710523
AX074382.1 GI:12710523
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Quality: 1322.50
Ratio: 5.652
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101 GCGCCCTGGGCCCTCCTGCTTGGGACGGGACGGACGCCCCCTGCTGC 150
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US-09-512-363-2 x AF117297
                                                                                                                                                           seq_name: gb_pr5:AF117297
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gb_pat2:AX093178
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1 X75962 H.sapiens mRNA for OX46
AR019518 Sequence 6 from patent
114933 Sequence 6 from patent
1 XX011588 Sequence 1 from Patent
1 X17037 Rat mRNA for OX40 antig
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95 i AL162741 Homo sapiens chromc
84 i AL390719 Homo sapiens chromc
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-YGAPEXT=0.500
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Query length: 234
Database: GenEmbl:*
Database sequences: 1144157
Database length: -856060004
Search time (sec): 1459.860000
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gb_htg20:AL162741
gb_htg22:AL390719
gb_pat1:A91704
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9b_pati:ANI709
9b_rol:AR229433
9b_rol:AR229434
9b_rol:AR229434
9b_rol:AR109216
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gb_pat2:AX077027
gb_pat2:AX074384
gb_pat1:AR108739
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gb_sts2:G28572
gb_pr9:HSU03397
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1 AX097545 Sequence 3 from Pat
1 AX09629 Sequence 3 from Pat
1 AX055373 Sequence 3 from Pat
1 AX056645 Sequence 1 from Pa
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Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
Kwon, B., Yu, K.Y., Ni, J., Yu, G.L., Jang, I.K., Kim, Y.J., Xing, L.,
Liu, D., Wang, S.X. and Kwon, B.S.
Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand
J. Biol. Chem. 274 (10), 6056-6061 (1999)
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/db_xref="G1:4378800"
/db_xref="G1:4378800"
/translation="MAQHGAMGARGAFALCGLALLCALSLGQRPTGGPGGCGPGRLLLGTG
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EPLGWLTVVLLAVAACVLLLFSAQLGLHIWQLRKTQLLLEVPPSTEDARSCGFPEEER
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Direct Submission
Submitted (30-DEC-1998) Micro. 6 Immunol., Indiana University, 635
Barnhill Dr ., Indianapolis, IN 46202, USA
Location/Qualiflers
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Homo sapiens TNF receptor superfamily activation-inducible protein
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/product="TNF receptor superfamily activation-inducible
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Gaps: 0
Percent Identity: 100.000
    936
936
936
1114
1114
    0.0131
0.0131
0.0131
0.0300
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/cell_type="T lymphocyte"
1. .705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .705
/organism="Homo sapiens"
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    194.74
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230 c 247
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195 ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSerCy 211
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                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                           Quality: 1317.50
Ratio: 5.655
Percent Similarity: 97.083
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                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-512-363-2 x AAA58588
                                                                                                                                                                                                                                               alignment_scores
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transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthemia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; nephritis; real neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammaticno; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli; ztnfr10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes tumour necrosis factor receptor zinfilo. The specification describes extracellular domains of BR43x2 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or BGMA (a related B cell protein). These contain a cysteine rich domain, and are used for inhibiting zinff activity. They may also be used for inhibiting BR43x2, TACI or BGMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                      227
                                                                                                                                                                                          820
                                                                                                                                                                                                                                                                                                seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA58588
                                                AGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGA
                                                                                                     210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG
                                                                                 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding tumour necrosis factor receptor ztnfr10
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                                                                                                                                                                                                                                           227 lyArgLeuGlyAspLeuTrpVal 234
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    AAA58588 standard; DNA; 813
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arthritis. The zinf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 GTTCACACGACGCGCTGCTGCCGCGATTACCCGGGCGAGGAGTGCTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 rGluTrpAspCysMetCysValGlnProGluPheH1sCysGlyAspProC
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                                                                                                                                                                                                                                                                                                                                Sequence 813 BP; 114 A; 276 C; 283 G; 140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 240
Gaps: 1
Percent Identity: 96.667
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The present sequence is a cDNA encoding molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06 cDNA library. This sequence is expressed in cardiovascular and haematopoletic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic, immunosuppressive, osteopathic, nephrotropic, antiathyroid, thyromimetic, immunosuppressive, osteopathic, antiarthitic, uropathic, antialcor, and ophthalmological activities. The present sequence is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= MACP-5_cDNA
/note= "This sequence is described as 764 bases long
in the Sequence Listing but a sequence of only 763 bases
is shown"
                                                                                                                                                                                                                                                                                                                                                                                Human; molecule associated with cell proliferation; MACP-5; Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-inflammatory; antipsorialic; anti-IV; antiasthmatic; anamatic; dermatological; antidabetic; nephrotropic; antithyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antiulicer; ophthalmological; diagnosis; treatment, prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides and polynucleotides useful for treating and detecting or proliferation disorders e.g. actinic keratosis, and immune disorders
                                                                                                                                                                                                                                                                                                                                                     Human molecule associated with cell proliferation, MACP-5 cDNA
seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ49948
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                                                    sGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysGlyA
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17..724
/*tag= a
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1..763
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                                                                                                                                                                                                                              seq_documentation_block:
ID AAZ49948 standard; cDNA; 763
                                                                                                                       228 rgLeuGlyAspLeuTrpVal 234
                                                                                                                                                         702 GGCTGGGAGACCTGTGGGTG 721
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P-PSDB; AAY44825.
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                602
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cell

Baughn MR;

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diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and
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                                                                     other;
                                                                                                                      Length: 240
Gaps: 1
Percent Identity: 96.250
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                                                                   Sequence 763 BP; 114 A; 252 C; 264 G; 133
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                                                                                                alignment_scores:
Quality: 1310.50
Ratio: 5.649
....ilarity: 96.667
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    88888
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alignment\_scores

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Goddard A, G
Shelton DL,
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                                                                                                                                                                                                      Ashkenazi AJ, Baker KP, Chan
Hebert C, Henzel W, Kabakoff
                                            99US-0144732.
99US-0144758.
99US-0146222.
                                                                    99WO-US21090
                                                                               99US-0162506
                                                                                     99WO-US28313
                                                                                           99WO-US28634
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2000WO-US13705
                            2000WO-US15264
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                                                                                                 99US-017
                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                             2001-025253/03.
                                                                                                                                                                                                                                   P-PSDB; AAB50910
     WO200073452-A2
                                                                                                                06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
                                                                                                                                 18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
15-MAR-2000;
                                                                                          01-DEC-1999;
09-DEC-1999;
20-DEC-1999;
                                                                                                                                                               21-MAR-2000;
                                                                                                                                                                    30-MAR-2000;
                                                                                                                                                         20-MAR-2000;
                                                                                                           05-JAN-2000;
                            02-JUN-2000;
                                                                                     30-NOV-1999
                07-DEC-2000
                                                                                                                                                                                                             Hebert C,
Wood WI;
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polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antigonists are useful for treating and diagnosing immune related alsorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vaculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepathits, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's diseases, autoimmune or immune-mediated skin diseases (such as bullous skin diseases such as asthma, allergic rhinitis, atopic dermatitis, cod hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, idiopathic pulmonary diseases including graft rejection and graft-versus-host diseases. present sequence is one of thirty three nucleic acids encoding PRO Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

seq\_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC97479

Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

821 GCCGCTGGGAGACCTGTGGGTG 843

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121 Argecacaccacceccarceccerrreseccererereseccres
                                                                                                                                                                                                                                                                                                                                                        GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134
                                                                                                                       1 MetalaGlnHisGlyalaMetGlyalaPheargalaLeuCysGlyLeuAl
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                                                                                                                                                                          17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
                                                                                                                                                                                                                                                                                                                                                                                               roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     621 CGTCGTCCTCCTGGCCGTGGCCGCTGCGTCCTCCTCACCTCGGCCC
                                                                                                                                                                                                                                                                                                                                            sSerGluTrpAspCysMetCysValGlnProGluPheH1sCysGlyAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG
 Length: 241
Gaps: 1
Percent Identity: 96.680
                                                                                             to: 1008
                                                                                             to: AAC91469 from: 1
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Quality: 1322.50
Ratio: 5.652
nilarity: 97.095
                                                     alignment_block:
US-09-512-363-2 x AAC91469
                         Percent Similarity:
                                                                                            Align seg 1/1
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Gurney AL; Watanabe CK;

Godowski PJ, Tumas D,

cancer;

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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via a dinistration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid for producing a PRO polypeptide, analyzing
                                                                                                                                                     cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatold arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; can Alzheimer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard A;
we. Marsters S/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                           Human angiogenesis-associated protein PRO364 cDNA, SEQ ID NO:141.
                                                                                                                                         protein; PRO; endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe CK, Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara N, Gerber H,
Hillan KJ, Kuo SS, M
                                                                                                                                                                                                                                 transgenic animal; ss
                 BP
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                                                                                                                                         Human; angiogenesis-associated
                 AAC97479 standard; cDNA; 1008
                                                                                                                                                                                                                                                                                                                                                                                                     99US-0123957.
99US-0134287.
99WO-US12252.
99US-0141037.
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99WO-US20111
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99WO-US28409
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurney AL,
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seq_documentation_block:
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                                                                                                                                                                                                                                 gene therapy;
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                                                                           28-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                          05-JAN-2000;
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05-OCT-1999;
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                                            AAC97479;
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cardiovascular, endothelial or angiogenic disorders, such as atheroscensis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate colNas with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a cDNA encoding a PRO
cell growth, cardiac hypertrophy or PRO-induced anglogenesis via the administration of a PRO protein, or an agonist or antegonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl
                                                                                                                                                                                                                                                                                                                  Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 96.680
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                          Length:
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                                                                                                                                                                                                                                                                                 protein of the invention.
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Ratio: 5.652
nilarity: 97.095
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US-09-512-363-2 x AAC97479
                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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SA;

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tructuating the prolitical compositions comprising the PRO polypeptide

or its antagonist have the opposite effect. A claimed method for
treating an immune related disorder, such as a T cell disorder,
treating an immune related disorder is selected from systemic
an antagonist antibody. The disorder is selected from systemic
lupus erythematcous, rheumatoid arthritis, osteoarthritis,
lupus erythematcous, rheumatoid arthritis, osteoarthritis,
lupus erythematcous, rheumatoid arthritis, osteoarthritis,
systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,
systemic vasculitis, arcoidosis, autoimmune haemolytic anaemia,
autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
commune-mediated renal disease, damyelinated diseases (such as
multiple sclerosis), autoimmune chronic active hepatitis, primary
bullary chrinosis, granulomatous hepatitis, sclerosing cholangitis,
inflammatcry bowel disease (ulcerative colitis and Crohn's disease),
colitical and sease (ulcerative colitis and crohn's disease),
dluten-sensitive enteropathy, Whipple's disease, (autolimmune-mediated
skin diseases (such as bullous skin disease, erythema multiforme and
colitical and and graft-versus-host disease) (all almed).

Colaimed methods of dispanosing these discoafers comprise detecting
the level of expression of the PRO gene. Also claimed are a method
cof identifiing the aepression or
antitity of the PRO molvorers host cells.
                                                                                            Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence is that of cDNA clone DNA47365-1206 (ATCC 209436)
                                                                                                                                                                                                                                                                                                                                                                                                                                encoding novel human immunomodulator protein PRO364 (UN0319) (see AAB20115). The clone was isolated from a small intestine library. The protein clo kba, pl 6.34 shows homology to mouse GITR protein and may be its human counterpart. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO364. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stimulating or enhancing an immune response in a mammal, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising the PRO polypeptide
                                                                                                                                                                                                                                                                  New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity of the PRO polypeptide, vectors, host ce and a method of stimulating the proliferation of
                                                                                               Goddard A,
Pitti RM,
                                                                                            KP, Fong S,
Marsters SA,
                                                                                                                                                                                                                                                                                                                                                               Claim 21; Fig 15; 127pp; English.
99US-0144758
                                               (GETH ) GENENTECH INC.
                                                                                                                   Hillan KJ, Mark MR,
Wood WI;
                                                                                                                                                                                         WPI; 2001-103149/11
                                                                                                                                                                                                                     P-PSDB; AAB20115
                                                                                            Ashkenazi AJ,
20-JUL-1999;
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Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:

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1 MetalaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
                       Percent Identity: 96.680
                  Gaps:
                                                                                                               from: 1 to: 1008
                                                                                                               to: AAF30057
             Ratio: 5.652
Percent Similarity: 97.095
Quality: 1322.50
                                                              alignment_block:
US-09-512-363-2 x AAF30057
                                                                                                               Align seg 1/1
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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34

sapiens

Homo

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Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease;
                                                                                                                                                                                                                                       roCysCysThrThrCysArgHisHisProCysProFroGlyGlnGlyVal 100
                                                                                                                                                                                            rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                         ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys
                                                                               sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP
                                                                                                                                                                                                                                                                                                       GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe
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Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                          KP, Ferrara N, Gerber H, OPJ, Gurney AL, Kuo SS, Ma:
Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                    Claim 60; Fig 7; 182pp; English.
                                                               990S-0141037.
990S-0144758.
990S-0146298.
990S-0146222.
                                                                                                        99WO-US28409.
99WO-US28469.
99WO-US28565.
99WO-US30095.
                                                                                                                                                                          2000WO-US05841
2000WO-US06319
                                                                                                                                         2000WO-US03565
2000WO-US04341
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                                       2000WO-US13705
                                                                                                                                                                   2000WO-US05004
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                                                                                                                                                                                                  2000WO-US07532
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Godowski PJ,
                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                     Goddard A, Godowski
Paoni NF, Pitti RM,
                                                                                                                                                                                                                                                                          WPI; 2001-025251/03.
P-PSDB; AAB50954.
       WO200073445-A2
                                                                                                                        02-DEC-1999;
16-DEC-1999;
11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
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Goddard A, Go
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10-MAR-2000;
                                                                                                                                                                                           15-MAR-2000;
21-MAR-2000;
                                       17-MAY-2000;
                                                                                                                                                                  24-FEB-2000;
                                                                                                        30-NOV-1999;
30-NOV-1999;
02-DEC-1999;
                       07-DEC-2000
                                                                                        28-JUL-1999,
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Marsters

Gerritsen ME; Mark MR, Marst 1, Wood WI;

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The present sequence is one of seventeen nucleic acids encoding PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO Polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
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Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0

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1 MetalaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
            Length: 241
Gaps: 1
Percent Identity: 96.680
                                                                                                                     to: 1008
                                                                                                                       from: 1
         Ouality: 1322.50
Ratio: 5.652
Percent Similarity: 97.095
                                                                                                                     to: AAC90566
                                                                        alignment_block:
US-09-512-363-2 x AAC90566
alignment_scores:
                                                                                                                       Align seg 1/1
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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34

Homo sapiens

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Human; PRO; antlinflammatory; dermatological; antlarthritic; antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy; ss.
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                                       GCGGCCCTGGCGCCTCCTTGGGACGGGACGGACGGACGCGCTGCTGC
                                                                                                       CGGGTTCACACGACGCGCTGCTGCCGCGATTACCCGGGCGAGGAGTGCTG
                                                                                                                                             CTTGCTGCACGACCTGCCGGCACCACCCTTGTCCCCCAGGCCCAGGGGGTA
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                                                                             ArgvalHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
                                                                                                                                                                                    roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal
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us-09-512-363-2.p2n.rng

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521 GCACCCAGTTCGGGTTTCTCACTGTTCCCTGGGAACAAGACCCACAAC
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Chimeric - Synthetic.
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                                                                                  167
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                                                                                                for
or
                                                                                              New composition useful for inhibiting neoplastic cell growth and treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide their antagonists
                              Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
                             Napier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 1
Percent Identity: 96.680
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                           Hillan K,
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                             Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1322.50
Ratio: 5.652
Percent Similarity: 97.095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
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(GETH ) GENENTECH INC
                           Goddard A,
                                                       2000-412325/35
                                                                    P-PSDB; AAY71467
                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
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PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor: TNFR; human umbilical vein endothelial cell; HUWEC; cardiac hypertrophy; myocardial infarction; PGF_2alpha; trauma; cancer; anglogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculatides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor anglogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis; ss.
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                                                                                                                                 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                             210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG 227
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                                                                                                                                                                                                                                                                                                                                         AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh
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524..550
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/note= "Probe binding site"
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/product= "PRO364"
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498..518
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GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe CAGTCCCAGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTGCCTC rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC GGGGACCTTCTCCCGGGGCCACGAAGGCCACTGCAAACCTTGGACT ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 

roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal

84 371 101 121 117 471 134 521

CTTGCTGCACGACCTGCCGGCACCACCCTTGTCCCCCAGGCCAGGGGGTA

670 193

....Arg

621 184

167

184

AlavalCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh

GCTGTGTGCGTCCCAGGGTCCCCGCCGCCAGAGCCGCTTGGGTGGCTGAC rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG

571

151

671

194 721 210

lnLeuGlyLeuHisIleTrpGlnLeu.....

LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe

GAGACCCAGCTGCTGCTGGAGGTGCCGCCGTCGACCGAAGACGCCAGAAG

rCysGlnPheProGluGluGluGluArgGlyGluArgSerAlaGluGluLysG 

210 770 227 820

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This sequence encodes a PRO364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGTTR). The corresponding ligand (hGTTRL), PRO156. given in AAB47056.

PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic disorder. The cardiovascular, endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNRP) family of polypeptides. The PRO175 cDNA sequence was isolated from an expressed sequence was isolated from an endothelial cells (HUVEC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting anglogenesis induced by PRO364 or PRO175 is useful for inhibiting anglogenesis induced the vaccular-related drug targeting or as theirapeutic targets for the
                                                                                                                                                                                               Composition for diagnosing and treating cardiovascular, endothelial and anglogenic disorders, comprises a PRO364 or PRO175 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system disease and neuropathies and rheumatoid arthritis.
                                                                                                                                                                                                                                                                          Example 1; Fig 1; 76pp; English.
                                                                        Gerritsen ME;
                       GENENTECH INC.
                                                                                                                       WPI; 20,01-138257/14
                                                                                                                                                 P-PSDB; AAB47054
                                                                        Williams PM,
                       (GETH)
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Sequence 1008 BP; 148 A; 336 C; 353 G; 171 T; 0 other;

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221 GCGCCCTGGCCCTCCTGCTTGGGACGGAACGGACGCGCGCTGCTGC 270
                                                                                                                                                                                                                171 GCTGCTGTGCGCGCTCAGCGTCAGCGCCCCACCGGGGGTCCCGGGGT 220
                                                                                                                                                                                          1 MetalaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
                                                                                                                                                                                                                                                                      17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34
                                                                                                                                                                                                                                                                                                                                                   ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                              ArgvalHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67
                                      Gaps: 1
Percent Identity: 96.680
                  Length:
                                                                                                                                                     to: 1008
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              Quality: 1322.50
Ratio: 5.652
Percent Similarity: 97.095
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                                                                                           alignment_block:
US-09-512-363-2 x AAC85433
alignment_scores:
                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                   34
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29 321

271 CGGGTTCACACGACGCGCTGCTGCCGCGATTACCCGGGCGAGGAGTGCTG 320

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PRO364; UNQ319; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipscriatic;
                                                  seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF30057
                                                                                                                                                                                                                                        antiasthmatic; antiallergic; immunostimulant; ss
                                                                                                                                                                                                                                                                                          Location/Qualifiers
121..846
                                                                                    AAF30057 standard; cDNA; 1008 BP
              HILLIHIHIHIHIHIHIHIHIH
821 GGGGCTGGGAGACCTGTGGGTG 843
227 lyArgLeuGlyAspLeuTrpVal 234
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2000; 2000WO-US06884
                                                                                                                                                                Human cDNA encoding PRO364
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                           /*tag= b
196..843
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                                                                                                                                                                                                                                                                                                                   /*tag= a
121..195
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                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                          WO200105972-A1
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                       30-APR-2001
                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2001
                                                                                                             AAF30057;
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15-SEP-1999;
05-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-SEP-1999
                                                                                                                                                                                                                                                                                                                                     AAA77604;
                                                                                                                                                                                                                210
                                                                                                                                                                                                                                                    227
                                                                                                    167
                                                                                                                       621
                            134
                                                                                                                                                                                                                                                                                                                            Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 CGGGTTCACACGACGCGCTGCTGCCGCGATTACCCGGGCGAGGAGGCTG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCGAGTGGGACTGCATGTGTCTCCAGCCTGAATTCCACTGCGGAGACC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTCCCAGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roCysCysThrThrCysArgHisHisProCysProFroGlyGlnGlyVal
                                                                                                                                                                                                                                                                                      Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                            Length: 241
Gaps: 1
Percent Identity: 96.680
                                                                                                                                                                                                                                                                                                                                                                                         to: 1008
                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                  Claim 23; Fig 35; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAC58596
                                                                                                                                                                                                                                                                                                                                   5.652
                                                                                                                                                                                                                                                                                                                           Quality: 1322.50
                                                                                                                                                                                                                                                                                                                                                                        US-09-512-363-2 x AAC58596
Tumas D,
                 WPI; 2000-572271/53
                          P-PSDB; AAB33431
                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Stewart TA,
                                                                                                                                                                                                                                                                                                                   alignment_scores
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Human; PRO; promotion; inhibition; anglogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; anglogenic; prollferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                184
                                                                                                                                                                                      184 InLeuGlyLeuHisIleTrpGlnLeu......Arg 193
                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AlavalCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
                                                                                                                                                                                                                                                                                        671 AGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGGA 720
                                                                                                                                                                                                                                                                                                                               194 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe 210
                                                                                                                                                                                                                                                                                                                                                                                                                 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA77604
                   rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG
ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrH1sAsn
                                                                                                                                                                                                                                                                                                                                                       Human PRO364 cDNA sequence SEQ ID NO:116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAA77604 standard; cDNA; 1008 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          821 GGCGGCTGGGAGACCTGTGGGTG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lyArgLeuGlyAspLeuTrpVal 234
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99US-0134287
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16-DEC-1998;
12-JAN-1999;
08-MAR-1999;
12-MAR-1999;
28-APR-1999;
20-JUN-1999;
20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2000
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99US-0162506

Goddard A;

or

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useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenesis and cardiovascularisation, andiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial angiogenic disorders in mammals (e.g. atheroscierosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24335 represent nucleotide and protein sequences used in
                                                                                                                                                                                                                                                                                      present invention describes nucleic acids encoding PRO polypeptides
                                                  Gerber H, Hillan KJ, Godó
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                     Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial angiogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 96.680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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                                                    Ferrara N,
Klein RD, F,
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                     Claim 61; Fig 43; 315pp; English
                                                                                       PM,
                                                    Baker KP,
Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1322.50
Ratio: 5.652
nilarity: 97.095
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                                                                                         Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-512-363-2 x AAA77604
              (GETH ) GENENTECH INC.
                                                                                                                        WPI; 2000-412154/35.
P-PSDB; AAB24409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                    Ashkenazi AJ,
                                                                          ΡJ,
                                                                                       Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
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                                                                        Godowski
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270

67

84

20

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PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumous breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue; tumour necrosis factor receptor; GITR protein homologue; ss.
                                                          570
                                                                                                                                                          670
                                                                                                                                                                                                                                   210
                                   150
                                                                                                           620
                                                                                                                                                                                  ....Arg 193
                                                                                                                                                                                                                                                           770
                                                                                                                                                                                                                                                                                                           820
           520
                                                                                    167
                                                                                                                                   184
                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human PRO364 protein"
/note= "Derived from clone DNA47365-1206"
121..195
                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAD01240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO364 protein encoding cDNA clone, DNA47365-1206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/product= "Mature human PRO364 protein"
                                                                                               rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG
                                                                                                                                                AGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGA
                                                                                                                                                                                                                                    194 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe
                                                                                                                                                                                                                                                                                     rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG
                                                                                                                                                                                                                                                                                                AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh
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                                  ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn
lnLeuGlyLeuHisIleTrpGlnLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
121..846
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                                                                                                                                                                                                                                                                                                                                                           821 GCCGCTGGGAGACCTGTGGGTG 843
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98US-0112850.
98US-0113296.
99US-0144758.
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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16-DEC-1998;
22-DEC-1998;
20-JUL-1999;
26-JUL-1999;
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                                                                                                                                                                                                                                                                                     210
                                                                                                                                    167
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GGCGCCTGGGAGACCTGTGGGTG 843

SXS

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alignment_scores:
821
                                   470
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                                                                                                                                                                                                                                             roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100
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                                                                                                                                                                                                                                                                                                                               ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
                                                                                                                                                                                                                                                                                                                                                                                      rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
                                                                                                                   121 ATGGCACAGCACGGGCGATGGGCGCGTTTCGGGCCCTGTGCGGCCTGGC 170
                                                                                                                                                                                                                                                                                                    rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134
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                                                                                                                                                                                                                  84
                                                                                                                                rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGluLysG
                                                                                                                                                                                                                                                     GGGGACCTTCTCCGGGGGCCACGAAGCCCACTGCAAACCTTGGACAGCT
                                                                                                                                                                                                                                                                                                                                       CSTCSTCCTCCTGCCGTGGCCGCCTGCGTCCTCCTCCTCCTGACCTCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCAGTTCCCCGAGGAAGAGCGGGGGGGAGGGATCGGCAGAGGAAGG
                                                                                                     MetalaGlnHisGlyalaMetGlyalaPheargAlaLeuCysGlyLeuAl
                                                                                                                                                                                                                   sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP
                                                                                                                                                                                        ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
              other;
                                                 Dercent Identity: 96.680
              T; 0
                                        Length:
Gaps:
             Seguence 1008 BP; 148 A; 335 C; 354 G; 171
                                                                                        to: 1008
mammalian cells (claimed)
                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyArgLeuGlyAspLeuTrpVal 234
                                                                                        Align seg 1/1 to: AAX87670
                                        Quality: 1322.50
Ratio: 5.652
Harity: 97.095
                                                                   alignment_block:
US-09-512-363-2 x AAX87670
                                                    Percent Similarity:
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                                 alignment_scores
responses
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Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and anglogenic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pitti RM;
                                                                                                                                                                                                                                                                   Cardiovascular; endothelial; anglogenic disorder; PRO179; PRO238; PRO238; PRO54; PRO844; PRO846; PRO1760; PRO205; PRO811; PRO833; PRO840; PRO877; PRO879; PRO899; PRO885; PRO885; PRO887; Gene therapy; Ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen ME;
Paoni NF, F
seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA99903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
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Gurney AL, Hillan KJ, Marsters
, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                       cDNA encoding human protein PRO364.
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                                           seq_documentation_block:
ID AAA99903 standard; cDNA; 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-USO5028.
99US-0123957.
99US-0144758.
99US-01447598.
99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28313.
99WO-US28355.
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                                                                                                                                                                     (first entry)
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/*tag= a
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P-PSDB; AAB27651.
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18-FEB-2000;
22-FEB-2000;
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Goddard A, G
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
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                                                                                                                                                                     26-JAN-2001
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12-MAR-1999,
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                                                                                                                    AAA99903;
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CDS
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241

Length:

Quality: 1322.50

Human PRO364 protein UNQ319 encoding cDNA SEQ ID NO:91

(first entry)

29-JAN-2001

AAC58596;

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GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGTGTGCGTCCCAGGGTCCCCGCCGGCAGAGCCGCTTGGGTGGCTGAC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
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                                                                                                                                                             17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
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  Gaps: 1
Percent Identity: 96.680
                                                                                to: 1008
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                                                                               to: AAA99903
                                                      US-09-512-363-2 x AAA99903
            Percent Similarity:
  Ratio:
                                                                                Align seg 1/1
                                         alignment_block
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seg\_name: /SIDS8/gcgdata/geneseg/genesegn/NA2000.DAT:AAC58596

seq\_documentation\_block: ID AAC58596 standard; cDNA; 1008 BP. XX

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dermatological; antiarthritis; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidlabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiallergic; antiasthmatic; systemic lugus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogran's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; pluten-sensitive enteropathy; autoimmune disease; immune—mediated skin disease; allergic disease; immunological disease; immune associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
                                                                   cardiant;
                                                                   immune related disease; diagnosis; antiinflammatory;
                                                                                                                                                                                                                       graft rejection; graft-versus-host-disease; ss
                                                                                                                                                                                                                                                                                                                                     99WO-US05028.
99US-0123618.
99US-0123957.
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99US-0132371.
99US-0134287.
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99US-0144758.
99US-0145698.
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99US-0128849
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99WO-US28409,
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2000WO-US00376.
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2000WO-US04342
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Kabakoff RC,
                                                                                                                                                                                                                                              Homo sapiens
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01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
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18-FEB-2000;
                                                                                                                                                                                                                                                                                           14-SEP-2000
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proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 GGGGACCTICTCCGGGGGCCACGAGGCCACTGCAAACCTTGGACAGACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys
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                                                                                                                                               Sequence 1006 BP; 156 A; 331 C; 337 G; 182 T; 0 other;
                                                                                                                                                                                                                     Length: 241
Gaps: 1
Percent Identity: 96.680
                                                                                                                                                                                                                                                                                                                                                to: 1006
                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                   Quality: 1322.50
Ratio: 5.652
Percent Similarity: 97.095
                                                                                                                                                                                                                                                                                                                                                to: AAV19153
                                                                                                                                                                                                                                                                                          alignment_block:
US-09-512-363-2 x AAV19153
                                                                                                                                                                                                    alignment_scores
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 88888888888
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This is the nucleotide sequence of a novel cDNA clone, termed UN0319 or DNA47365-1206 (APCC 209436), that codes for PR0384 (see AAY06605), a novel member of the tumour necrosis factor receptor family. UN0319 was isolated from a human bone marrow tissue cDNA library by PCR amplification and probe hybridisation (see also CRA87876-75 and AAX87720-23). Nucleic acids comprising the present sequence, the PR0364 coding region, and DNA having at least 95% comprising amino acids 1-241, 1-X, 26-441 or 26-X of PR0364, where X is any of residues 157-167, and (b) DNA encoding mature PR0364, are claimed. PR0364 nucleic acids can be used in the recombinant C production of PR0364 nucleic acids can be used in the recombinant c production of PR0364 polypeptides, as probes, in gene and chromosome mapping, in the generation of antisense sequences, and c in gene therapy. PR0364 polypeptides are useful. for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory autoimmune responses
                                                                                                                                                                                                                                                                                                                                                                                                                          "a nucleic acid comprising nucleotides
121-843 is specifically claimed in
Claim 3"
              PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy; ds.
                                                                                                                        seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX87670
rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG
                                                                                                                                                                                                                                                             Human TNF receptor homologue PRO364 cDNA clone UNQ319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA;
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                                                           lyArgLeuGlyAspLeuTrpVal 234
                                                                            701 GGGGGTGGGAGACCTGTGGGTG 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1; 104pp; English.
                                                                                                                                                                   AAX87670 standard; cDNA; 1008
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/*tag= a
/note= "a :
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/*tag= b
196..843
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P-PSDB; AAY06605.
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, Digeorge syndrome, HIV infection, severe combined immunodeficiency fortunat. They can be used for treating immune deficiency blood coagulation disorders, blood coagulation disorders, blood coagulation disorders, blood coagulation disorders, blood also be used to treat heart attacks, strokes, Addison's disease, has be used to treat heart attacks, strokes, Addison's disease, also be used to treat heart attacks, strokes, Addison's disease, and tiple sclerosis, myasthenia gravis, Stiff-Man syndrome, gisease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lugus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's neuropathies, and shy-brager syndroms). The products can also be used for detection, diagnosis and prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ATGGCACAGCACGGGCGATGGGCGCTTTCGGGCCCTGTGCGGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 983 BP; 144 A; 326 C; 346 G; 167 T; 0 other;
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Gaps: 0
Percent Identity: 100.000
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Percent Similarity: 100.000
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Quality: 1340.00
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US-09-512-363-2 x AAZ37762
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                                                                                                                                                                                                                                       roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal
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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
             168 GCTGCTGTGCGCTCAGCCTGGGTCAGCCCCCACCGGGGGTCCCGGGT
                                                         34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys
                                                                                                                     ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
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                                                                                                                                                                                                                                                                                                                                                            rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC
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318

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Engagement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             develop products for treating, transplantation rejection and
                                                                                                                                                                                                                GTGCCGCCGTCGACGAAGACGCCAGAAGCTGCCAGTTCCCCGAGGAAGA 767
                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV19153
AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh
                                                                          CGTCGTCCTCCTGGCCGTGCCTGCGTCCTCCTCCTGACCTCGGCCC
                                                                                                                        184 InLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuLeuGlu
                                                                                                                                                      668 AGCTTGGACTGCACATCTGGCAGCTGAGGAAGACCCAGCTGCTGGAG
                                                                                                                                                                                                                                              uArgGlyGluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpV
                               568 GCTGTGTGCGTCCCAGGGTCCCCGCCGGCAGAGCCGCTTGGGTGGCTGAC
                                                             rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG
                                                                                                                                                                                                                                                                              GCGGGGCGAGCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACCTGTGGG
                                                                                                                                                                                     ValProProSerThrGluAspAlaArgSerCysGlnPheProGluGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of the human 312C2 T cell gene.
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/product= "human 312C2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Pages 58-59; 71pp; English.
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ID AAV19153 standard; DNA; 1006
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96US-0689943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorders.
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16-AUG-1996;
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which includes an open reading frame coding for a 25 kbm human tumour necrosis factor receptor-like protein, designated TR11 (see AAY9589), which shows 58.6% identity to murine glucocorticolid induced tumour necrosis factor receptor family-related gene. The induced tumour necrosis factor receptor family-related gene. The TR11 CDNA was discovered in a cDNA library derived from T-helper cells, and was not found in any other CDNA library examined. TR11 activation-inducible. The TR11 ligand is constitutively expressed in an endothelial cell line. This suggests that TR11 and its ligand may be involved in activated T-cell trafficking. The invention provides TR11 xR11Styl and TR11Sty nucleic acids (see AAA50304-06) and encoded proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TR11styl and/or TR11Styl polypetides are useful for treating, preventing, preventing, preventing, preventing, preventing, preventing, munnodeficiency, especially common variable immunodeficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is that of cDNA clone HHEAC71 (ATCC 209341),
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                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
118..822
                                                                                                                                                         ВР
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ID AAA50304 standard; cDNA; 983
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99US-0134172.
99US-0144076.
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13-MAY-1999;
16-JUL-1999;
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/SIDSB/gcgdata/geneseqn/geneseqn/NA1997.DAT:AAT91027
/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:AA086126
/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:AA075424
/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:AA791026
of: US-09-512-363-2 to: N_Geneseq_0601:*
                                                                  Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd
                                                                    the GenCore
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Query: US-09-512-363-2
Query length: 234
Database: N_Geneseq_0601:*
Database sequences: 730101
Database length: 313950809
Search time (sec): 111.920000
                                 Date: Sep 4, 2001 3:57 PM
                                                                                                                 Command line parameters:
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                                                                    About: Results
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TR11; human; tumour necrosis factor receptor-like protein; immunodeficlency; autolmanne disease; rheumatcid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; gene therapy; diagnosis; ss.
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197.00
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/SIDS8/gcgdata/geneseg/genesegn/NA1999.DAT:AAX02162
/SIDS8/gcgdata/geneseg/genesegn/NA1996.DAT:AAT39546
   'SIDS8/gcgdata/geneseg/genesegn/NA1999.DAT:AAZ09769
                                    /gcgdata/geneseg/genesegn/NA1999.DAT:AAZ08961
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X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TRILS' TRILS' Ind\or TRILS' and or TRILS' antagonists (e.g. antibodies) are used to treat, prevent, prognose and\or diagnose an autolmmune disease, especially rheumatoid
                                                                                                        arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGTTCACACGCGCGCTGCTGCTGCCGGGTTACCCGGGCGAGGAGTGCTG 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 983 BP; 144 A; 326 C; 346 G; 167 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           Length: 234
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                     agonist/antagonist compounds are also provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 983
                                                                                                                                                                                                                                                                                                                                         Ouality: 1340.00
Ratio: 5.726
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-512-363-2 x AAA50304
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This is the nucleotide sequence of the human tumour necrosis factor receptor-like protein (TR11 receptor). The invention relates to TR11 and two splice variants TR11sV1 and TR11sV2. The nucleotide sequences were determined by sequencing cloned cDNAs AA237765-237766. The TR11 receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GTRR). TR11, TR11sV1 and TR11sV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for
                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor-like protein (TR11), nucleotide sequence.
                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV: SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntingdon's disease; ss; inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Tumour necrosis factor receptor-like protein"
118..192
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 217
                                                        234
                                                                                   817
                                                                                                                                                                   seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ37762
/*tag= b
/note= "Putative signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= TR11_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "TR11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US22085
                                                                                                                                                                                                                                                                    01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193..820
                                                                                                                                                                                                             AAZ37762 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..822
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                                                                                                                                                                                                seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY52158
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                              al 234
                                                                                                                                                                                                                                          AAZ37762;
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 201
                            718
                                                        217
                                                                                   768
                                                                                                               234
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/note="Vector: lambda pSB; Site_1: BamHI; Site_2: ECORI; First strand cDNA was primed with an anchored Ahol-oilgo(dT) primer [5'GGAGGACTCGAGCGCCGCAGGAGGAG(T)VN Strand was primed with a nd then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGAGCTGGATCGCGGCCGCAATAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and Salistes of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block: 374 bp mRNA EST 30-NOV-1998
LOCUS AI214481 Soares_NFL_T_GBC_51 Homo sapiens CDNA clone
DEFINITION qg690401.x1 Soares_NFL_T_GBC_51 Homo sapiens CDNA clone
IMAGE:1840417 3' similar to TR:035714 035714 GLUCOCORTICOID INDUCED
TNFR_FAMILY RELATED PROTEIN PRECURSOR.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Euthoria; Primates; Catarrhini; Hominidae; Homo. I to 274)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Trace consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 695 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualiflers
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Gaps: 0
Percent Identity: 98.438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 CGGGTTCACACGACGCGCTGCTGCCGGGTTACCCGGGTAAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGlu 64
  /dev_stage="pediatric 2 years"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 370
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                                                                                                                                                                                                                                                                                                             130 g
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: BE244247
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5.578
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US-09-512-363-2 x BE244247
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[E. 1 (bases 1 to 370)
[S. Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.

[Pediatric Leukemia cDNA Sequencing Project
[Unpublished (2000)
[Contact: Dr., Judith F. Margolin
[Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
[102 Bates, MC3-3320 Houston, Tx 77030, USA]
[Tel: 832-824-4536]
[Fax: 832-825-4038]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE244247 370 bp mRNA EST 15-NOV-2000 TCBAP2E0971 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP0971, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project=TCBA"
                                                                                                                                                                                                                                                                                                                                   85 ysCysThrThrCysArgHisHisProCysProFroGlyGln.GlyValGl 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 nSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerG 118
                        212 AGGAGAAGCACTATGGGGGCATGGCCATGCTATGGAGTCTCGATGCT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 lyThrPheSerGlyGlyHis.GluGlyHisCysLysProTrpThrAspCy 134
                                                                                             35
                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                     52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe 68
                                                                                                                                                                                                                                                                                                                                                                               68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProC 85
GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg
                                                                                             uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG
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/cell_type="pre-B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 sThrGlnPheGlyPheLeuThrValPhe 143
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Location/Qualifiers
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BE244247.1 GI:9095987
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/clone_lib="Soares_NFL_T_GBC_SI"
/clone_lib="Soares_NFL_T_GBC_SI"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_l: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH13W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-667239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
57 a 86 c 87 g 44 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 sThrHisAsnAlaValCysValProGlySerProProAlaGluProLeuG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 GACCCACATCGCTGTGAGTCCGAGGGTCTCCGCCGACAGCCGCTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 TrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLy 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 319.50 Length: 90
Ratio: 4.318 Gaps: 1
Percent Similarity: 82.222 Percent Identity: 74.444
                          /clone="IMAGE:1840417"
/db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to reverse of: Al214481
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US-09-512-363-2 x AI214481/rev
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FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                       494.50
                                                                                                                                                                                                                                                                                                                                                                                                                             70.303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-512-363-2 x AW659186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est45:AW335806
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LOCUS AW335806
 PCR PRimers
                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
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                                                                                                                       source
                                                                                                                                                                                                                                                                                            BASE COUNT
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                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoidea; Bovoinae; Bos.

1 (bases 1 to 552)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid, W.W. and Reele, J.W.

Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                   141 rValPheProGlyAsnLysThrHisAsnAlaValCysValProGlySerP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHisProCysProProGlyGlnGlyValGlnSerGlnGlyLysPheSerP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heGlyPheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHis 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluGlyHisCysLysProTrpThrAspCysThrGlnPheGlyPheLeuTh 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 CCTGTTTCCCGGAAACAAGACGCACAATGCTGTGTGCAGCCTGGGGCTGC 376
                                                                                                                                                                                                                                                    1 GGCCAGCGACCCTCAGCGATCTGAGCTGCAGCCTGGCCAAGTTCTGCA 50
                                                                                                                                                                                                                                41 uGlyThrGlyThrAspAlaArgCysCysArgValHisThrThrArgCysC 58
                                                                                                                                                                                                                                                                                                          58 ysArgAspTyrProGlyGluGluCysCysSerGluTrpAspCysMetCys 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW659186 552 bp mRNA EST
96144 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW659186
                                                                                                                                                       25 GlyGlnArgProThrGlyGlyProGlyCysGlyProGlyArgLeuLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 2
Percent Identity: 63.768
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                 to: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                   from: 1
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Contact: Smith TPL
                                                                                                                 Align seg 1/1 to: AW483085
Ratio: 4.721
Percent Similarity: 80.435
                                                       alignment_block:
US-09-512-363-2 x AW483085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roProAlaGluPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 CGCCCACTGAACCA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est50:AW659186
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AUTHORS
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SOURCE
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/tissue_type="pooled"
/lab_host="pooled"
/lab_host="DH10B"
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 GlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCy 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 sAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 pLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 AGTGACCATCGTCTCTCTCTGGCTGCCTGCATCCTGGCCCTGACCG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 TGCTGATTGCAGCCCCTCTGCAGAGACCCAGGCTCCTGGAGGCCCCGCCAC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 erAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLys......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 GGAGTGCAGCCTGAGGGCAACTTCAAATTCGGCTTTGAGTGTGTTGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ThrGlnLeuLeuGluValProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 roSerThrGluAspAlaArgSerCysGlnPheProGluGluArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 GluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpVal 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 56.364
                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 552
                                                       Location/Qualifiers
1. 552
/ Organism="Bos taurus"
/ db_xref="taxon:9913"
/ clone_lib="MARC 1BOV"
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 83 row: A column: 19
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                  Smith T. P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
GOT discovery in cattle
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fax: 402 762 4366
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 AGTGACCATCGTCATCTCTCTCTGGCTGCCTGCATCCTGGCCTGACCG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 hrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThr 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 HisAsnAlaValCysValProGlySerProProAlaGluProLeuGlyTr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 pLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrS 182
22020 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 143
Gaps: 1
Percent Identity: 53.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: AW335806 from: 1 to: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 15 row: F column: 18 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
                                       AW335806.1 GI:6832445
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4.170
67.832
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                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                     AW335806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                      COM
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DEFINITION
                                                                                                        ORGANISM
                   ACCESSION
VERSION
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                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                              AUTHORS
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                                                            KEYWORDS
SOURCE
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BE373185 620 bp mRNA EST 21-JUL-2000 601225221F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3583589 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In Interest to account to the second to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1585389"
/clone=lib="NCI_CGAP_Mam1" .
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/cloue_stage="a months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pcWV-SPORT6; Site_1: Sal1; Site_2: NotI: cloned unidiractionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
a 145 c 200 g 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 620)
                                194
                                                                                                                                                                                                                               362
                                                                                                                                                                                                                                                                                                                                                     363_TGCTGATTGCAGCCCTCTGCAGAGACCCAGCTCCTGGAGGCCCCGCCAC 412
                                                                                                                                                                                                                               .....ThrGlnLeuLeuLeuGluValProP
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Gaps: 5
Percent Identity: 45.833
erAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 620
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/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 roSerThrGluAspAlaArgSerCysGln 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 CCCCACCTGAGGATGCCTGCAGTTGCCAG 441
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BE373185
BE373185.1 GI:9318548
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3.405
72.917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .620
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US-09-512-363-2 x BE373185
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                                                                                                                                                              house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.
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JOURNAL
COMMENT
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/note="Organ: colone" unidirectionally. Primer: Oligo dT.
Normalized to Cot 500. Average insert size 1.11kb.
Normalized version of NCI_CGAP_CO18. Library constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu:
1 (bases 1 to 606)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP nttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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LOCUS BF117994 606 bp mRNA EST 29-DEC-2000

DEFINITION u210e09.yl NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3668680

similar to TR:035714 035714 GLUCOCORTICOID INDUCED TNFR FAMILY

RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAlav 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVal 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 sCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGlnS 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 CIGCACGACTGCGGGCACCACCT.TGTCCCCCAGGGCGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 GAGTGGAACTGCATGTGTGTCCAGCCTGAATTCCACTGCGAAGACCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 113
Gaps: 0
Percent Identity: 94.690
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    .340
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                                                                                                                                                                                                                                                                                                   by Life Technologies."
100 c 115 g
       High quality sequence stop: 75
                            Location/Qualifiers
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BF117994.1 GI:10987470
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AUTHORS
TITLE
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SOURCE
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                            FEATURES
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Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Itssue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D., cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW300857 340 bp mRNA EST 18-JAN-2000 KSYSOVO.X.1 NCI_CGAP_CCO20 Homo sapiens cDNA clone IMAGE:2666028 3' simflar to TR:095851 095851 THF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN. ; contains MER22.bl TAR1 repetitive
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 340)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                 97 lyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIle 113
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                                                                                                                                                                                                                             114 AspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysPr 130
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                                                                                                                                                                                                                                                                                                                                              ysThrHisAsnAlaValCysValProGlySerProProAlaGluProLeu 163
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AAGGAGGACTGTCCAAAAGAAAGGTGCATATGTGTCACACCTGAGTACCA 181
                                                                                                                                                               eProGluGluGluArg.....GlyGluArgSerAlaG
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TGTGTCCTCGAGAGACCC.....AGCCATTCGCGGAGGTGCAGTTG
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                                               sCysGlyAspProCysCysThrThrCysArgHisHisProCysProProG
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AW300857
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Unpublished (1997)
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DEFINITION
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COMMENT

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                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGl 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GlnH1sGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysArg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProC 85
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Percent Identity: 51.980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
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                                                                                                                                                                                                                                                     Seq primer: -40kF Lioum class. High quality sequence stop: 427.
Location/Qualifiers
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US-09-512-363-2 x BF117994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                  JOURNAL
                                                                                                                                                                                                                                                                                              FEATURES
                                      COMMENT
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l (bases 1 to 39)
Smith, T. P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,
W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
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                                                                                                                                450
                                                                                                                                                                                    168
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AW483085
152 ValCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVa
                                                                                                                                                                                                                                                                                               168 lValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL
                                                                                                                                                                                                                                                                                                                                             501 CATCTTCCTGGTCATGCTGCATGCATAGTCTTCCTAACCACAGTCCAGC
                                                                               hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAla
                                                                                                          451 GTGTGCATCCCGGAGCCACTGCCCACTGAGCAATACGGCCATATGACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Plate: 26 row: K column: 17
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est47:AW483085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
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Length:

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DEFINITION
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                                                                                                                                                                                                                                                       118
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                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail nih.gov
Tissue Productment: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples 4 providing samples 4 provided by Life to 2 others
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
    ŝ
                                                                                                                                                                                                       1 (bases 1 to 644)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
uo63d10.yl NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:2647219 similar to TR:035714 035714 GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AGGAGAAGCACTATGGGGGCATGGCCATGCTGTATGGAGGTCTCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 lyProGlyArgLeuLeuClyThrGlyThrAspAlaArgCysCysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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/clone=lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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    644
    /organism="Mus musculus"

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Location/Qualifiers
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Unpublished (1997)
Other_ESTs: uo63d10.x1
                                                              AW230423
AW230423.1 GI:6559719
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3.867
75.701
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US-09-512-363-2 x AW230423
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Ratio:
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ORGANISM
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AUTHORS
TITLE
                                                              ACCESSION
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UNC10605.11 Scares thy Land Mus musculus cDNA clone IMAGE:3470242 5' similar to TR:035714 035714 GLUCOCORTICOID INDUCED INFR FAMILY RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Emall: cgapbs.+e@nall.nih.gov
This clone is available ropatty-free through LLNL; contact the IMAGE Consortium (info@image.ilnl.gov) for further information.
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                                                                                                                                   250 AGTGCAAGATCTGCAAGCACTACCCCTGCCAACCAGGCCAGAGGGTGGAG
                                                                                                                                                                                                                                      135 hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAla 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                152 ValCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVa 168
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                                                                                                           85 ysCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGln 101
68 rGluTrpAspCysMetCysValGlnProGluPheH1sCysGlyAspProC :::
                                                                                                                                                                                                                                                                                                                  yThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysT
                                                                                                                                                                                                              SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGl
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/db_xref="taxon:10090"
/clone="InAGE:3470242"
/clone=lib="Soares_thymus_2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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1 (bases 1 to 609)
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Unpublished (1997)
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145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 CCAGGCAAGGACGACTGTCCAAAAGAAAGGTGCATATGTGTCACACCTGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 CyslleAspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCy 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 ......ArgLysThrGlnLeuLeuGluValProProSer 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 roProGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGln 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 sLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProG
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Gaps: 3
Percent Identity: 54.412
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3.997
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                                                                                                                                                                                                                             alignment_scores
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BESJ 4685 689 bp mRNA EST 21-JUL-2000 60124187F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3582548 5',
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. n column: 21
High quality sequence stop: 580.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDM Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GGAGTCTCGATGCTCTGTGTGTGCTGGACCTAGGTCAGCCGAGTGTAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 yGlyProGlyCysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGCCTGGCTGTGGCCTGGCAAGGTTCAGAACGGAAGTGGCAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 laArgCysCysArgValHisThrThrArgCysCysArgAspTyrProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluGluCysCysSerGluTrpAspCysMetCysValGlnProGluPheHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 219
Gaps: 5
Percent Identity: 50.228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                      BE374685.1 GI:9320048
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3.733
74.429
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US-09-512-363-2 x BE374685
                                seq_name: gb_est73:BE374685
                                                                                                                        mRNA sequence.
BE374685
ACTGAAGATGCC 597
                                                                                                                                                                                                          Mus musculus
                                                                    seq_documentation_block:
                                                                                                                                                                          EST.
house mouse.
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Ratio:
Percent Similarity:
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JOURNAL
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                                                                                                                                                        VERSION
KEYWORDS
SOURCE
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586
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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Wed

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BF539340 953 bp mRNA EST 11-DEC-2000 602049520F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4188724 5',
                                                                                                                                                                                                                                                                          SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                   yThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 CACCTICICCCCAGGTCGTGACGTCACTGCAGACTTTGGACCAACTGTT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lvalLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL 185
                   82
                                                                                                                                                                                                                                                                                                                      85 ysCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGln 101
                                                            19 uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG 35
3 GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
                                                                                                                            35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51
                                                                              ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 ATCTGGGGGGTCGGTGG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est89:BF539340
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BF539340
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LOCUS BF539340
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KEYWORDS
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Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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/clone="IMAGE:4168724"
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/lab_host="DH10B (T] phage-resistant)"
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NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                        þe
1 (bases 1 to 953) "NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9513 row: h column: 05
High quality sequence stop: 649.
Location/Qualifiers
                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 sLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AGTTGAGGAGCCTGGCTGTGGCCTGGCAAGGTTCAGAACGGAAGTGGCA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 roProGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGln 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 oThrGlyGlyProGlyCysGlyProGlyArgLeuLeuLeuGlyThrGlyT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 hrAspAlaArgCysCysArgValHisThrThrArgCysCysArgAspTyr 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlyGluGluCysCysSerGluTrpAspCysMetCysValGlnProGl 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 uPheHisCysGlyAspProCysCysThrThrCysArgHisHisProCysP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LeuCysGlyLeuAlaLeuLeuCysAlaLeuSerLeuGlyGln...ArgPr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 218
Gaps: 3
Percent Identity: 54.587
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="FVB/N"
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3.859
76.606
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US-09-512-363-2 x BF539340
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Ratio:
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152 ValCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVa 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGln 101
                                                                                                                                                                                                                                                                                                                       21 AGGAGAAGCACTAFGGGGGATGGGCCATGCTGTATGGAGTCTCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                      19 uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                71 CTGTGTGCTGGACCTAGGTCAGCCGAGTGTAGTTGAGGAGCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 CACCTTCTCCGCAGGTCGTGACGGTCACTGCAGACTTTGGACCAACTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 euGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuLeu...Glu
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                                                                                                                                                                                                                                                                                               3 GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProC
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                                                                                                                                     Percent Identity: 51.364
                                                                                                                Gaps:
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3.792
75.455
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US-09-512-363-2 x AW230447
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LOCUS     AW230423
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Ratio:
Percent Similarity:
                                                                   alignment_scores
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Producement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Context Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

178 c 188 g 149 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Emmanlais; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 659)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                          384 GGAACAAGACCCACAAATGCTGTGTGCATCCCGGAGCCACTGCCGACAGAG 433
                                                                                                                                                                                                                           584 GCTGAGGATGCTTGCAGCTTCCAGTTCCCTGAGGAGGAACGCGGGGAGCA 633
                                                                                                                                                                                                    178 uLeuLeuThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLys. 194
                                                                                                                                                                                                                                                                                               204
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                  145 lyAsnLysThrHisAsnAlaValCysValProGlySerProProAlaGlu 161
                                                                                                                                     534 AACACATGTGTCTCGAGAGACCCAGCCATTCGCGGAGGTGCAGTTGTCA
                                                                                                           162 ProLeuGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLe
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/clone=lib="NCI_CGAP_Mam1"
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Inpublished (1997)
Other ESTs: uo63f10.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -40RP from Gibco
High quality sequence stop: 434.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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AW208743 uo63d10.x1 NCI_CGAP_MG
BF318127 ux01e06.x1 NCI_CGAP_GG
A1117445 ub88b01.x1 Scares_thym
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AW659189 96150 MARC 1BOV Bos ta
AW659189 xx84g01.x1 NCI_CGAP_ES
ANG94829 xx64f08.x1 NCI_CGAP_ES
ANG94829 xx64f08.x1 NCI_CGAP_ES
AR326084 EST232646 Normalized I
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BG327151 602426382F1 NIH_MGC_1
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-ALIGN-15 -NORDE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-ILGN-13 -LONGLOG -NO_XLPXY -WAIT -THREADS-1
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L Jumpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/Amage/Amage.html
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Seq primmer: -40UP from Gibco
High quality sequence stop: 459.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT773D-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tunnor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 650)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                           'n
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/clone=lib="NKI_CGAP_Lu19"
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LOCUS A1923712 650 bp mRNA EST 08-MAR-2000
DEFINITION W159906.x1 NCI_CGAP_LU19 Homo sapiens cDNA clone IMAGE:2449786
similar to TR:035714 035714 GLUCOCORTICOID INDUCED TNFF FAMILY
RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
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to: 1026
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end: BamHI. Host: DH10B.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
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3.847
76.569
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US-09-512-363-2 x AK020762
                                                                                                                                          4 (sites)
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
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                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                          REFERENCE
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                                                          TITLE
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (sites)
Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Kikuchi,N., Ishil,Y., Nakamura,S., Hazama,M., Nishine,T.,
Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430104A12, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordatà; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAP trapper.
Mus musculus (strain:C57BL/6J) 0 day neonate thymus cDNA to
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:A430104A12.
                                 euLeuGluValProProSerThrGluAspAlaArgSerCysGlnPhePro 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 yPheLeuThrValPheProGlyAsnLysThrHisAsnAlaValCysValP 155
                                                                                                                                                                                                                                                                                                                                                               roGlySerProProAlaGluProLeuGlyTrpLeuThrValValLeuLeu 171
                                                                                                                                                                                                                                                                                                                                                                                    100 CAGGGTCCCCGCCGCCGCAGAGCCGCTTGGTGGTGGCTGACCGTCGTCCTCCTCTCG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                           172 AlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnLeuGlyLeuHi 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sIleTrpGlnLeu................ArgLysThrGlnLeuL 198
650 TGCATGTGTGTCAGCCNTGAATCCCACTGCGGAGACCTTGCTGGCACGAC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 CATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGAGAGACCCAGCTGC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 TGCTGGAGGTGCCGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTCCCC 201
                                                                                                                   ysPheSerPheGlyPheGlnCysIleAspCysAlaSerGlyThrPheSer
                                                                                                                                                                                                  122 GlyGlyHisGluGlyHisCysLysProTrpThrAspCysThrGlnPheGl
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High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
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LOCUS AK020762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 CCTGTGGGTG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 pLeuTrpVal 234
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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Thuctional annotation of a full-tength mouse count collection.

The functional annotation of a full-tength mouse count collection.

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakwa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Hiraoka, T., Hori, F., Hangaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Nomura, K., Sato, H., Kawa, J., Miyazaki, A., Nishi, Y., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Kojima, Y., Kolno, H., Saito, H., Sakai, C., Sakai, K., Sakai, K., Sakai, K., Sakai, T., Sagaki, D., Shibata, K., Shibata, Y., Shibata, M., Tagawa, A., Takahshi, F., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahshi, F., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

AL Submitted (18-ANG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reséggec.riken.go.jp, Fax:81-45-503-9212, Phase visit our web site (http://genome.gsc.riken.go.jp/) for first-har Adalasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="WGD:MGT:1911656"
/db_xref="MGD:MGT:894675"
/clone="A430104A12"
/tissue_type="thymus"
/clone_lib="RtEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
269 c 301 g 232 t
Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E. Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                   The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
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Percent Identity: 53.975
                                                                                                                                                                                       Genome Res. 10 (11), 1757-1771 (2000)
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10 CCTGCACGTGTGTAACCTCAGAAGTGGGAGTGAGCGGAAGCAGCTGTG 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 TGGGGCTGAGCACCGTGACGGGGCTCCACTGTGTCGGGGACACCTACCC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 CGTGCGGCCGGCTTCTACAACGACGTGGTCAGCTCCAAGCCGTGCAAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 sThrThrCysArgHisHisProCysProProGlyGlnGlyValGlnSerG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 lnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGlyThr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 InArgProThrGlyGlyPro.GlyCysGlyProGlyArgLeuLeuLeuGl 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GGCTCGGCGCTGGGCCGCGGGCCGTGTGCGGCTTGCTCCTGGGCC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ......AlaLeuCysAlaLeuSerLeuGlyG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 yThrGlyThrAspAlaArgCysCysArgValH1sThrThrArgCysCysA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 rgAspTyrProGly.....GluGluCysCysSerGluTrpAspCysMet 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 ...CysValGlnProGluPheHisCysGlyAsp.....ProCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeu.......
                                                                                        COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,967
FILING DATE: 10-FEB-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SALLH, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET UNMBER: 05490A-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2402
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE (ALRANCTERISTICS:
LENGTH: 1057 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 253
Gaps: 8
Percent Identity: 25.692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .; LOCATION: 15.845
; OTHER INFORMATION: /standard_name= "ACT-4 CDNA"
US-08-195-967-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-195-967-1 from: 1
                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-512-363-2 x US-08-195-967-1
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Ratio: 1.518
Percent Similarity: 43.874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
     ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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Sequence 1, Application US/08195967
Patent No. 6242566
GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: CD4+T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Litton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 CGTGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGCCGTGCAAG 260
                                                                                                                                                                                                                                                                                                                             261 CCCTGCACGTGTGTAACCTCAGAAGTGGGAGTGAGCGGAAGCAGCTGTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                       sThrThrCysArgHisHisProCysProProGlyGlnGlyValGlnSerG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 nPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAlaValC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 alValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGln 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuLeuGluVa 201
                                                                                                                                                                                            59 rgAspTyrProGly.....GluGluCysCysSerGluTrpAspCysMet 73
                                                                                                  42 yThrGlyThrAspAlaArgCysCysArgValHisThrThrArgCysCysA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 ACAGGGACCCTCCACCCGGCCCGTGGAGGTCCCCGGGGGGCCGTGCGGTTG
                                                                                                                                                                                                                                                                                       ...CysValGlnProGluPheHisCysGlyAsp.....ProCysCy
26 lnArgProThrGlyGlyPro.GlyCysGlyProGlyArgLeuLeuGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    561 CCGGCCAGGCCCATCACTGTCCAGCCCAGAAGCCTGGCCCAGAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 CCGCCATCCTGGGCCTGGGCCTGGGGCTGCTGGGCCCCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 ATCCTGCTGGCCCTGTACCTCCGGAGGGACCAGAGGCTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-195-967-1
                                               126 AGCAACGACCGGTGCTGCCACGAGTGCAGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 lProPro 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 .....
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120 Pheser(        411 TTCTCC	120 PheserGlyGlyHisGluGlyHisCysLysDroTrpThraspCysThrGl	136 460
136 nPheGly    461 GGCTGG	136 nPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAlaValC	153 510
153 ysvalP:     511 GTGAGG	153 ysValProGlySerProProAlaGlu	161 560
161		161
561 CCGGCC	561 CCGCCCAGCCCATCACTGTCCAGCCCACTGAAGCCTGGCCCAGAACCTC	019
162	ProLeuGlyTrpLeuThrV	
611 ACAGGG	ACCCTCCACCGGCCCGTGGAGGTCCCCGGGGGCCGTGCGGTTG	099
168 alvalLe :::::: 661 CCGCCA	alValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGln 184 :::::::   ::::::: ccgccAlccrGGGccrGGTGCTGGGGCTGCTGGGCCCCTGGCC 710	184 710
185 LeuGly) ::: 711 ATCCTG	LeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuLeuGluVa :::	201 752
201 lProPro 203	0 203 0 203 0 758	

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130 ProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAs 146
                                                                                   146 nLysThrHisAsnAlaValCysValProGlySerProProAlaGluProL 163
                                                                                                                                                                         163 euGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeu 179
                                                                                                                                                                                                  180 LeuThrSerAlaGlnLeuGlyLeuHisIleTrp......GlnLe 192
                                                                                                                                                                                                                                                                                        550 CCAACCACTGTCCAA...TCCACCACAGTCTGGCCCAGGACTTCTGAGTT 596
                                                                                                                                                                                                                                                                                                                                                                              192 uArgLysThrGlnLeuLeuLeuGluValProProSer.....ThrG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/l/ina/5A_COMB.seq:US-08-192-480A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Andrew D. Weinberg and Arthur A.
APPLICANT: Vandembark
TITLE OF INVENTION: MEDIATED CONDITIONS
INUMBER OF SEQUENCES: 3
CORRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Leigh & Whinston
STREET: 121 S.W. Salmon Street, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: ::: |||| |||| |||| 644 ACACATGCCACCACCAGCACCTGAAGCCGAG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                         206 luAspAlaArgSerCysGlnPheProGluGluGlu 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: Wordperfect 5-1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/192,480A FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA: N/A APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28,107
ER: 4282-38649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: RICHARD J. POLIEY, ESQ.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 4282-3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEPRA: (503) 228-946
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 848 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Portland
STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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201 lProPro 203

261 CCCTGCACGTGTGTAACCTCAGAAGTGGGAGTGAACGGAAGCAGCTATG 310 76 TGGGGCTGAGCACCGTGACGGGGCTCCACTGTGTCGGGGACACCTACCCC 125 211 CGTGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGCCGTGCAAG 260 103 lnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGlyThr 119 361 TGGACAGCTACAAGCCTGGAGTTGACTGTGCCCCCTGCCCTCCAGGGCAC 410 120 PheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysThrGl 136 136 nPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAlaValC 153 561 CCGCCCAGCCCCATCACTGTCCAGCCCACTGAAGCCTGGCCCAGAACCTC 610 162 .....ProLeuGlyTrpLeuThrV 168 611 ACAGGGACCCTCCACCCGGTCCGTGGAGGTCCCCGGGGGCCCGTGCGGTTG 660 168 alValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGln 184 661 CCGCCATCCTGGGACTGGACTGGTGCTGGGCTGCTGGGACCCCTGGAC 710 SThrThrCysArgHisHisProCysProProGlyGlnGlyValGlnSerG 103 511 GTGAGGACAGGGACCCCCAGGCACCCCCAGGAGACCCAGGGTCCC 560 185 LeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuLeuGluVa 201 5 GlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeu..........16 26 GGCTCGGCGGCTGGGCCGGGGCGTGTGCTCCTCCTGGGCC 75 17 ..........AlaLeuLeuCysAlaLeuGlyG 26 26 lnArgProThrGlyGlyPro.GlyCysGlyProGlyArgLeuLeuGl 42 42 yThrGlyThrAspAlaArgCysCysArgValHisThrThrArgCysCysA 59 ...CysValGlnProGluPheHisCysGlyAsp.....ProCysCy Length: 253
Gaps: 8
Percent Identity: 25.692 to: US-08-192-480A-1 from: 1 126 AGCAACGACCGGTGCTGCCACGAGTGCAGGCCA... 153 ysValProGlySerProProAlaGlu... alignment\_block: US-09-512-363-2 x US-08-192-480A-1 1.531 44.269 Quality: Ratio: Percent Similarity: ; FRAGMENT TYPE: US-08-192-480A-1 alignment\_scores 161 ..... Align seg 1/1 98 74

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APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-147-784-1
                                                                                                                                                                                                                                                                                                           Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 253
Gaps: 8
Percent Identity: 25.692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name= "ACT-4 cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-147-784-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-220
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                seq_documentation_block:
; Sequence 1, Application US/08147784
; Patent No. 5821332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-512-363-2 x US-08-147-784-1
                                                                                                                                                                                                                                                                                                                        STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168.50
1.518
43.874
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 15..845
; OTHER INFORMATION:
US-08-147-784-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
753 . CCCCCC 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
AUWBER OF SEQUENTON: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807 AGACCAGTACAAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCC 856
rValPheProGlyAsnLysThrHisAsnAlaValCysValProGly.... 156
                                                                                                         :::: ||||:::||| ::::::::|||||| | |||:::
                                                                                                                                                                                                        607 ccgaccrcrcrccgggagcarccrcrgrgaccccgccrgcccrgcgaga 656
                                                                                                                                                                                                                                                                     GluProLeuGlyTrpLeuThrValVal.....LeuLeuAlaValAlaAl 175
                                                                                                                                                                                                                                                                                                                                aCysValLeuLeuLeuThrSerAlaGlnLeuGlyLeuHis.....I 189
                                                                                                                                                                                                                                                                                                                                                                                                                                           189 leTrpGlnLeuArgLysThrGlnLeuLeuLeuGluValProPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....SerThrGluAspAlaArgSerCysGlnPhePr
                                                                                                                                                                    ...SerProProAla....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-816-605-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/CDCKET NUMBER: PF25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oGluGluGluArgGly 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MD
COUNTRY: U
                                                                                    141
                                                                                                                                                                                                                                                                                        657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214
                                                                                                                                                                                                                                                                                                                                175
                                                                                                                                                                                                                                                                                                                                                                        707
                                                                                                                                                                    157
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167 hrValVal.....LeuLeuAlaValAlaAlaCysValLeuLeuThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 AGATCATCTTCTTTCTTGCGCTGACGTCGGTTGCTTTCTTCTG 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 SerAlaGlnLeuGlyLeuHis......IleTrpGlnLeuArgLysTh 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 caccagcaargcagagrergacrec.....acrecagggrrrcaer 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 GCCTGGGGGCAGGATGCAGCATGTGT...GAACAGGATTGTAAACAAGGT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 GlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAs 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 CTGTTGCTTTGGGACATTTAACGATCAGAAACGTGGCATCTGTCGACCCT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 rpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLys 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 ......ProProAla.....GluProLeuGlyTrpLeuT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 rGlnLeuLeuLeuGluValProPro......S 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 CAAGAACTGACAAAAAAGGT.....TGTAAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 pCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 CTGTTCTTCCTCACGCTCCGTTTCTCTGTTAAACGGGGCAGAAGAA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672 ACTCCTGTATATTCAAACAACCATTTATGAGACCAGTACAAACTACTC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ysGlyAspProCysCysThrThrCysArgHisHisProCysProProGly 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 r......GluTrpAspCysMetCysValGlnProGluPheHisC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-097-827-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 erThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGly 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 ATCCTCTGTGACCCCGCCTGCCAGAGAGAGCCAGGACACTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GluGluCysCysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 ThrHisAsnAlaValCysValProGlySer......
                                                                                                                                                                                                                                                                                      Length: 199
Gaps: 10
Percent Identity: 31.156
                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 946
                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-816-605-1
                                                                                                                                                                                                                                                                                                                                                                                               US-09-512-363-2 x US-08-816-605-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 CysArgAspTyrProGly....
                                                                                      sig_peptide
124..177
                                                                                                                                                      mat_peptide
178..780
                                                                                                                                                                                                                                                                                      194.00
1.940
50.251
                                             124..780
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                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                      NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                             LOCATION:
                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                             ;
US-08-816-605-1
                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                    FEATURE:
                                                                                                                                    FEATURE
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No. 5783665el Cytokine Which is a Ligand for OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 ATGATACCTGCAAGCAGTGTACACAGTGCAACCATCGAAGTGGAAGTGAA 270
                                                                                                                                                                                                                                                                                                                                 96 oGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysI 113
                                                                                                                                                                                                                                                                                                                                                                            321 AGGCACCCAACCTCGGCAGGACAGCGGCTACAAGCTTGGAGTTGACTGTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                           113 leAspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLys 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 TTCCCTGCCCTCCTGGCCACTTTTCTCCAGGCAACAACCAGGCCTGCAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 nLysThrHisAsnAlaValCysValProGlySerProProAlaGluProL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 euGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 LeuThrSerAlaGlnLeuGlyLeuHisIleTrp.......GlnLe 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 uArgLysThrGlnLeuLeuLeuGluValProProSer.....ThrG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seg_name: /cgn2_6/ptodata/1/ina/5A_COMB.seg:US-08-494-574-10
                                                                                                                                                                                                                                                                                   271 CTCAAGCAGAATTGCACACCTACTCAGGATACTGTCTGCAGATGTAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 GAAGCCTCCTGGCCACACTGCTCTGGGAGACCCAGCGCCCTACATTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......CysThrThrCysArgHisHisPro.....
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 luAspAlaArgSerCysGlnPheProGluGluGlu 217
       145 GTGAACCGCTGTGATCATACCAGGGATACTCTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/494,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08494574 Patent No. 5783665 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                    79 eHisCysGlyAspProCys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NO TITLE OF INVENTION: OX NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
                                                                                                                                                                                                                                      94
                                                                       APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William .
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 y.....ThrGlyThrAspAlaArg.....CysCysArgValHisThr. 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...GluGluCysCysSerGluTrpAspCysMetCysValGlnProGluPh 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GlnArgProThrGlyGlyProGlyCysGlyProGlyArgLeuLeuLeuGl 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 .....ThrArgCysCysArgAsp...TyrProGly....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 ACTCACACTTGGAGTTACAGCAAGGCGGCTCAACTGTGTTAAACATACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    STREET: 51 University Street CITY: Seattle
Sequence 10, Application US/08097827
Patent No. 5457035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: PERKINA, PALTICIA A.
REGISTRATION UNMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-097-827-10
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US-09-512-363-2 x US-08-097-827-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1317 base pairs TYPE: nucleic acid
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 175.50
Ratio: 1.610
Percent Similarity: 44.490
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                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                      USA
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-097-827-10
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320

549

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182 TGTCCTCCAAATAGTTTCTCCAGCGCAGGTGGA.....CAAAGGACCTG 225
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                                                                                                                                                                                                              sHisProCysProProGlyGlnGlyValGlnSerGlnGlyLysPheSerP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ......TGTAAAGACTGTTGCTTTGGGACATTTAACGATCAGAAA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluGlyHisCysLysProTrpThrAspCysThrGlnPheGlyPheLeuTh 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......SerProProAla..... 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 CTGACCTCTCTCGGGAGCATCCTCTGTGACCCCGCCTGCCCTGCGAGA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GluProLeuGlyTrpLeuThrValVal.....LeuLeuAlaValAlaAl 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628 GACTGCGTTGCTCTTCCTGCTGTTCTTCTCTCTGTTG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ::: 111111
678 TTAAACGGGCCAGAAGAACTCCTGTATATATTCAAACAACCATTTATG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728 AGACCAGTACAAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCC 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 heGlyPheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHis 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......SerThrGluAspAlaArgSerCysGlnPhePr 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:PCT-US96-03965-7
34 CysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCy 50
                                                                                      50 sArgValHisThrThrArgCysCysArgAspTyrProGly......63
                                                                                                                                                                                  64 .....GluGluCysCysSer......GluTrpAspCysMetCys 74
                                                                                                                                                                                                                                                                             75 ValGlnProGluPheHisCysGlyAspProCysCysThrThrCysArgHi 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 aCysValLeuLeuThrSerAlaGlnLeuGlyLeuHis.....I
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Sequence 7. Application PC/TUS9603965

GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se

APPLICANT: Kang, Chang Yull

TITLE OF INVENTION: Monoclonal antibody against human

TITLE OF INVENTION: receptor 4-1BB

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, Brown & Michaels

STREET: 306 East Street, Suite 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 leTrpGlnLeuArgLysThrGlnLeuLeuLeuGluValProPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 oGluGluGluArgGly 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Ithaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                      226
                                                                                                                                                                                                                                                                                                                           305
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182 TGTCCTCCAAATAGTTTCTCCAGCGCAGGTGGA.....CAAAGGACCTG 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 CysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 12
Percent Identity: 30.180
ZIP: 14850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: PCT-US96-03965-7 from: 1 to: 838
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CELL TYPE: Lymphocyte
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/number= 1
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/number= 1
                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-198
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REGISTRATION NUMBER: 34,390
REGISTRATION NUMBER: 34,390
REGISTRATION NUMBER: 34,390
REGISTRATION NUMBER: WWOS
TELECOMMUNICATION INFORMATION:
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US-09-512-363-2 x PCT-US96-03965-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: 41..802
OTHER INFORMATION: /cod
OTHER INFORMATION: /roo
OTHER INFORMATION: /num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 838 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 607-273-2609 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 197.00
Ratio: 1.807
nilarity: 49.099
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LOCATION: 41..805
OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US96-03965-7
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305 TGACATA.....TGCAGGCAGTGTAAAGGTGTTTTCAGGA 339 ...GA 427 91 sHisProCysProProGlyGlnGlyValGlnSerGlnGlyLysPheSerP 108 heGlyPheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHis 124 64 .....GluGluCysCysSer......GluTrpAspCysMetCys 74 34 CysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCy 261 TGTCCTCCAATAGTTTCTCCAGCGCAGGTGGA.....CAAAGGACCTG 75 ValGlnProGluPheHisCysGlyAspProCysCysThrThrCysArgHi 340 CCAGGAAGGAGTGTTCCTCCACCAGCAATGCAGAGTGTGACTGC..... 50 sArgValHisThrThrArgCysCysArgAspTyrProGly...... Length: 222 Gaps: 12 Percent Identity: 30.180 to: 1415 428 ACAGGATTGTAAACAAGGTCAAGAACTGACAAAAAAAGGT SOFTWARE: Microsoft Word, Version #6.0.1 CURRENT APPLICATION DATA: Align seg 1/1 to: US-08-236-918A-7 from: 1 APPLICATION NUMBER: US/08/236,918A NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 707-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: alignment\_block: US-09-512-363-2 x US-08-236-918A-7 CDNA to mRNA 06-May-1994 LENGTH: 1415 base pairs sig\_peptide 120..188 1.807 mat\_peptide 189..884 TYPE: nucleic acid STRANDEDNESS: sing 120..887 linear 2 ANTI-SENSE: NO IMMEDIATE SOURCE: hu4-1BB Quality: Percent Similarity: TOPOLOGY: 11 MOLECULE TYPE: Ratio: HYPOTHETICAL: NAME/KEY: LOCATION: alignment\_scores: NAME/KEY: LOCATION: NAME/KEY: ; LOCATION: US-08-236-918A-7 FEATURE:

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281 AGCTGCCCTCCAAGTACCTTCTCCAGCATAGGTGGACAGCCGAACTGTAA 330
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369 AGTITIGCTCCTCTACCCACAACGCGGAGTGTGAGTGCATTGAA...GGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uLeuLeuThrSerAlaGlnLeuGlyLeuHisIle.....TrpGlnLeuA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 ProSerThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGl 219
                                                                                                                                                            137 CATTTCGCCATGGGA.....AACAACTGTTACAACGTGGTGGTCATTGT 180
                                                                                                                                                                                                                                                         181 GCTGCTGCTAGTGGGCTGTGAGAAGGTGGGAGCCGTGCAGAACTCCTGTG 230
                                                                                                                                                                                                                                                                                                                                       TICCATIGCTIGGGCCACAGTGCACCAGAIGT...GAAAAGGACIGCAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oProGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ysIleAspCysAlaSerGlyThrPheSerGlyGlyHis...GluGlyHis 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPhePr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 IGTCGACCCTGGACGACTGCTCTAGACGGAAGGTCTGTGCTTAAGAC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 ProLeuGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLe 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           792 AAAAATTCCCCCACATATTCAAGCAACCATTTAAGAAGACCACTGGAGCA 841
                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheHisCysGlyAspProCysCysThrThrCysArgHisHisProCysPr 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luCysCysSerGluTrp.....AspCysMetCysValGlnProGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 yGluArgSerAlaGluGluLys.....GlyArgLeuGlyAspLeuTrp 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642 CTCCCAGTACCACCATTTCTGTGACTCCAGAGGAGGACGACCAGGAGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 HisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLeuCy
                                                                                                                                                                                                                                                                                                                                                                                                    gCysCysArgValH1sThrThrArgCysCysArgAspTyrProGlyGluG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGACCACGGAGAAGGACGTGTGTGTGGACCCCCTGTGGTGAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCCTGATCTTCATTACTCTCTGTTCTCTGTGCTCAAATGGATCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 oGlyAsnLysThrHisAsnAlaValCysValPro.....
                                                                    to: 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 GCCTGGCCAGGAGCTAACGAAGCAGGGT.....
                                                                    from: 1
                                                                                                                                                                                                                                                                                                       roGlyCysGlyProGlyArgLeuLeu.....
                                                                  Align seg 1/1 to: PCT-US96-03965-1
                   US-09-512-363-2 x PCT-US96-03965-1
alignment_block:
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-236-918A-5
                                                                                                                                                                                                                         St. Kathryn A. Anderson, Immunex Corporation
51 University Street
                                                                                       GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 28.704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-236-918A-5 from: 1 to: 768
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                          Apple Power Macintosh
                                    seq_documentation_block:
; Sequence 5, Application US/08236918A
; Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-512-363-2 x US-08-236-918A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              768 base pairs
nucleic acid
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70..768
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1..69
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1.883
49.537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple P
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..768
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                                                                                                                                                                                                                                            STATE: Wack:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mu4-1BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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LOCATION:
FEATURE:
                                                                                                                                                                                                                           ADDRESSEE:
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US-08-236-918A-5
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34 CysGlyProGlyArgLeu...LeuLeuGlyThrGlyThrAspAlaArgCy 49

APPLICATION NUMBER: PCT/US94/10457

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seq_documentation_block:
    Sequence 1, Application PC/TUS9410457
    GENERAL INFORMATION:
    APPLICANT: Byoung Se Kwon
    TITLE OF INVENTION: New Human Receptor and Related Products
    TITLE OF INVENTION: and Methods
    NUMBER OF SEQUENCES: 1
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 leAspCysAlaSerGlyThrPheSerGlyGlyHis...GluGlyHisCys 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 CCAGTACCACCATTTCTGTGACTCCAGAGGAGGACCAGGAGGCACTCC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 oGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                    .....TGCA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 AAACCIGIAGCIIGGGAACAITIAAIGACCAGAACGGIACIGGCGICIGI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......GlySerProProAlaGluPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 LeuGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLe 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 uLeuThrSerAlaGlnLeuGlyLeuHisIle.....TrpGlnLeuArgL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 AATTCCCCCACATATTCAAGCAACCATTTAAGAAGACCACTGGAGCAGCT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US94-10457-1
                                                                                                                           189 CTGCAGAGTG......TGTGCAGGCTATTTCAGGTTCAGAAGT 226
                                                                                                                                                                                                                                                                                 80 HisCysGlyAspProCysCysThrThrCysArgHisHisProCysProPr 96
                                                                      49 sCysArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 SerThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGly 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700 CAAGAGGAAGATGCTTGTAGCTGCCGATGTCCACAGGAAGAAGAAGAA747
                                                                                                                                                                             66 ysCysSerGluTrp.....AspCysMetCysValGlnProGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 yAsnLysThrHisAsnAlaValCysValPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                    321 TGGCCAGGAGCTAACGAAGCAGGGT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Barnard & Brown
STREET: 306 E. State St., Sulte 220
CITY: Ithaca
TATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 ysThrGlnLeuLeuLeuGluValPro....
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Similarity to mouse 4-1BB and other members of NGFR superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Kwon, B.S., and Weissman, S.M.
TITLE: CDNA sequences of two inducible T-cell genes
JOURNAL: Proc. Natl. Acad. Sci. USA
VOLUME: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 222
Gaps: 12
Percent Identity: 30.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: PCT-US94-10457-1 from: 1
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                                                                                                                                                                                                                                                  kwnh41bb
                                               FILING DATE: 2/1/93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,996
FILING DATE: 7/30/92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/267,577
FILING DATE: 11/7/88
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       NAME: Michaels, Christopher A. REGISTRATION NUMBER: 34,390 TREFRENCE/DOCKET NUMBER: kwnh41 TELECOMMUNICATION: TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; RELEVANT RESIDUES IN SEQ ID NO: PCT-US94-10457-1
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,269
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-512-363-2 x PCT-US94-10457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Lymphocytes
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197.00
1.807
49.099
                                                                                                                                                                                                                                                                                      TELEPHONE: 607-273-17
TELEFAX: 607-273-2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: n/a ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: H4-1BB
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAP POSITION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANELLE
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485 GIGTGCATCCCGGAGCGACTGCCCACTGAGCAATACGGCCATTTGACTGT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSerCy 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111111:::111 | 11 | 11 | 12 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 yThrPheSerGlyGlyH1sGluGlyH1sCysLysProTrpThrAspCysT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 ValCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVa 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 lValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 53.975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-911-423-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-512-363-2 x US-08-911-423-1
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1073 base pairs
                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     704.00
3.847
76.569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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1.602
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COMPUTER READABLE FORM:
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LOCATION: 146..916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March
1963-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                          USA
                                                                                                                                                                               CITY: Ithaca
                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US96-03965-1
                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGES:
                                                                                                                                                                                                                                               ; Sequence 72, Application US/09188930A
; Patent No. 1615050
; GENERAL INFORMATION;
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, Compositions Isolated From Skin Cells
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; TITLE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 72
LENGTH: 267
                                       211 sGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysGlyA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-03965-1
635 ACCCAGCCATTCGCGGAGGTGCAGTTGTCAGCTGAGGATGCTTGCAGCTT 684
                                                             57 CysCysArgAspTyrProGlyGluGluCysCysSerGluTrpAspCysMe 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 uGlyGln...ArgProThrGlyGlyProGlyCysGlyProGlyArgLeuL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 euLeuGlyThrGlyThrAspAlaArgCysCysArgValHisThrThrArg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 tCysValGlnProGluPheHisCysGlyAspProCysCysThrThrCysA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GlyalaPheArgAlaLeuCysGlyLeuAlaLeuLeuCysAlaLeuSerLe 24
                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-188-930-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 95
Gaps: 2
Percent Identity: 46.316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 rgHisHisProCysProProGlyGlnGlyValGln 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 AGCACTACCCTGCCAACCAGGCCAAAGGGTGGAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
    Sequence 1, Application PC/TUS9603965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-188-930-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-512-363-2 x US-09-188-930-72
                                                                                                                       228 rgLeuGlyAspLeuTrp 233
                                                                                                                                                            732 ATCTGGGGGGTCGGTGG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255.00
3.806
70.526
                                                                                                                                                                                                                                             seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: mouse US-09-188-930-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inducible T-cell genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 283
Gaps: 13
Percent Identity: 26.502
                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                     306 East State Street, Suite 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390 REFERENCE/DOCKET NUMBER: KWOS TELECOMMUNICATION INFORMATION: TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two
                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: et al.,
TITLE: cDNA sequences of tv
JOURNAL: Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Kwon, Byoung Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 2347 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: murine 4-1BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide LOCATION: 146..913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                   NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213.00
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181.95
181.95
164.89
166.83 (
                                                                                                                                                                                                                            APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: REAGENTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGCCACAGCACGGGGCGATGGGGCGCGTTTCGGGCCCTGTGCGGCCCTGGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetalaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
 /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-071-433-85 + 126.50
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-041-886.26 + 126.50
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-042-785A-1 + 123.50
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-466-589-5 + 122.50
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-700-636-5 + 122.50
                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-911-423-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 1
Percent Identity: 96,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 SEE: DNAX Research Institute
: 901 California Avenue
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       Align seg 1/1 to: US-08-911-423-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-512-363-2 x US-08-911-423-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1006 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650-496-1200
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Ratio: 5.652
Percent Similarity: 97.095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
LOCATION:
US-08-911-423-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2612
1815
                                                                                                                         Command line parameters:
-MODEL=frame+_p2n.model -DEV-xlp
-Q-Coq012_1VGPPTO_spool_VG09512363/runat_04092001_154255_21802/app_query.fasta_1.293
-Q-Coq012_1VGPPTO_spool_VG09512363/runat_04092001_154255_21802/app_query.fasta_1.293
-DB-ISSUEd_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni
-GAPOP=12.000 -GAPOP=4.500 -MINMATCH=0.100 -LOOPEL—0.000
-XGAPEXT=0.000 -GAPOP=4.500 -GAPEXT=7.000 -XGAPOP=10.000
-YGAPEXT=0.500 -PGELOP=6.500 -PGEEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09512363_eCGN1_1_57 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197.08
+ 139.50 193.94
+ 137.50 192.58
137.50 192.58
133.00 198.76
131.50 192.50
131.50 198.76
131.50 198.40
129.50 178.84 0.
                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
   out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-042-785A-22 +
OM of: US-09-512-363-2 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query length: 234
Database: Issued_Patents_NA:*
Database sequences: 324599
Database length: 94655562
Search time (sec): 67.430000
                                     Date: Sep 4, 2001 3:55 PM
                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
Query: US-09-512-363-2
Query length: 234
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17

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California
                                                                                94304-1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
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    Sequence 5, Application US/08911423
    Pagtent No. 6111000
    GENERAL INFORMATION:
    APPLICANT: Gorman, Daniel M.
    APPLICANT: Bandall, Troy D.
    APPLICANT: 2lotnik, Albert:
    TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
    TITLE OF INVENTION: REAGENTS
    MAMMALIAN CELL SURFACE ANTIGENS RELATED
    MAMMALIAN CELL SU
                                                                                     ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 GCACCCAGITCGGGITTCTCACIGIGITCCCIGGGAACAAGACCCACAAC 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84
                                      aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
                                                                                                                                                                                                                     34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys
                                                                                                                                                                                                                                                                                                                                                                                                          51 ArgvalHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701 GGCGGCTGGGAGACCTGTGGGTG 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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134

167

651

E: DNAX Research Institute 901 California Avenue

STREET: YOU

ADDRESSEE:

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51 NYTHYTHTGYGCNYTHWSNYTHGGNCARMGNCCNACNGGNGGNCCNGGNT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 CNTGYTGYACNACNTGYMGNCAYCAYCCNTGYCCNCCNGGNCARGGNGTN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGCNCARCAYGGNGCNATGGGNGCNTTYMGNGCNYTNTGYGGNYTNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 1
Percent Identity: 76.349
                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 723
                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY-AGENT INFORMATION:
REGISTATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
INFORMATION FOR SEQ. 1D NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                       14-AUG-1997
14-AUG-1997
18: 536
                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-911-423-5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-512-363-2 x US-08-911-423-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1075.50
Ratio: 5.487
Milarity: 81.328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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22 LCGLALL 28

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A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, A:Reference number: A82950; MUID:20437337
A:Reference number: A82950; MUID:20437337
A:Accession: B83642
A:Status: pre-liminary
A:Molecule type: DNA
A:Residues: 1-200 <STO>
A:Cross-references: GB:AE004442; GB:AE004091; NID:g9945843; PIDN:AAG03418.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
                                                            C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83642
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-206 <KUN> A:Residues: 1-206 <KUN> A:Residues: 1-206 <KUN> A:Zross-references: GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14350.1; PID:e1185687; A:Experimental source: strain 168 C;Genetics: A:Genetics: A;Genetics:
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                                      hypothetical protein PA0028 [Imported] - Pseudomonas aeruginosa (strain PA01)
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100.0%; Pred. No. 42;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.0
Best Local Similarity 100.
Matches 7; Conservative
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Search completed: September 5, 2001, 09:47:28 Job time: 69 sec

Wed Sep 5 10:00:53 2001

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Gaps

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0; Indels

Length 69;

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hypothetical protein ytfA [imported] - Lactococcus lactis subsp. lactis (strain IL140 c; Species: Lactococcus lactis subsp. lactis
C; Species: Lactococcus lactis lactic lact
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Reference number: A8304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <STO>
A;Cross-references: GB;AE004895; GB;AE004091; NID:g9951083; PIDN:AAG08208.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4823
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C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 30-May-1997
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 30-May-1997
C;Accession: B25429
C; Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 30-May-1997
C;Accession: B25429
C;Author T;Author C;Author C
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C;Keywords: T-cell receptor
F;11-120/Product: T-cell receptor beta chain V region SJL73 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005176; NID:g12724914; PIDN:AAK05979.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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100.0%; Pred. No. 23;
ive 0; Mismatches
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100.0%; Pred. No. 18;
ive 0; Mismatches
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7: Conservat
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K.; Lim,
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:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Libronectin Mouse (Iragment)
C; Species: Was musculus (house page 20-Aug-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C; Dates: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C; Dates: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C; Dates: 02-Jul-1996 #sequence_revision N.C.
Gene 137, 353-354, 1993
A; Title: Sequence of the mouse fibronectin gene promoter region.
A; Reference number: 148349; MUD:94131313
A; Molecule type: DNA
A; Molecule type: DNA
A; Reference number: S33445
A; Cross-references: EMBL:222729; May 1993
A; Description: Nucleotide sequence of the murine fibronectin gene promoter region.
A; Reference number: S33445
A; Molecule type: DNA
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                               A.Consorreferences: GDB:120019; OMIM:105120; OMIM:137350
A.Map position: 9q33-9q33
A.Antrons: 48(A.) 11/71
C.Superfamily: qelsolin; gelsolin repeat homology
C.Keywords: actin binding: alternative splicing; amyloid; calcium; duplication
C.Keywords: actin binding: alternative splicing; amyloid; calcium; duplication
C.Keywords: actin binding: alternative spredicted <SIG>
F.1-27/Domain: signal sequence #status predicted <SIG>
F.3-782/Product: gelsolin, plasma #status experimental <MATI>
F.51-176/Domain: actin-severing #status predicted <SEV>
F.53-782/Pondin: actin-severing interfilament contact
F.53-126/Region: actin-actin interfilament contact
F.434-782/Domain: gelsolin repeat homology <GEL1>
F.434-782/Domain: gelsolin repeat homology <GEL2>
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C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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100.0%; Pred. No. 13;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches
     with high affinity to fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibronectin - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ALLCALSL 24
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A; Cross-references: EMBL:X59889; NID:g62621; PIDN:CAA42543.1; PID:g62622
R;Chang, Y.S.; Huang, C.J.; Huang, F.L.; Lo, T.B.
Int. J. Pept. Protein Res. 32, 556-564, 1988
A;Title: Primary structures of carp gonadotropin subunits deduced from cDNA nucleotid A; Reference number: JK0024; MUID:89233593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-144 < CH2>
R; Jolles, J.; Burzawa Gerard, E.; Fontaine, Y.A.; Jolles, P.
R; Jolles, J.; By 893-898, 1977
A; Title: The evolution of gonadotropins: some molecular data concerning a non-mammali A; Reference number: A90673; MUID: 78124308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: G83342
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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: G83342
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, RStover, C.X.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: pituitary glycoprotein hormone beta chain C;Superfamily: pituitary pituitary C;Keywords: glycoprotein; pituitary F;1-27/Domain: signal sequence #status predicted <SIG> F;28-117/Product: gonadotropin beta chain #status predicted <MAT> F;33-38,47-81,50-112,62-134,96-124,114-117/Disulfide bonds: #status predicted F;37/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                           A;Cross-references: EMBL:X59888; NID:g62619; PIDN:CAA42542.1; PID:g62620
A;Accession: S29678
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00.0%; Pred. No. 33;
ve 0; Mismatches
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100.0%; Pred. No. 33;
iive 0; Mismatches
submitted to the EMBL Data Library, May 1991
A;Reference number: $29677
A;Accession: $29677
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A; Residues: 28-36, 'X', 38-53; 141-142 <JOL>
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Conservative 0;
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A:Molecule type: DNA
A:Residues: 1-144 <CHA>
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-144 <STO>
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Best Local Similarity
                                                                                                                     A; Molecule type: DNA
A; Residues: 1-144 <CH1>
                                                                                           A;Status: preliminary
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A;Gene: PA2436
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                                                                                                                                                            hypothetical protein PH0581 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Ju1-2000
C;Accession: A71173
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohituu, Y.; Yamashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137
A;Recession: A71173
A;Recession: A71173
A;Recession: A71173
A;Recession: A71173
A;Recession: A71173
A;Recession: A7173
A;Recession: A7173
A;Recession: A7173
A;Recession: A7173
A;Recession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0581
C;Superfamily: hypothetical protein MJ1081
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C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accssion: G75053
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: G75053
A;Status: preliminary
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A;Experimental source: strain Orsay
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C;Species: Cyprinus carpio (common carp)
C;Bate: 31-Aug-1979 #sequence_revision 16-Feb-1996 #text_change 23-Mar-2001
C;Accession: S29677; S29678; Jrd462; A01504
R;Chang, Y.S.; Huang, F.L.; Lo, T.B.
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100.0%; Pred. No. 31;
iive 0; Mismatches
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100.0%; Pred. No. 31;
iive 0; Mismatches
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Best Local Similarity luv...
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A; Residues: 1-133 <KAW>
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Matches 7; Conserv
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GPGCGPG 11
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summaries

Post-processing: Listing first 45

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

	Description	hypothetical prote	- 0			gelsolin precursor	fibronectin - mous	hypothetical prote	hypothetical prote	u	. hypothetical prote		gonadotropin beta	hypothetical prote		N-acetylmuramoyl-L	conserved hypothet	CD1b protein - she	thiamin biosynthes	chitinase (EC 3.2.	guanylate kinase -	leukocyte differen		puff II/9-1 protei	thiamin biosynthes	syntaxin - human	4-	probable D-amino a	probable ABC-type	transforming prote
SUMMARIES	QI	35	E70470	S61245	H70597	FAHUP	I48349	A83044	A86860	B25429	A71173	G75053	UTCAB	G83342	B83642	E69961	675303	S58353	D69845	B42424	C75291	B45887	507533	S07532	675613	138517	S52726	T35265	T36062	51001
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30 31	32	3 4 2 4	35	36	37	38	38	40	41	42	43	44	45	

## ALIGNMENTS

MENOUR: 1 T33566 hypothetical protein R160.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000 C;Cacession: T33566 R;Nelson, J; Gattung, S submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid R160. A;Reference number: 221370 A;Reference num			-2000								P:R160.6									Gaps 0;	
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National Landon R160.6 - Caenorhabditis elegan hypothetical protein R160.6 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: 29-Oct-1999 Rsquence_revision 29-Oct-1999 C.Accession: T33566 R.Accession: T33566 A.Accession: T33566 A.Accession: T33566 A.Accession: T33566 A.Accession: T3356 A.Accession: T3376 A.Accession: T3376 A.Accession: A.Access		กร	#text_change (			160.		J.			; GSPDB:GN00028	90					protein R160.6	•	Length 215;	0; Indels	
WESULT 1 193566 hypothetical C;Species: Ca C;Date: 29-06 C		protein R160.6 - Caenorhabditis elegal	t-1999 #sequence_revision 29-Oct-1999	T33566	carrung, s. the EMBL Data Library, October 1998	i: The sequence of C. elegans cosmid R	T33566	liminary; translated from GB/EMBL/DDB.	rpe: DNA	215 <nel></nel>	ences: EMBL:AF099001; PIDN:AAC68733.1	il source: strain Bristol N2; clone Rl		R160.6	. <b>x</b> :u	./2; 74/1; 96/2	caenorhabditis elegans hypothetical		3.4%; Score 8; DB 2; Statilarity 100 0%. Dred NO 4 8.	8; Conservative 0; Mismatches	AVAAC 176
•	T33566	hypothetical	C; Date: 29-0c	C; Accession:	K;Nelson, J.; submitted to	A; Description	A; Accession:	A;Status: pre	A; Molecule ty	A; Residues: 1	A;Cross-refer	A; Experimenta	C; Genetics:	A; Gene: CESP:	A; Map position	A; Introns: 31	C;Superfamily		Query Match	Matches	0v 169 VLI

169 VLLAVAAC 176 ||||||||| 24 VLLAVAAC 31 g RESULT 2
E70470
conserved hypothetical protein aq\_1986 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: B70470
C;Accession: E70470
R;Deckert; G:; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUD:9819666
A;Accession: E70470
A;Accession: E70470
A;Accession: E70470
A;Accession: E70470
A;Accession: E1241 <AQF>
A;Cross-references: GB:AE000766; NID:92984216; PIDN:AAC07762.1; PID:92984233; GB:AE00
A;Cross-references: GB:AE000766; NID:92984216; PIDN:AAC07762.1; PID:92984233; GB:AE00
C;Genetics:
A;Gene: aq\_1986
C;Superfamily: conserved hypothetical protein aq\_1986

Conservative

24

17 ALLCALSL

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Query Match Best Local Similarity Matches 8; Conserv

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A; Wolecule type: protein
A; Residues: 200-213, NY,215-270 <MAU>
A; Experimental source: familial amyloid polyneuropathy (Finnish-type) heart and kidne
A; Note: the substitution of Asn for 214-Asp causes disease
R; Haltia, M.; Prelli, F.; Ghiso, J.; Kiuru, S.; Somer, H.; Palo, J.; Frangione, B.
Biochem. Biophys. Res. Commun. 167, 927-932, 1990
A; Title: Amyloid protein in familial amyloidosis (Finnish type) is homologous to gels
A; Reference number: A34562; MUID:90211339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. Experimental source: kidney, Finnish hereditary amyloidosis patient C. Comment: Gelsolin is a calcium-regulated, actin-modulating protein that binds to the can promote the assembly of monomers into filaments (nucleation) as well as sever fil C. Comment: A single gene encodes two forms of gelsolin; one remains associated with t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Cell Biol. 102, 1439-1446, 1986
A;Title: Definition of an N-terminal actin-binding domain and a C-terminal Ca(2+) reg
A;Reference number: A60849; MUID:86168493
A;Accession: A60849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Maury, C.P.J.
J. Clin. Invest. 87, 1195-1199, 1999, 1991
A; Title: Gelsolin-related amyloidosis, Identification of the amyloid protein in Finni A; Reference number: A61263; MoID: 91185597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for cytos
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N;Alternate names: actin-depolymerizing factor; brevin
N;Contains: amyloid protein, 12K; gelsolin, cytosolic
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
C;Accession: A03011; A36797; S03073; A60849; A36029; A61263; A34562; A34137
R;Kwiatkowski, D.J.; Stossel, T.P.; Orkin, S.H.; Mole, J.E.; Colten, H.R.; Yin, H.L.
Nature 323, 455-458, 1986
A;Title: Plasma and cytoplasmic gelsolins are encoded by a single gene and contain a A;Reference number: A93383; MUID:87014807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence homology between the amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 28-52;178-194, XX', 197;279-290,'S',292-294,'XX',297-303;434-449,'XX',452-
R; Watatkowski, D.J.; Mehl, R.; Yin, H.L.
J. Cell Biol. 106, 375-384, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 'XX',150-153,'X',155,'X',157-159;486-492,'X',494-498,'X',500,'X';628-641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genomic organization and biosynthesis of secreted and cytoplasmic forms of A;Reference number: S03073; MUID:88115587
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A;Residues: 200-214 GHAL-
A;Experimental source: diseased kidney, familial amyloidosis (Finnish type)
R;Lind, S.E.; Janmey, P.A.
J. Blol. Chem. 259, 13262-13266, 1984
A;Title: Human plasma gelsolin binds to fibronectin.
A;Reference number: A92450; MUID:85030446
                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-782 <KMI>
A;Cross.references: EMBL:XO4412; NID:935447; PIDN:CAA28000.1; PID:9736249
A;Accession: A38797
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A;Realdues: 'X',52-55,'X',57-59,'X',61-62 <BRY>
R;Vandekerckhove, J.; Bauw, G.; Vancompernolle, K.; Honore, B.; Celis,
J. Cell Biol. 111, 95-102, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Comparative two-dimensional gel A; Reference number: A36029; MUID:90307803
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A; Residues: 235-237;240-252;258-269 <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Maury, C.P.J.; Alli, K.; Baumann, M.
FEBS Lett. 260, 85-87, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-116 <KW3>
A;Cross-references: EMBL:X07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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H70597
probable membrane protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-oct-1999
C;Accession: H70597
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-509 <col>
A;Accession: H70597
A;Coss-references: GB:Z94121; GB:AL123456; NID:93261736; PIDN:CAB08087.1; PID:e312290; C;Genetics: Rv3887c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V.; Rock, D.; Letchworth, G.J.; Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the bovine herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: bovine herpesvirus 1
Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Aug-1999
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C;Species: bovine herpesvirus 1
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Au
C;Accession: S61245
R;Vicek, C; Benes, V; Lu, Z.; Kutish, G.F.; Paces, V; Rock, D.; Le
submitted to the EMBL Data Library, January 1995
A;Description: Nucleotide sequence analysis of a 30-kb region of the
A;Reference number: S6123
A;Accession: S61245
A;Accession: S61245
A;Accession: S61245
A;Accession: S61245
A;Catus: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <-VLC>
A;Cross-references: EMBL:248053; NID:9971311; PIDN:CAA88123.1; PID:99
C;Superfamily: herpesvirus 51K protein
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5.2;
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                                                            3.4%; Score c,
100.0%; Pred. No. 5.2
**** 0; Mismatches
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Mismatches
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100.0%; Pred. No.
ive 0; Mismatch
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100.0%; Pred. No
:ive 0; Mismat
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Conservative

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Query Match
Best Local Similarity
The By Conserve

Query Match 3.4 Best Local Similarity 100. Matches 8; Conservative

RESULT

g δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- DEVELOPMENTAL STAGE: ABUNDANT IN THE BLASTULA UNTIL GASTRULATION, BARELY DEFECTABLE DURING GASTRULATION, AND INCREASE AGAIN DURING NEURILATION DEFECTED THROUGHOUT THE REMAINING DEVELOPMENT AND IN HATCHED LARVAE.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MECH. DGV. 40:63-72(1993).

-I- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUBS. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
-I- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDITRE-93183769; PubMed-8443107; MEDLIKE-93183769; PubMed-8443107; Busse U., Sequin C.; Sequin C.; Sequin C.; Sequin C.; Sequin C.; More two closely related members of the axolotl Wht family, Awnt-5A and Awnt-5B, and analysis of their expression
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR MATRIX.
-1- TISSUE SPECIFICITY: NEUROECTODERMAL AND NON-NEUROECTODERMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .) (POTENTIAL)
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                                                      Length 335;
                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WNT-5A PROTEIN.

N-LINKED (GLCNAC. .) (POT
W; 533FFB0414DAAA14 CRC64;
37717 MW; EA041C1C45A5777F CRC64;
                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
WNT-5A PROTEIN PRECURSOR.
                                                    Query Match 3.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 28; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00110; wnt; 1.
PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein; Signal.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                      359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.0%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                 Ambystoma mexicanum (Axolotl).
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                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
305
359 AA;
335 AA;
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                                                                                                                                                 1/1/1/1
216 GPGRLLL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8296;
                                                                                                                           35 GPGRLLL 41
                                                                                                                                                                                                                                                    WN5A_AMBME
Q06442:
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17 ALLCALS 23
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@license.)
                                                                                                                                                                                                                                                                 MEDILINE-97422605; PubMed-9268631; Schweltne-97422605; PubMed-9268631; Schwelter N., Valk P.J., Delwel R., Cox R., Francis F., Meier-Ewert S., Lehrach H., Barlow D.P., "Characterization of the C3 YAC contig from proximal mouse chromosome "Characterization of the C3 YAC contig from proximal mouse chromosome I7 and analysis of allelic expression of genes flanking the imprinted
                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-i- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR ANGIOTENSIN
                                                                                                                                         Expression of the mouse and rat mas proto-oncogene in the brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      # (POTENTIAL).

EXTRACELULAR (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

G (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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(GLCNAC. ..) (POTENTIAL).
                                                            STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-95094925; PubMed-8001672;
Metzger R., Bader M., Ludwig T., Berberich C., Bunnemann B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.0%; Score 7; DB 1; Length 324;
100.0%; Pred. No. 27;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCRDb; GCR_20660; --
GCRDb; GCR_2448; --
GCRDb; GCR_2448; --
MGD; MGT:96918; Masl.
Interpro; IPR000276; --
Interpro; IPR0001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
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24F4AB7299E6016F CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U96273; AAB69120.1; -. PIR; S29619; S29619.
                                                                                                                                                                 peripheral tissues.";
FEBS Lett. 357:27-32(1995).
                                                                                                                                                                                                                                                STRAIN-BCBA; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                           1gf2r gene.";
Genomics 43:285-297(1997).
-1- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                             SEQUENCE OF 1-25 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                          SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proto-oncogene
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                                                                                                                          Santen D.
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TRANSMEM
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  NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
0144767E25525509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-CELL SURFACE GLYCOPROTEIN CD1B-1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                 01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
T-CELL SURFACE GLYCOPROPEIN CD1B-1 PRECURSOR (CD1B-1 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam:
Pfam: PF00047; ig; 1.
Glvcoprotein; Signal; Immunoglobulin domain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 333;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                 333 AA
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100.0%; Pred. No. 28;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fetal thymocytes;
MEDLINE=96269982; Pubmed=8662069;
                                                                                                                                                                     01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last seq
01-0CT-2000 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z36890; CAA85359.1; -. HSSP; P11609; 1CD1.
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                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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302
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333
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279
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333 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
153 ALLCALS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111
216 GPGRLLL 222
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
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C1B2_SHEEP
ID C1B2_SHEEP
                                                                                  RESULT 12
C1B1_SHEEP
ID C1B1_SHEEP
AC Q28565;
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DOMAIN
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                                                                                                                                                                                                                   Rhind S.M., Hopkins J., Dutia B.M.; "Amino-terminal sequencing of sheep CD1 antigens and identification of
                                                                                                                                                    Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.; "The sheep CD1 gene family contains at least four CD1B homologues."; Immunogenetics 44:86-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                     -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
                                                                Vus aries (Sheep).
Eukaryota: Metazooa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMICARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
W; 861BAE9617DB9BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-CELL SURFACE GLYCOPROTEIN CD1B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
        01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CDIB-2 PRECURSOR (CDIB-2 ANTIGEN)
(SCDIB-42) (ANTIGEN IAH-CC14).
                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 236891; CAA8B360.1; -.
HSSP; P11609; 1CD1.
InterPro; IPR003006; -.
Pfam, PF00047; ig; 1.
Glycoprotein; Signal; Immunoglobulin domain; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 333; 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL). POTENTIAL.
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01-APR-1990 (Rel: 14, Created)
01-APR-1990 (Rel: 14, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.0%; Score 7; DB 1
100.0%; Pred. No. 28;
ttive 0; Mismatches
                                                                                                                                                                                               SEQUENCE OF 21-33.
MEDLINE=99115506; PubMed=9914336;
                                                                                                                                   TISSUE-Thymus;
MEDLINE-96269982; PubMed-8662069;
                                                                                                                                                                                                                                       a sheep CD1D gene.";
Immunogenetics 49:225-230(1999).
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Best Local Similarity
7; Conserve
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75
146
333 AA;
                                                                                                                        SEQUENCE FROM N.A.
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216 GPGRLLL 222
                                                                                                    NCBI_TaxID=9940;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-OCT-2000 (Rel. 40, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CDID PRECURSOR (CDID ANTIGEN) (R3G1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89098892; PubMed=2463622;
Balk S.P., Bleicher P.A., Terhorst C.;
Isolation and characterization of a cDNA and gene coding forfourth CDI molecule.;
Proc. Natl. Acad. Sci. U.S.A. 86:252-256(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-CELL SURFACE GLYCOPROTEIN CD1D. EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89196496; PubMed-2467814;
Calabi F., Jarvils J.M., Martin L., Milstein C.;
"Two classes of CD1 genes.";
Eur. J. Immunol. 19:285-292(1989).
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BY SIMICARITY.
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N-LINKED (GLCNAC.
T-SC.
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/FTId=VAR_010211
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EMBL, L38815, AAA59672.1; JOINED.
EMBL, L38817, AAA59672.1; JOINED.
EMBL, L38816, AAA59672.1; JOINED.
EMBL, L38818, AAA59672.1; JOINED.
EMBL, L38819, AAA59672.1; JOINED.
EMBL, X14974; CAA33099.1; -.
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MIM; 188410; -.
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PIR; A32217; A32217
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CARBOHYD
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61 2
156 1
286 AA;
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160
275
275 AA;
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                                                                                                                                        195 GPGRLLL 201
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PU91_SCICO
P22311;
                                                                                                                                                                                                                                                                                                                                                             STRAIN-6980
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   CARBOHYD
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PU92_SCICO
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                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN
T-CELL LEUKEMIAS, AND IN VARIOUS OTHER TISSUES.
-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
Pfam; PF00187; chitin_binding; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
HydroLase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-90035137; PubMed-2478462; Calabi F., Belt K.T., Yu C.Y., Bradbury A., Mandy W.J., Milstein C. "The rabbit CD1 and the evolutionary conservation of the CD1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                           Sylvilagus floridanus (Cottontail rabbit).
Wakaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               famlly.";
Immunogenetics 30:370-377(1989).
-1- FUNCTION: NOT KNOWN.
-1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991 (Rel. 20, Created)
1-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
T-CELL SURRANCE GIFCOPROTEIN CDID (LEUCOCOTTE DIFFERENTIATION-LIKE ANTIGEN TA) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                           POTENTIAL.
ENDOCHITIANSE B.
CHITIN-BINDING (BY SIMILARITY).
HINGE REGION (GLY-RICH).
CATALYTIC.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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SIMILARITY.
3D38B1BADF75DE8F CRC64;
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ilarity 100.0%; Pred. No. 24;
Conservative 0; Mismatches
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269
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53
8166 MW;
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InterPro: IPR003006; -
Pfam; PF00047; 1g; 1.
Glycoprotein; Immunoglobulin
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258
17
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                              269 AA;
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7 GLALLCA 13
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P23043;
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Sciaroldea;
Sciaridae; Bradysia.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
AA6A7B55F191BB1D CRC64;
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                                                                                                                                                                         Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 286;
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Signal; Coiled coil; Glycoprotein.
OR 21 (POTENTIAL).
                                                                                                                                                                         3.0%; Score 7; DB 1;
100.0%; Pred. No. 24;
tive 0; Mismatches
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PUFF II/9-1 PROTEIN PRECURSOR.
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100.0%; Pred. No. 25;
tive 0; Mismatches
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Best Local Similarity 100..
7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Gene 143:303-304(1994).
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                  J. Mol. Biol. 210:531-540(1989).
-!- MISCELLANDEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR DISULPIDE BRIDGES FORMED BY NUMBROUS CYSTEINE RESIDUES IN POSTITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;
Sciaridae; Bradysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .) (POTENTIAL). 720AC8CCC22A869C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta; wbwed-8206394; mbDirne-94266173; PubMed-8206394; Li H., Hodge D. R., Pei G. K., Seth A.; Isolation and sequence analysis of the human syntaxin-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                           MEDLINE-90133907; PubMed-2614832;
Dibartolomeis S.M., Gerbi S.A.;
"Molecular characterization of DNA puff II/9A genes in Sciara coprophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 286; . 25;
                                                                                                                                                                                                                                                                D OF THE HEPTAD REPEAT.
SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             OR 21 (POTENTIAL).
PUFF II/9-2 PROTEIN.
HELICAL (POTENTIAL).
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE HUMAN STANDARD; PRT; 297 AA. 012846; Q15525; Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 39, Last annotation update) 30-MAX-2000 (Rel. 39, Last annotation update) SYNTAXIN 4. STYAA OR STX4. Homo sapies (Human). Homo sapies (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebri Mammalia; Eutheria; Primates; Catarrhini; Homini
    our-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
00-Cor-1996 (Rel. 34, Last annotation update)
11/9-2 PROTEIN PRECURSOR.
 286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.0%; Score 7; DB 1
100.0%; Pred. No. 25;
tive 0; Mismatches
 PRT;
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                                                                             Sciara coprophila (Fungus gnat).
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235
156
N-32621 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
156
186 AA;
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                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=38358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 LTWYLLA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                     "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2."; Biochem. J. 317:945-954(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENTIALLY INVOLVED IN DOCKING OF SYNAPTIC VESICLES
AT PRESYNAPTIC ACTIVE ZONES.
-!- SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASI OR MAS-1 OR MAS.

Was musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                     Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J., Ward C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE-PETIPHERS; Nabokina S. Lazo P.A., Mollinedo F.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil; Transmembrane.
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A -> V (IN REF. 1).
5084FDIC49A86BAA CRC64;
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Pred. No.
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE-96332494; Pubmed-8760387;
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100.0%; Pre
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PROSTTE; PS00914; SYNTAXIN; 1.
Neurotransmitter transport; C
DOMAIN 43 163 C
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276
276
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297 AA;
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MIM; 186591; -.
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283 TVVLLAV 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. . .) (PROBABLE).
W, 854FE80D4A39DCF8 CRC64;
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P54525; P54526; 032017;
01-0CT-1996 (Rel. 34, Created)
30-MXZ-2000 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 22.2 KDA PROTEIN IN SPOOM-MMGA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
STRAIN=168 / JH642;
KObayashi Y., Yakeulino M., Masuda S., Takemaru K., Hosono Sato T., Takeuchi M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                             EMBL: X59889; CAA42542.1; -
EMBL, X59889; CAA42543.1; -
PIR; S29677; S29677; S29677; S29677; S29677; S29678; S29678. -
PIR; A01504; UTCAB.
PIR; TOT462; JT0462.
HSP: P01233; JHRP:
INTERPRO; IPR001359; -
INTERPRO; IPR001359; -
INTERPRO; IPR001455; -
INTERPRO; IPR001455; -
Pfam: PF00007; Cyg_knot; 1.
PRINTS; PR004438; GEVCQ_HORMONE_BETA_1; 1.
PROSITE; PS00689; GLYCQ_HORMONE_BETA_2; 1.
PHORMONE; BETA_2; 1.
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100.0%; Pred. No. 15;
tive 0; Mismatches
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134
1134
112
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Matches 7; Conserv
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19 VVLLAVA 25
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Chang Y.S., Huang C.-J., Huang F.-L., Lo T.-B.;
"Primary structures of carp gonadotropin subunits deduced from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinus carplo (Common carp).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Etafinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 28-53 AND 141-142.

MEDLINE-78124308; PubMed=607993;

Jolles J., Burzawa-Gerard E., Fontaine Y.-A., Jolles P.;

Jolles J., Burzawa-Gerard E., Fontaine Y.-A., Jolles P.;

"The evolution of gonadotropins: some molecular data concerning a non-mammalian pituitary gonadotropin, the hormone from a teleost fish (Cyprinus carpio L.).";

Biochinia 59:893-898(1977).

-I- FINCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENSIS.

-I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

-I- SIMILARITY: BELONGS TO THE GLXCOPROTEIN HORMONES BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-07-2000 (Rel. 40, Last annotation update)
GONADOTROPIN BETA-II CHAIN PRECURSOR (GTH-II-BETA) (LUTEINIZING HORMONE-LIKE GTH).
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                                                                                                                                                                                                                           POLYPHOSPHOINOSITIDE BINDING (BY SIMILARITY).
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Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_007719.
8CEBC52257A160F7 CRC64;
                                                                                                                                                                                                                                                                                   IN PLASMA FORM ONLY.
D -> N (IN FAF).
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D -> Y (IN FAF).
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. 5.6;
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[2]
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100.0%; Pred. No. 5.6
Live 0; Mismatches
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Best Local Similarity
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3326
3342
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                          REPEAT
REPEAT
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REPEAT
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                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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Glydm: PF00047; ig; 1.
Glydm: pr00047; imunoglobulin domain; Transmembrane; Multigene family.
NON_TER 1 1 1 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #EDINE-96269983; PubMed-8662069;
Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
"The sheep CDI gene family contains at least four CDIB homologues.";
Immunogenetics 44:86-96(1996).
-i. FUNCTION: NOT KNOWN.
-i. SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY). SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CDIB-3 (CDIB-3 ANTIGEN) (SCDIT10)
                                                                                                                                                                                                                                                                         3.0%; Score 7; DB 1; Length 206; 100.0%; Pred. No. 19; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       170 170 E -> D (IN REF. 1).
206 AA; 22235 MW; B0950FA7E4D12D1E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                        232 AA
                                                                                                                            EMBL; D84432; BAA12584.1; ALT_FRAME. EMBL; D84432; BAA12585.1; ALT_FRAME. EMBL; 293116; CAB14350.1; -201116; CAB14350.1; -101112; BG11717; yq1I. InterPro; IPR002508; -Pfam; PF01520; Amidase_3; 1. Hypothetical protein; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fetal thymocytes;
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Best Local Similarity
Matches 7; Conserv
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|9 ALCGLAL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                        C1B3_SHEEP
P80943;
                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
C1B3_SHEEP
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01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (SEED CHITINASE B) (FRAGMENT).
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panlcoideae;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huynh Q.K., Hironaka C.M., Levine E.B., Smith C.E., Borgmeyer J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shah D.M.;
"Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed.";
J. Biol. Chem. 267:6635-6640(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92156129; PubMed=1740436;
Werburg J.G., Smith C.E., Lisek C.A., Huynh Q.K.;
Identification of an essential tyrosine residue in the catalytic site of a chitinase isolated from Zea mays that is selectively modified during inactivation with
1-ethyl-3-(3-dimethylaminopropyl)-carbodilmide.";
J. Blol. Chem. 267:3886-3893(1992).
-i-FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL). C96DB93840B56158 CRC64;
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                                                                                                                                                                                             Length 232;
  CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                          3.0%; Score 7; DB 1;
100.0%; Pred. No. 21;
iive 0; Mismatches
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InterPro; IPR001002; -.
Pfam; PF00182; Glyco_hydro_19; 1.
232 CY
83 BY
178 BY
45 N-
26023 MW;
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HSSP; P02877; 1HEV.
MaizeDB; 25130; -.
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Matches 7; Conserv
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P29023;
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DISULFID
CARBOHYD
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                                         homo sapien
saccharomyc
rattus norv
homo sapien
caenorhabdi
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pseudonaja
orf virus (
               homo sapien
mycoplasma
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10323;
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                                                                                                                                                                                                                                                                                 VGLM_HSVBC STANDARD; PRT; 411 AA. P52370; 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) GLYCOPROTEIN M.
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                                                                                                                                                                                                             ALIGNMENTS
                                         COMP_HUMAN
YJG2_YEAST
SYJ2_RAT
SYJ2_HUMAN
DP27_CAEEL
FINC_MOUSE
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NXLB_PSETE
VF09_ORFN2
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InterPro; IPRO00785; -.
Pfan: PF01538; Herpes_glycop; 1.
PRINTS; PR00333; HSYINTEGRLMP.
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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GELS_HUMAN
GTH2_CYPCA
YQII_BACSU
C1B3_SHEEP
CHIB_MAIZE
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C1B1_SHEEP
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NUSM_BRAFL
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NUSM_GORGO
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NUSM_ALLMA
CCMF_RHOCA
NUSM_CHOCR
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PU91_SCICO
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NUSM_HYLLA
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                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match 1
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93 VVLLAVAA 100

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protein in familial amyloidosis (Finnish type) is homologous
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Maury C.P.J., Alli K., Baumann M.;
"Finnish hereditary amyloidosis. Amino acid sequence homology between the amyloid fibril protein and human plasma gelsoline.";
FEBS Lett. 260:85-87(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93361115; PubMed-8395021;
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"Structure of gelsolin segment 1-actin complex and the mechanism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional consequences of disulfide bond formation in gelsolin.";
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-87014807; PubMed-3020431;
Kwiatkowski D.J., Stossel T.P., Orkin S.H., Mole J.E., Colten H.R.,
                                                                                                                                                                                                                                                                                                                   "Plasma and cytoplasmic gelsolins are encoded by a single gene and contain a duplicated actin-binding domain.";
Nature 323:455-458(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96167246; Pubmed=8599675; Xian W., Vegners R., Janmey P.A., Braunlin W.H.; Spectroscopic studies of a phosphoinositide-binding peptide from glasolin: behavior in solutions of mixed solvent and anionic micelles.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wen D., Corina K., Chow E.P., Miller S., Janmey P.A., Pepinsky "The plasma and cytoplasmic forms of human gelsolin differ in disulfide structure.";
                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-GT-2000 (Rel. 06, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90211339; Pubmed-2157434;
Haltia M., Prelli F., Ghiso J., Kiuru S., Sommer H., Palo J.,
Frangione B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to gelsolin, an actin-binding protein.";
Biochem. Biophys. Res. Commun. 167:927-932(1990).
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                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN BINDING.
MEDLINE-88030446, PubMed-6092370,
Lind S.E., Janmey P.A.,
"Human plasma gelsolin binds to fibronectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY OF FAF AMYLOID PROTEIN WITH GELSOLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY OF FAF AMYLOID PROTEIN WITH GELSOLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 259:13262-13266(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96312883; PubMed-8703941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97157527; PubMed-9003812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 35:9700-9709(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 177-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 401:89-94(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       filament severing.";
Nature 364:685-692(1993).
                  STANDARD;
                                                                                                                                                           Homo sapiens (Human).
                                                                                                                          (BREVIN) (AGEL).
                                                                                                                                                                                                                NCBI_TaxID=9606;
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                GELS_HUMAN
P06396;
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                                                                                                                                                                                                                                                                                                     Yin H.L.;
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GELS_HUMAN
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R.B.;

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                                                                                                         MEDLINE-93265143; PubMed-1338910;

MEDLINE-93265143; PubMed-1338910;

A ela Chapelle A. Tolvanen R., Boysen G., Santavy J.,

Bleeker-Wagemakers L., Maury C.P.J., Kere J.;

Celsolin-derived familial amyloidosis caused by asparagine or

Tyrosine substitution for aspartic acid at residue 187.";

NAL. Genet. 2:157-160(1992).

PROTEIN THAT BINDS TO THE PLUS (OR BARBED) ENDS OF ACTIN MONOMERS

PROTEIN THAT BINDS TO THE PLUS (OR BARBED) ENDS OR ACTIN MONOMERS

CAPPING). IT CAN PROMOTE THE ASSEMBLY OF MONOMERS INTO FILAMENTS

(NUCLEATION) AS WELL AS SEVER FILAMENTS ALREADY FORMED.

CONDINGS. PRODUCTS: PLASMA GELSOLIN AND CYTOPLASMIC.

CONDINGS. PRODUCTS: PLASMA GELSOLIN AND CYTOPLASMIC.

ALTERNATIVE PRODUCTS: PLASMA GELSOLIN AND CYTOPLASMIC.

TISSUE SPECIFICITY: MHACOCYTIC CELLS, FIBROBLASTS,

CONTINUES SPECIFICITY: CONTINUES CONTINUES. FIBROBLASTS,
                                                                                                                                                                                                                                                                                                                                                NONMUSCLE CELLS, SMOOTH AND SKELETAL MUSCLE CELLS.
-!- DISEARS: DEPECTS IN GSN ARE THE CAUGE OF FAMILIAL AMYLOIDOSIS,
FINNISH TYPE (FAR), AN INHERITED FORM OF SYSTEMIC AMYLOIDOSIS,
CLINICALLY CHARACTERIZED BY CRANIAL NEUROPATHY AND LATTICE CORNEAL
                                        MEDLINE-91097517; PubMed-2176481;
Ghiso J., Haltia M., Prelli F., Novello J., Frangione B.;
Gelsolin variant (Asn-187) in familial amyloidosis, Finnish type.";
Biochem. J. 272:827-830(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: IN ADDITION TO ITS ROLE IN ACTIN REGULATION, THIS PROTEIN IS KNOWN TO BIND WITH HIGH AFFINITY TO FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-BINDING, CA-SENSITIVE (POTENTIAL)
ACTIN-ACTIN INTERFILAMENT CONTACT POINT
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FOR CYTOPLASMIC ISOFORM.
ACTIN-SEVERING (POTENTIAL).
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Pfam; PF00626; Gelsolin; 6.
Brings; PR00597; GELSOLIN; 7.
Actin-binding; Repeat; Calcium; Alternative initiation; S.
Capping protein; Amyloid; Disease mutation; 3D-structure.
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Biophys. J. 69:2695-2702(1995).
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; A34137; A34137.
; A34562; A34562.
; ISOL; 08-MAR-96.
                            VARIANT FAF ASN-214
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MIM; 105120; -
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g	252	252 RHYYYKGVCVPACPPGTYRFEGWRCVDRDFCANIPNAESSDSDGFVIHDGFC- 303	ACPP	GTYRFE	GWRCVDRD	FCANIDNA	PSSDSDGFV	THDGEC-	303

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Search completed: September 4, 2001, 16:12:11 Job time: 1108 sec

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F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                            Best Local Similarity 26.39
Matches 41; Conservative
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-474 <GOO>
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A; Residues: 1-22 <KIS>
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tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequenc_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885
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R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A)Description: Characterization of the promoter region of the murine p75-TNF receptor A;Reference number: S54816
A;Accession: S54816
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A; Residues: 1-474 <LEW>
A; Residues: 1-474 <LEW>
A; Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828
B; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.;
Mol. Cell. Biol. 11, 3020-3026, 1991
A; Title: Molecular cloning and expression of the type 1 and type 2 murine receptors
A; Reference number: A40254; MUID: 91246168
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C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
C;Keywords: cytokine receptor; transmembrane protein
E;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;70-17/Domain: NGF receptor repeat homology <NG2>
F;79-120/Domain: NGF receptor repeat homology <NG3>
F;166-203/Domain: NGF receptor repeat homology <NG4>
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                                                                                   Gaps
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   Length 461;
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; Score 119; DB 1;
; Pred. No. 0.022;
14; Mismatches 63;
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C; Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
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                                                                                                                                         Query Match 12.1%;
Best Local Similarity 25.6%;
Matches 42; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pb
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A; Residues: 1-277 cSTA.
A; Residues: 1-277 cSTA.
A; Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851
A; Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851
B; Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A; Reference number: A60771; MUID:89093941
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 21-50 cBRA>
A; Experimental source: Burkitt lymphoma cell line Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:215268; OMIM:109535
A; Map position: 20q12-20q13.2
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Reywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F; 21-193/Domain: extracellular #status predicted <EXT>
                                                          B-cell activation protein CD40 precursor - human N.Alternate names: B-cell surface antigen Bp50 (5.Species: Homo Sapiens (man) (5.Species: Homo Sapiens (man) (5.Species: Homo Sapiens (man) (5.Species: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000 (5.Accession: 504460; A60771 (5.Lark, E.A.; Seed, B. EMBO J. 8, 1403-1410, 1982 (1.Species) (1.Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: 154182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen A;Reference number: 154182; MUID:93252381
A;Accession: 154182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
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F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 NKTHNAVCVP 155
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Best Local Similarity
Matches 36; Conserv
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A;Gene: GDB:LTBR
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insulin-like growth factor I receptor precursor - rat
N;Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I be
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Mar-1990 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: JC2461; A33897; PC1131
R;Pedrini, M.T.; Giorgino, F.; Smith, R.J.
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994
A;Title: cDNA cloning of the rat IGF I receptor: Structural analysis of rat and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues; 1.1371 (RBD)
A; Residues; 1.1371 (RBD)
R: Werner, H: Woloschak, M: Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D.
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989
A; Title: Developmental requlation of the rat insulin-like growth factor I receptor ge
A; Reference number: A33837; MUID:90017496
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Jochem. Biophys. Res. Commun. 187, 934-939, 1992
Jille: A new member of the insulin receptor family, insulin receptor-related recept
*Reference number: PC1130; MUID:92412145
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A;Residues: 913-984, PY, 987-1017 <KUR>
A;Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359
C;Superfamily: insulin receptor; protein kinase homology
C;Keywords: ATP: growth factor receptor; kinase-related transforming protein; transme
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F;31-741/Product: insulin-like growth factor I alpha chain *status predicted <IGB>
F;742-1371/Product: insulin-like growth factor I beta chain *status predicted <IGB>
F;937-959/Domain: transmembrane *status predicted <TMM>
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                                                                               10;
                                                                                                                                                                                                                                   62 CPP----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                   CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                           117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
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                                                                               Gaps
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                                                                                                                                                       ---CRDYPGEE----C
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   Length 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 ONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC---KNPLEP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP
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Score 117; DB 2; 1
Pred. No. 0.031;
; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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A; Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A; Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A; Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A; Note: sequence extracted from ncbir annotated in GenBank entry MUSCD40A, release 113.0
R; Ginaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J; Ilmmunol. 149, 3921-3926, 1992
A; Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A; Reference number: A46515; MUID:93094586
A; Accession: A46515
A; Accession: A46515
A; Accession: A46515
A; Residues: Dreliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-287, 'LV, <GRI>A; Residues: 1-287, 'LV, <GRI>A; Residues: Brain, NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126
A; Coss-references: GB:MB312, NID:91553058; PIDN:AA66515.
C; Comment: For an alternative splice form, see PIR:A46476.
C; Comment: For an alternative splice form, see PIR:A46476.
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laminin beta-2 chain precursor - rat
Nalternate names: laminin chain B3; S-laminin
Nalternate names: laminin chain B3; S-laminin
Sapeciaes: Rattus norvegicus (Norway rat)
C; Speciaes: Rattus norvegicus (Norway rat)
C; Accession: S03539
E; Accession: S03539
E; Anuncer, D.D.; Shah, V; Merile, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A; Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne
A; Reference number: S03539; MUID:89159410
A; Residues: 1-1801
A; Mesidues: 1-1801
A; Mesidues: 1-1801
C; Complex: EMBL: X16563; NID:957250; PIDN: CAA34561.1; PID:957251
C; Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: interact with cells and with other basement membrane proteins to promo C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C; Keywords: basement membrane; calcium binding; cell binding; colled coll; extracellu F;1-35/Domain: signal sequence #status predicted <SIG>F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 CHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 1.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-11ke homology <LE02>
EGF-11ke homology <LE03>
EGF-11ke homology <LE04>
EGF-11ke homology &LE04>
EGF-11ke homology #status atypical <LE05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LCALWGCLLTAVHLGQCVT----CSDKQYL----HDGOCCDLCOPGSRLTSHCTALEKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 135.5; DB 2; 26.1%; Pred. No. 0.00089; 11ve 10; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LCGL--ALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like homology
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F;350-410/Domain: laminin-type
F;413-470/Domain: laminin-type
F;473-522/Domain: laminin-type
F;525-555/Domain: laminin-type
F;556-784/Domain: IV <DOM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 NKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Species: Phytolacca americana (Virginian pokeweed)
C. Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
C. Accession: JC5599
E. Yourino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Blotechnol. Blochem. 61, 690-698, 1997
A. Fittle: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phyto A. Reference number: JC5559; MUID:97290889
A. Reference number: JC5559; MUID:97290889
A. Reference number: JC5559; MUID:97290889
A. Residues: 1-295 < VAM>A. Residues: 1-295 < VAMA < VAM
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B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
J: Immunol: 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine A;Reference number: A46476; MUID:92105763
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                       8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 CGVDFGNRTCPNDLCCSEWGWCGITEGYCGEGCOSOC---NHORCGKDFAGRTCLNDLCC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 SEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ-C---IDCASGTFSGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
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                                                                                                                                                                                                                                                                                                                                                                                                             26 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD---
                                                                                                                                                                                                                                                    Length 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163
C;Keywords: growth factor receptor; transmembrane protein F:1-15/Domain: signal sequence #status predicted <SIG> F:20-271/Product: OX40 antigen #status predicted <MAT> F:211-235/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                15.6%; Score 151; DB 2; 28.5%; Pred. No. 5.1e-05; tive 12; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 139; DB 2;
Pred. No. 0.00046;
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                                                                                                                                                                                                                                                                                                                                   47; Conservative
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                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 47; Conserve
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A;Molecule type: mRNA
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NDAHC 243
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C; Accession: S53869
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           SP 192
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F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
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C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
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R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: 148854; MUID:95178848
A;Accession: 148854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
148854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 : | | | | | 944 TSCHRDGYSQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDPGAC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 HTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SORHFA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 GVQSQGKFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 HTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQGKFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840 GALSALCEGTSGQCLCRTGAFGLRCDHCQRGQWGFPNCRPCVCNGR------ADECDA 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GAFRALC-GLALLCALSLG-----QRPTGG-PGCGP----GRLLLGTGTDARCCRV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004 DPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTCNLLGTDP 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 -----SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134.5; DB 1; Length 1801;
Pred. No. 0.0034;
6; Mismatches 60; Indels 105;
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E;786-831/Domain: laminin-type EGF-like homology <LED6>
F;788-1196/Domain: III <LDOM3>
F;884-97/Domain: laminin-type EGF-like homology <LED7>
F;880-927/Domain: laminin-type EGF-like homology <LED8>
F;980-986/Domain: laminin-type EGF-like homology <LED9>
F;981-986/Domain: laminin-type EGF-like homology <LE10>
F;104-1095/Domain: laminin-type EGF-like homology <LE11>
F;104-1109/Domain: laminin-type EGF-like homology <LE11>
F;1146-1190/Domain: laminin-type EGF-like homology <LE12>
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                      F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
F;1446-1801/Region: heptad repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.9
Best Local Similarity 26.9
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                            F;1446-1801/Domain: I <DOM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-459 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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R; Livanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tr Matrix Biol. 14, 489-497, 1994
A; Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal the A; Reference number: S53869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 #text_change 08-Dec-2000
C; Accession: A35356; A36475; A48416; A36007; A33666; B35010; I38094
R; Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
A; Title: A receptor for tumor necrosis factor defines an unusual family of cellular a A; Reference number: A3536; MUID:90260639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 3p21.3-3p21.2
C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C; Seywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33.1798/Product: laminin beta-2 chain #status predicted <MAT>
F;283-344/Domain: laminin-type EGF-like homology <LE01>
F;347-407/Domain: laminin-type EGF-like homology <LE02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                  C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885 ECNTHTGACLGCRDHTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPEGPGSQRH 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     837 GALSSLCEKTSGQCLCRTGAFGLRCDRCQRGQWGFPSCRP------CVCNGHAD 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 -CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQ-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor receptor 2 precursor [validated] - human N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atypical <LE05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 -------SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPPAE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GAFRALC----GLALLCALSLGQR-----PTGGPGCGPGRLLLGTGTDARC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F)410-467/Domain: laminin-type EGF-like homology <LEG03>
F)470-519/Domain: laminin-type EGF-like homology <LEG04>
F)522-552/Domain: laminin-type EGF-like homology <LEG04>
F)783-828/Domain: laminin-type EGF-like homology <LEG05>
F)813-84/Domain: laminin-type EGF-like homology <LEG07>
F)87-924/Domain: laminin-type EGF-like homology <LEG08>
F)927-963/Domain: laminin-type EGF-like homology <LEG08>
laminin beta-2 chain precursor (version 2) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:LAMB2
A;Cross-references: GDB:132363; OMIM:150325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.9%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1798 <IIV>
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version	- 2000
GenCore	(c) 1993
	Copyright

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ow process	Run on:	Title:

tes/sec

969 1 MAQHGAMGAFRALCGLALLC......FPGNKTHNAVCVPGSPPAEP 162 Perfect score: Sequence:

BLOSÚM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

insulin-like growt	notch 3 protein -	alpha-2-macroglobu	MEGF8 protein - hu	notch protein homo	agglutinin isolect	insulin receptor-r	apolipoprotein E r	gene shuttle craft	ultra high-sulfur	lectin precursor -	agglutinin isolect	latent transformin	alpha-2-macroglobu	cartilage oligomer	crumbs protein - f
IGHUR1	S45306	A53102	T00209	S18188	A28401	B47417	JE0237	T13938	S18946	LNRZ	AEWT2	A55494	S02392	A44315	A35672
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1367	2318	4543	1737	2531	186	540	966	1106	169	227	213	1820	4544	755	2139
10.5	10.5	10.4	10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.2
101.5	101.5	101	100.5	100.5	100	100	100	100	99.5	99.5	66	66	66	98.5	98.5
30	31	32	.33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
gene 0x40 protein - mouse
N;Alternate names: Ox40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J
A;Title: Cloning of mouse Ox40 a T cell activation marker that may mediate T-B cell
A;Reference number: I48700; MUID:94044750
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
```

A Residues: 1-272 <RES>
A; Residues: 1-272 <RES>
A; Cross-references: RMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
A; Cross-references: RMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R; Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A; Reference number: 148334; MUID:95255413

A,Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: 1-14,'G',16-272 <RE2>
A;Residues: 1-14,'G',16-272 <RE2>
C;Genetics: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:

A;Gene: 0x40 A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1 C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 16.7%; Score 162; DB 2; Length 272; Best Local Similarity 28.3%; Pred. No. 7.2e-06; Matches 45; Conservative 11; Mismatches 51; Indels 9

7;

86 ------CTTCRHHP-----CPPGQGVQSQGKFSFGFQCID 114 39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85 14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC-----HPCET 65 qq õ

66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125

qq õ QQ RESULT 2
137552
0x40 homolog - human
C;Species: Homo sapiens (man)

N

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A; Molecule type: mRNA
A; Residues: 1-256 < KRO>
A; Cross-references: GB: J04492; NID: g201121; PIDN: AAA40167.1; PID: g201122
A; Cross-references: GB: J04492; NID: g201121; PIDN: AAA40167.1; PID: g201122
J. Immunol. 152, 2256-2262, 1994
A; Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B
A; Reference number: 148879; MUID: 94179805
A; Accession: 148879: MUID: 94179805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: 30.5ep-1993 #sequence_revision 30.5ep-1993 #text_change 05-Nov-1999
C;Accession: $12783; $08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Fitle: Characterization of the MRC 0X40 antigen of activated CD4 positive
A;Reference number: $12783; MUID:90214614
                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: U02567; NID: 91117783; PIDN: AAA93113.1; PID: 9409178
                                                CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1 superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: CDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.8%; Score 153; DB 2; ilarity 31.5%; Pred. No. 3.4e-05; Conservative 17; Mismatches 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Supertamily: Uper which protein C;Reywords: transmembrane protein C;Reywords: transmembrane protein #status predicted <: F;1-23/Domain: signal sequence #status predicted : F;24-256/Product: 4-1BB protein #status predicted :
                                                                                                                                                                                                                150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                       I-cell antigen 4-1BB precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: B32393; 148879
                                                                                                                                                 145 GNKTHNAVCVPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
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A; Residues: 1-271 <MAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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A.Molecule type: mRNA
A.Residues: 1-106, "K',108-255 <SCH>
A.Stesidues: 1-106, "K',108-255 <SCH>
C.Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neord
C.Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neord
C.Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix
C.Superfamily: CD27 antiquen, NGF receptor repeat homology
C.Keywords: glycoprotein; phosphorotein; receptor; transmembrane protein
F:117/Domain: signal sequence #status predicted <SIG>
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <NAT>
F:187-213/Domain: transmembrane #status predicted <TWN>
F:187-213/Domain: carbohydrate (Asn) (covalent) #status predicted
F:234,235/Binding site: phosphate (Thr) (covalent) (by protein kinase II) #status predicted
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C; Accession: 137552
R; Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Bur. J. Immunol. 24, 677-683, 1994
A; Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c A; Reference number: 137552; MUID: 94170844
A; Reference number: 137552; MUID: 94170844
A; Reference special problem ox and chromosomal assignment c A; Restaus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-277 cRES
A; Residues: 1-277 cRES
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphocyte activation-induced receptor ILA precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacie: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C;Accession: I38426; JT0752
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, Eur. J. Immunol. 24, 2219-2227, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Molecular and biological characterization of human 4-1BB and its ligand. A;Reference number: I38426, MUID:94374434
A;Accession: I38426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-255 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 TRCCRDYPG--BECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GAMGAFRALCGLALLCALSLG------QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GARRIGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCS----EWDCMCVQPEFHCGDP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPPNSFSSAGG--QRICDI-----CRQCKGVFRIRKECSSTSNAECDC---TPGFHCLGA 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 160.5; DB 2; Length 255; 30.9%; Pred. No. 9e-06; Live 12; Mismatches 52; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%; Score 162; DB 2;
ilarity 29.7%; Pred. No. 7.2e-06;
Conservative 11; Mismatches 92;
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Best Local Similarity
Matches 51; Conserv
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Best Local Similarity
Matches 47; Conserv
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7:

Gaps

18;

Length 256;

positive T lymphoc

Length 1798;

DB 1;

Score 111.5;

11.5%;

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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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-> A (IN REF. 2).
9555CF5B24850CB7 CRC64;
LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 8.

LAMININ EGF-LIKE 9.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 13.

DOMAIN II.

DOMAIN II.

COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

BY SIMILARITY.

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13;
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                                                                                                                                                                                Gaps
                                                                  50 -CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGD--PCCTTCRHHPCPPGQGVQ--- 101
                                                  GAFRALC----GLALLCALSLGQR-----PTGGPGCGPGRLLLGTGTDARC----- 49
                                                                                                                                                                                                                                         121 ------SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPPAE 161
Pred. No. 0.017;
......trhes 65; Indels 107;
                                                                                                                                                                  ----SQGKFS------FGFQCIDCASGTF---------
                       10; Mismatches
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1000 CDPHTGOCLRCLHHTEGPHCAHCKP
        23.2%;
          Best Local Similarity 23.2
Matches 55; Conservative
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Search completed: September 4, 2001, 16:15:21 Job time: 1133 sec

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kidney.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                   -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CPP----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 TSKRKTOCRC-OPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CRDYPGEE---C 66
                                                                                                          -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
     Ware C.F., Hession C.,
Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C., Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; "A lymphotoxin-beta-specific receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 117; DB 1; Length 435; 25.6%; Pred. No. 0.002; Live 12; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
LYMPHOTOXIN-BETA RECEPTÓR
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
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(Rel. 35, Last sequence update)
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Pfam: PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
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Matches 42; Conservative
                                                      Science 264:707-710(1994)
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185
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435 AA;
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01-NOV-1997
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P24062;
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-1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGE II WITH A LOWER AFFINITY. IT HAS A
TYROSINE-PROTEIN KINASE ACTIVITY.

-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.

-1- SUBGNIT: TETRAMER OF 2 AAPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
BINDING DOMAIN, HHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                    Du J., Delafontaine P.; "Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA."; Circ. Res. 76:963-972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leroith D.; "Developmental regulation of the rat insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
)1-OCT-2000 (Rel. 40, Last annotation update)
INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
"A new member of the insulin receptor family, insulin
receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASES.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90017496; Pubmed=2477843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 913-1017 FROM N.A. MEDLINE-92412145; PubMed-1530648;
                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-95277910; PubMed-7758167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01030; Recep_L_domain;
Pfam; PF00041; fn3; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L29232; AAA41392.1; -. EMBL; M27293; AAA41384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-364 FROM N.A. STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000494; ...
Interpro; IPR000719; ...
Interpro; IPR001777; ...
Interpro; IPR002011; ...
Interpro; IPR002011; ...
Interpro; IPR002174; ...
Pfam; PF00757; Furin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A33837; A33837.
HSSP; P06213; 11RK.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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DOMAIN
 20;
                                                                                                                                                                                                                                                                                                            90 RHH------PCPPGQGVQSQGKFSF-GFQCID---CAS-----GTFSGG---HEGHCK 129
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                   8 GAFRA-----LCGLA------LLCALS-----LGQRPTGGPGCG---PGRL------L 40
               INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                             INSULIN-LIKE GROWTH FACTOR I RECEPTOR
                                                                                                                                                                                                                                                                                                                                 41 LGTGTDARCCRVHTTRC---CRDYPGEECCSEWDCMCVQPEFHCGDPC-----CTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                            (POTENTIAL)
                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                      ; Score 115.5; DB 1; Length 1370;
; Pred. No. 0.0064;
22; Mismatches 52; Indels 79;
Phosphorylation; Repeat; Signal. POTENTIAL.
                                                                                                                                                                                                                                                  A5946897A41CB145 CRC64;
                                           EXTRACELLULAR (POTENTIAL)
                                                          CYTOPLASMIC (POTENTIAL)..
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                      BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
                                                                                PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).
                                                                                                                      N-LINKED (GLCNAC
                                                                                                                                     (GLCNAC
                                                                                                                                            (GLCNAC
                                                                                                                                                   (GLCNAC
                                                                                                                                                           (GLCNAC
                                                                                                                                                                         (GICCNAC
                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                           (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1798 AA.
                                      BETA-CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                          130 PWIDCTQFGFLTVFPGNKTHNAVCVPGSPP 159
                                                                                                                                                                                                                                                                                                                                                                                                   304 -MQECPS-GFIR----NSTQSMYCIPCEGP 327
                                                    POTENTIAL.
                                                                                                                                                                        N-LINKED
N-LINKED
                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                   N-LINKED
N-LINKED
N-LINKED
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N-LINKED
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N-LINKED
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                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95213013; PubMed-7698745;
                                                                                                                                                                                                                                                                                                                                                                                                                                             IMB2_HUMAN STANDARD; F P55268; Q16321; O1-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequol-0CT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                       11.9%;
27.1%;
                                                                                                                                                                                                                                                  155395
Glycoprotein; ATP-binding; SIGNAL 1 30
                                                                                                                                                                                                                                                                                     57; Conservative
                                                                                       1014
1034
1034
1136
1166
102
135
135
                              1370
                                                                                                                                                                                                                                         985 98
1370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                       ACT_SITE
MOD_RES
                                                    RANSMEM
                                                                                                                                                                  CARBOHYD
                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                              CARBOHYD
                                                                 DOMAIN
DOMAIN
DOMAIN
NP_BIND
                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                          CONFLICT
                                            DOMAIN
                                                            DOMAIN
                 CHAIN
                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
LMB2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMB2
                                                                                                                                                                                                                                                                                      Matches
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RN SEQUENCE FROM N.A.

REQUENCE FROM N.A.

REAL STATE OF THE PARTY OF THE LAMBE Gene.";

REAL ILSSUES and chromosomal assignment of the LAMBE gene.";

REAL ILSSUES AND CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ

RECEIN INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING

TELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING

WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROPIEN, CONSISTING OF THREE

- DIFFERENT POLYPEPTIDE CHAINS (ALCHA, BETA, GAMMA), WHICH ARE BOUND

COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT BACH END.

THE BETA -2 CHAIN IS A SUBUNIT OF LAMININ), LAMININ-4

(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

- TISSUE SPECIFICITY: FOUND IN THE SYNAPTIC

COMPONENT OF THE NUMBER OF LAMININ IN THE SYNAPTIC

COMPONENT OF THE NUMBER OF LAMININ IN THE SYNAPTIC

CONTROLLED OF THE NUMBER OF LAMININ IN THE SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: THE ALPHA HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
-!- DOMAIN: DOMAINS 'VI AND IV ARE GLOBULAR.
-!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 X LAMININ EGF-LIKE REPEATS (DOMAIN
Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattel M.-G., Champliaud M.F., Burgeson R.E., Albrechtsen R.; Human beta 2 chain of laminin (formerly S chain): cDNA cloning, chromosomal localization, and expression in carcinomas."; Genomics 24:243-252(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LÁMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    III).
LAMININ EGF-LIKE 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 268155; CAA92279.1; -.
EMBL, 268156; CAA92279.1; JOINED.
EMBL; X79683; CAA56130.1; -.
EMBL; S77512; AAB34682.2; -.
HSSP; P02468; IKLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001886; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
33
281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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TISSUE-Liver;
                                                                                                                                                                                specific."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
DISULFID
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DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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REPEAT
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REPEAT
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      ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGPG---RLLLGTGTDARC------71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKED (GLCNAC. . .) (POTENTIAL)
LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%; Score 121; DB 1; Length 461; 26.3%; Pred. No. 0.00096; Live 14; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNR2_MOUSE STANDARD; PRT; 474 AA.
925119; P97893;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMON NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2)
TUMON TREPS OR TNRR-2.
                                                                                                                                                                                                                                                                       Receptor, Transmembrane; Glycoprotein; Repeat; Signal;
Phosphorylation; Pharmaceutical; 3D-structure.
                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P (IN REF. 4).
M (IN REF. 1 AND 3).
T (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603B580ECD67636F CRC64;
                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
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N-LINKED (GLCNIN).
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 4.
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EMBL, U52160, AAC50622.1, JG
EMBL, U52161, AAC50622.1; JG
EMBL, U52162, AAC50622.1; JG
EMBL, U52163, AAC50622.1; JG
EMBL, U52164; AAC50622.1; JG
EMBL, M5594, AAA36755.1; -
PIR, A36007; A36007.
PIR, A36007; A36007.
PIR, A36475; A36475.
PIR, B35010, B35010.
PIR, B35010, B35010.
PIR, B35010, B35010.
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Best Local Similarity 26.3
Matches 41; Conservative
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461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
GOODWIN R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.,
"Molecular cloning and expression of the type 1 and type 2 murine
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                         SEQUENCE FROM N.A.
MEDLINE=91187885; PubMed=1849278;
MEDLINE=91187885; PubMed=18.A., Lee A. Bennett G.L., Rice G.C.,
Lewis M., Tartugila L.A., Goeddel D.V.;
Wong G.H., Chen E.Y., Goeddel D.V.;
"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NOD;
Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P19438; B38634.
HSSP; P19438; BNCF.
MGI: 1314883; Tnfrsflb.
P1042Fro; PF00020; TNFR.c6; 4.
PROSITE; PS00652; TNFR.NGFR_1; 2.
PROSITE; PS00652; TNFR.NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
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TNFR-CYS 3.
TNFR-CYS 4.
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SEQUENCE OF 1-26 FROM N.A.
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                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 22, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD401. RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
(TUMOR NECROSIS FACTOR RECEPTOR 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98266353; Pubmed-9605317; Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.; "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40."; Protein Sći. 7:1124-1135(1998).
                                                                                                                                                        46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQG 104
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELING OF 24-144.
MEDLINE=97189482; PubMed=9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";
Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
-1- SIMILARITY: CONTAINS A LA-NGFKTNFR-TYPE CYSTEINE-RICH REGION.
-1- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

462EAE398C4D6563 CRC64;
                                                                                                                                                                                        105 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth
                                                                                                                 18;
                                                                                       Score 119; DB 1; Length 474; Pred. No. 0.0015; 8; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89356608; PubMed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
A B-lymphocyte activation molecule related to the nerve of factor receptor and induced by cytokines in carcinomas.";
EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
                                                                                                                                                                                                                                                                           277 AA.
                                                      MM:
                                                                                        12.3%;
31.0%;
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 163
181
69
195
50319 1
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                              STANDARD;
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                                                474 AA;
                                                                                                    Local Similarity
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P25942;
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CD40_HUMAN
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62 CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
12MPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
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Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. .) (POTENTIAL)
BC8776EC2C4A5680 CRC64;
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                                                                                    Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93252381; PubMed-8486360;
Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen
"Construction and evaluation of a hncDNA library of human 12p
transcribed sequences derived from a somatic cell hybrid.";
Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                    CD40L RECEPTOR. EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
            InterPro; IPR001368; -.
Ppfam; PF00020; TNRR_G5; 4.
PROSITE; PS00055; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
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Mammalla; Eutheria;
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Matches 36; Conserv
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109535;
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01-AUG-1991 (Rel. 19, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
1-GT-2000 (Rel. 40, Last annotatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 CGKGEFLSTWNREKYC---HEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQ-HCTSHTCE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 TCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| | | | | | | | : | : | SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKGLVEQHV 177
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Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy F
Dower S.K., Cosman D., Goodwin R.G.;
A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins.";
Science 248:1019-1023(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; A second tumor necrosis factor receptor gene product can shed naturally occurring tumor necrosis factor inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
Pfam; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 122.5; DB 1; Length 269; 28.7%; Pred. No. 0.00048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70; Indels
                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29983 MW; 746903F30F95F387 CRC64;
                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 AA.
                                                                                                                                        CD40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                             4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                 TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Conservative
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P20333;
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AYERST): USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LICAND-BINDING PORTION OF THREZ LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TINE-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
-!- DATABASE: NAME-BROW; NOTE-CD guide CD120b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-31.
MEDLINE-90110215; PubMed-2153136;
Engelmann H., Novick D., Wallach D.;
Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.; "Blochemical properties of the 75-kba tumor necrosis factor receptor Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91056048; PubMed=2173696;
Loctscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;
                                                                                                                              "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.", Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99221490; PubMed-10206649;
Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
"Structural basis for self-association and receptor recognition of
"Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and partial amino acid sequence analysis of tw
distinct tumor necrosis factor receptors from HL60 cells.";
J. Biol. Chem. 265:20131-20138(1990).
                                                                                             <u>.</u>
                                                      SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 267:21172-21178(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93016040; PubMed=1328224;
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                                                                                                                Ringold G.M.;
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SEQUENCE OF
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AACS0622.1; JOINED. AACS0622.1; JOINED. AACS0622.1; JOINED. AACS0622.1; JOINED.

U52158; U52159;

EMBL; EMBL; EMBL;

052157;

EMBL;

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              DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Basement membrane; Extracellular matrix; Colled coll; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                      LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
BY SIMILARITY.
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EGF-LIKE 7
EGF-LIKE 8
EGF-LIKE 9
EGF-LIKE 1
EGF-LIKE 1
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DOMAIN I.
    CLEFT OF THE NEUROMUSCULAR JUNCTION,
                                                                                                                                                                                                                                                                                            InterPro; IPR002049; -.
Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
PROSITE; PS00124; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
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LAMININ EG
LAMININ EG
LAMININ EG
DOMAIN II.
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LAMININ E
LAMININ E
LAMININ E
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                                                                                                                                                                                                                                                                  InterPro; IPR000561; -. InterPro; IPR001886; -.
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472
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785
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HSSP; P02468; 1KLO.
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    *** MEDLINE-89159410; PubMed-2922051;

*** MEDLINE-89159410; PubMed-2922051;

*** Hurter D.D., Shah V., Merlie J.P., Sanes J.R.;

*** A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";

*** A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";

*** A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";

*** A laminin-like adhesive protein cleft of the neuromuscular junction.";

*** A laminin-like adhesive protein cleft of the neuromuscular junction.";

*** CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING CLELS INTO TISSUES DURING EMBRYONIC DEVELOPMENT.

*** CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT.

*** CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT.

*** CELLS INTO TISSUES CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND CLESSUE AT EACH END.

*** TO EACH OTHER BY DISLUEIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

*** THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 CLOSSUES SPECIFICIAR: FOUND IN THE BESEMENT MEMBRANES (MAJOR COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                                                                                                                        C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                                                                                                                                                                                                                                            59 CHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                   C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                 55;
                                         Glycoprotein; Transmembrane; Repeat; Signal.

19 POTENTIAL.

289 CD40L RECEPTOR.

193 EXTRACELLULAR (POTENTIAL).

215 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
                                                                                                                                                                                                                                                     Length 289;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                           CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CXS 2.
TNFR-CXS 3.
                                                                                                                                                                                                                                                    Query Match 14.0%; Score 135.5; DB 1; Best Local Similarity 26.1%; Pred. No. 3.8e-05; Matches 49; Conservative 10; Mismatches 74;
                                                                                                                                                                                                                                                                                                            LCGL - - ALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCC
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Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
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289 AA;
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                                            Receptor; B-cell;
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179 TSQTNVIC 186
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TRANSMEM
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                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                             SEQUENCE
                                                        SIGNAL
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REPEAT
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                                                                                                                                                                                                                                                                                                                         s-laminin/laminin beta 2.";
Nature 374:258-262(1995).
-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR NERVE TERMINALS.
                                                                                                                                                                                           TISSUE-Lung;
MEDLINE-94319092; PubMed-8043959;
Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
A. S. Laminin gene (Lams) maps to Fl band of mouse chromosome 9.";
Mamm. Genome 5:393-394(1994).
                                                                                                                                                                                                                                                                                STRAIN=129/J;
MEDLINE-95191650; PubMed-7885444;
Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
"Aberrant differentiation of neuromuscular junctions in mice lacking
                                                                                       Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
Albrechtsen R., Wewer U.M.;
"Structural organization of the human and mouse laminin beta2 chain
genes, and alternative splicing at the 5' end of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix; Coiled coil;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Basement membrane; Extracellular matrix;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                      genes, and alternative splicing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMINI_TYPE_EGF; 12.
                                                                                                                                                      Biol. Chem. 271:13407-13416(1996).
                                                                           MEDLINE-96278760; PubMed-8662701;
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EMBL; U42624; AAC53535.1; JOINED.
EMBL; X75928; CAA53532.1; -.
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Pfam; PF00055; laminin_Nterm; 1
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                              SEQUENCE OF 348-428 FROM N.A.
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PROSITE; PS01186; EGF_2; 2.
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InterPro; IPR000561; -.
InterPro; IPR001886; -.
InterPro; IPR002049; -.
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      FUNCTION
              15;
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Pred. No. 0.00018;
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INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                             "Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
-1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                   -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED
                                                                                                              Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-1BB LIGAND RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
3 X TNFR-CYS.
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                                            Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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Interpro; IPR001368; ...
Pfam; PF00020; TWFR_C6; 2.
PROSITE; PS00652; TWFR_NGFR_1; 1.
PROSITE; PS50050; TWFR_NGFR_2; 1.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E3A563FE5EF00460 CRC64;
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                                                                                                  MEDLINE-95347766; PubMed-7622190;
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30.9%;
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255 AA;
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REVISION TO 107.
                               Schwarz H.;
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41BB\_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATES WITH P56-LCK.
-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
-- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
-- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T., Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 150:771-781(1993).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY ACTIVE DURING T CELL ACTIVATION.
-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                     MEDLINE-94179805; PubMed-8133039; Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.; "Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFR-CYS 3.

TNFR-CYS 3.

TNFR-CYS 4.

N-LINKED (GLCNAC. . .) (POTENTIAL).

93A10D03C60813C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Inducible T cell antigen 4-1BB. Analysis of expression and
01-FEB-1991 (Rel: 17, Created)
01-FEB-1991 (Rel: 17, Last sequence update)
15-JUL-1999 (Rel: 38, Last annOtation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB).
TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
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PROSITE; PS50050; TWFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
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                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89184547; Pubmed-2784565;
KWON B.S., Welsseman S.M.;
"CDMA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
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TNFR-CYS 1.
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MEDLINE=93139510; Pubmed=7678621;
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HSSP; P25942; ICDF.
MGD; MGI:1101059; Tnfrsf9.
InterPro; IPR001368; -.
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                           antigen 4-1BB
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CARBOHYD
SEQUENCE
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                                  7;
                                                                                                                                    102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                     90 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                              MEDLINE-90214614; PubMed-2157591;
Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC 0X40 antigen of activated CD4 positive J "Characterization of the MRC 0X40 antigen of activated CD4 positive J I Jymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J.,9:1063-1068(1990).
-- FUNCTION: RECEPTOR FOR THE OX40L/GD34 CYTOKINE.
-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                  Gaps
                                                             34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . ) (POTENTIAL).
C06465136816E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                  18;
; Score 153; DB 1; Length 256;
; Pred. No. 1e-06;
17; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (0X40 ANTIGEN) (MRC 0X40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 X TNFR-CYS.
TNFR-CYS 1.
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    15.8%;
31.5%;
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                                                                                                                                                                                                                                                                                                                                                                     TNFRSF4 OR TXGP1L OR OX40. Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001368; -. Pfam; PF00020; INFR_c6; 3.
                                  Conservative
                                                                                                                                                                                                                                                                                 STANDARD;
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271
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PIR; S12783; S12783.
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    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                         154 KDVVCGP 160
                                                                                                                                                                              149 HNAVCVP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=T-cell
                                  40;
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DOMAIN
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15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
THERSF5 OR CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
                                                                                                                                     72 CMCVQPEFHCG----DPC--CTTCRHH--------------PCPPGQGVQSQGKFSF 108
                                                                                                                                                                CHPCEPGFYNEAVNYDICKQCIQCNHRSGSELKQNCIPIEDIVCQCRPGIQPRQDSSHKL 118
                                     Gaps
                                                                  26 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----- 71
                                                                                                  QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-92105763; PubMed-1370315;
Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";
J. Immunol. 148:620-626(1992).
                                   Indels .44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C; TISSUE-Liver;
BDDLINE-93094586; Pubmed-1281194;
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.,
 Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Torres R.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                        GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                          62;
15.6%; Score 151; DB 1; 28.5%; Pred. No. 1.6e-06; ive 12; Mismatches 62.
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EMBL; M94126; AAA37404.1; -.
EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M94127; AAA37404.1; JOINED.
PIR; A46476; A46476.
HSSP, P25942; 1CDF.
MGD; MGI:88336; Tnfrsf5.
                                     Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                   Similarity
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STRAIN-BALB/C;
                                 47;
                                                                                                                                                                                                                                                                                                                             CD40_MOUSE
   Query Match
Best Local S
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CD40_MOUSE
                                     Matches
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triticum ae homo sapten mus musculu

hordeum vul mus musculu

triticum ae homo sapien

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
MEDLINE-94044750; PubMed-8228223;
Caldachead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
T-B cell interactions.";
J. Immunol. 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.";

Eur. J. Immunol. 25:926-930(1995).

-- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:104512; Thfrsf4.
InterPro: IPR001368; -.
Pfam; PF00020; TNFR_G5; -.
PR051TE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                            P35444
P10040
P18519
Q16787
P98133
P10968
P15312
P22105
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MEDLINE-95255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Barclay A.N.;
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                        RESULT 1
0X40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 34, Last sequence update)
DT 01-CCT-2000 (Rel. 40, Last annotation update)
DE 0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
                                                                                                                                                                                                                ALIGNMENTS
                            COMP_RAT
CRB_DROME
NGFR_CHICK
LMA3_HUMAN
FINI_BOVIN
AGII_WHEAT
AGI_HORVU
AGI2_WHEAT
LRP1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                 TNFRSF4 OR TXGP1 OR OX40.
213
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; Search time 43.78 Seconds
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P20334
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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CD40_BOVIN
TNR2_HUMAN
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CD40_HUMAN
TNRC_HUMAN
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NTC1_MOUSE
LMA5_MOUSE
IG1R_MOUSE
FBN2_HUMAN
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CD40_MOUSE
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LMB2_HUMAN
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LRP1_CHICK
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AGI_ORYSA
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Maximum Match 100%
Listing first 45 summaries
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OX40_HUMAN
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB :
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Result

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Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDINDE-95219871; PubMed-7704935; Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.; "Identification of OX40 ligand and preliminary characterization of
                                                                                                                                                                                                                                                                           86 -----CPPGQGVQSQGKFSFGFQCID 114
                                                                                                                                                                                                                                                                                                     66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                    39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94170844; PubMed=7510240;
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
Hummel M., Fonatsch C., Stein H.;
"The human OX40 homolog: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROFEIN.
-i- SIMILARITY: COUTAINS A LA-NGFK/TNFR-TYPE CYSTEINE-RICH REGION.
-i- DATABASE: NAME-PROW; NOTE-CD guide CD134 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  OX40_HUMAN STANDARD; PRT; 277 AA.
P43489; Q13663;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
OX40L RECRETOR PRECURSOR (ACCT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPHOTEIN 1 RECEPTOR) (CD134 ANTIGEN).
                                                                                                                                                                                         52;
                                                                                                                                                     ; Score 162; DB 1; Length 272;
; Pred. No. 1.8e-07;
11; Mismatches 51; Indels :
                                                                                                   A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                        TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  115 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                  126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                       TNFR-CYS 4.
N-LINKED (GLCNAC.
              4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              its activities on OX40 receptor.";
Circ. Shock 44:30-34(1994).
                                                                                                                   Ψ.
                                                                                                                                                           16.7%;
28.3%;
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                                                                                                                  30153
                                                                                                                                                                       Local Similarity 28.3 les 45; Conservative
272
165
61
103
124
165
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                                                                                                                  272 AA;
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                                                                       REPEAT
CARBOHYD
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REPEAT
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55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GARRIGRGPCAALLILGLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GAMGAFRALCGLALLCALSLG------ORPTGGPGCGPGRLLLGTGTDARCCRVHT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwarz H., Tuckwell J., Lotz M.;
"A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Indels 18;
                                                                                                                                                                                                                                                    Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-027-2000 (Rel. 31, Last sequence update)
01-027-2000 (Rel. 40, Last annotation update)
4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
(T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. .) (POI N-LINKED (GLCNAC. .) (POI N-LINKED (GLCNAC. .) (POI N-49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                                                                              OX40L RECEPTOR.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 162; DB 1;
Pred. No. 1.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AA
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TNFR-CYS 1.
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EMBL; S76792; AAB33944.1; ALT_INIT.
HSSP; P25942; 1CDF.
MIM; 600315; -.
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                                                                                                                                                                           PROSITE; PS00652; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94085794; PubMed-8262389;
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                                                                                                         InterPro; IPR001368; -. Pfam; PF00020; TNFR_c6; 3.
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277 AA;
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Matches 51
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CARBOHYD
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R;Stamenkovic, I; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-1ymphocyte activation molecule related to the nerve growth factor recept A;Reference number: S04460; MUID:89356608
A;Accession: S04460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross references: GDB:215268; OMIM:109535
A.Map position: 20q12-20q13.2
B.S.D.Map position: 20q13.2
B.S.D.Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (min)
C;Date: 24 May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Date: 24 May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: 154182
K;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
A;Reference number: 154182; MUID:93552381
A;Accession: 154182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-277 <STRA.
A; Cross-teferences: SEMBL: X60592; NID: 929850; PIDN: CAA43045.1; PID: 929851
A; Cross-references: SPA: SPAUlie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-A; Reference number: A60771; MUID: 89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
                     ---KTHSGS--CROCMRLSKCGPGFGVASSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                         80 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 133
                                                                                                                                                                             14.1%; Score 118.5; DB 2; Length 277; 27.7%; Pred. No. 0.01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-cell activation protein CD40 precursor - humanyAlternate names: B-cell surface antigen Bp50
                     107 EIRACTKQQNRVCACEAGRYCAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A60771
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A; Residues: 1-474 <GOO>
A; Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
A; Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R; Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
Submitted to the EMBL Data Library, May 1995
A; Description: Characterization of the promoter region of the murine p75-TNF receptor.
A; Reference number: S54816
A; Retus: preliminary
A; Molecule type: DNA
A; Residues: 1-22 <KIS>
A; Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
A; Residues: 1-22 <KIS>
A; Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C; KGywords: Cytokine receptor; transmembrane protein
F; 1-27 Domain: signal sequence #status predicted <AIG>
F; 23-474/Product: tumor necrosis factor receptor type 2 #status predicted <AMT>
F; 23-474/Product: tumor necrosis factor receptor type 2 #status predicted <AMT>
F; 21-27/Domain: NGF receptor repeat homology <AIG>
F; 21-20,70main: NGF receptor repeat homology <AIGS>
F; 21-20,70main: NGF receptor 
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R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A;Reference number: A40254; MUID:91246168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor receptor type 2 precursor - mouse
(Species: Mus musculus (house mouse)
(Spate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
(SAccession: B38634; A40254; S54816
(R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID:91187885
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8
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG3>
F;20-152/Domain: NGF receptor repeat homology <NG4>
F;20-152/Domain: transmembrane #status predicted <TMN>
F;20-461/Domain: intracellular #status predicted <INN>
F;20-461/Domain: are arbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CGPG---RLLLGTGTDARC------46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
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14; Mismatches 63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.18; Score 119; 26.38; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.1
Best Local Similarity 26.3
Matches 41; Conservative
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Best Local Similarity
Matches 36; Conserv
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A; Residues: 1-474 < LEW>
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A; Cross-references: EMBL: 249886; PIDN: CAA90055.1; GSPDB: GN00020; CESP: C06A1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Caenorhabditis elegans
:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                              972 HFGDPSRPGGRCQLCECSGNIDPMDPDACDPHTGQCLRCLHHTEGPHCAHCKP----- 1024
61 GCGGG----GGGCGCCCCR---PRCC-----CCCRPKCCTCCRTCCCTRCCTCCR-- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C06A1.6 - Caenorhabditis elegans
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A;Molecule type: DNA
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0; Mismatches
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                                                                                         94 TF--------
                                                                                                                                                                                                                                                     1025 GFHGQAARQSCHRCTCNLLGTNPQQ 1049
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                                                                                                                                                                                                               113 GFLTVFPGNKTHNAVC-VPGSPPAE 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: clone C06A1
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34.9%;
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Best Local Similarity 34.9°
Matches 30; Conservative
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R;Ilvanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Trygg Maring Biol. 14, 489-497, 1994
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss A;Reference number: S53869
A;Accession: S53869
                                                 A)Cross references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics: A)Gene: GBB:L130195; OMIM:600979
A)Cross references: GDB:1230195; OMIM:600979
A)Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3p21.3-3p21.2
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------CVCNGHADECNTHTGACLGCRDHTGGEHCER----CI-AGF 912
                                                                                                                                                                                                                                                                                                                                                                                                                            ----- CRDYPGEE---- 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 HCGDPCCT---TCRHHPCPPGQGVQ-----SQGKFS------FGFQCIDCASG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GGPGCGPGRLLLGTGTDARC-----CRVHTTRC--CRDYPGEECCSEWDCMCVQPEF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;283.344/Domain: laminin-type EGF-like homology <LEG1>
F;347-407/Domain: laminin-type EGF-like homology <LEG1>
F;410-467/Domain: laminin-type EGF-like homology <LEG1>
F;410-467/Domain: laminin-type EGF-like homology <LEG1>
F;420-519/Domain: laminin-type EGF-like homology <LEG1>
F;522-552/Domain: laminin-type EGF-like homology %LEG1>
F;783-828/Domain: laminin-type EGF-like homology <LEG6>
F;831-84/Domain: laminin-type EGF-like homology <LEG6>
F;877-944/Domain: laminin-type EGF-like homology <LEG9>
F;927-983/Domain: laminin-type EGF-like homology <LEG9>
                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                   Score 117; DB 2; Length 435;
Pred. No. 0.018;
2; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 QNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC---KNPLEP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laminin beta-2 chain #status predicted
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F;1095-1140/Domain: laminin-type EGF-1ike homology <LE12>
F;1143-1187/Domain: laminin-type EGF-1ike homology <LE13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Domain: laminin-type EGF-like homology <LE10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-32/Domain: signal sequence #status predicted <5173
33-1798/Product: laminin beta-2 chain #status nredio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin beta-2 chain precursor (version 2) - human N;Alternate names: s-laminin
                                                                                                                                                                                                                                                                                                   Query Match 13.9%; Score 117; DE Best Local Similarity 25.6%; Pred. No. 0.01 Matches 42; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:132363; OMIM:150325
                                                                                                                                                                                                                                                                                                                                                                                                                         9 CGPGRLLLGTGTDARCCRVHTTRC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 23...
Best Ag, Conservative
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A; Residues: 1-1798 <IIV>
C; Genetics:
A; Molecule type: mRNA
A; Residues: 1-435 <RES>
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24; Gaps

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A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 23-461 CDBM>
A; Residues: 23-461 CDBM>
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons A; Reference number: A36007; MUID:90349572
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M32315; NID:g189185; PIDN:AAAS9929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally oc A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-195, R. 197-461 <KOH>
A; Residues: 1-195, R. 197-461 <KOH>
A; Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758
A; Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758
B; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokinne 2, 231-237, 1990
A; Title: Two human TNF receptors have similar extracellular, but distinct intracellul A; Reference number: A48416; MUID:91370690
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A;Residues: 23-40;65-69;136-141;300-306 <LOE>
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
A;Residues: 23-40;65-69;131-1536; D.
J. Biol. Chem. 265, 1531-1536; 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A;Reference number: A35010; MUID:90110215
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A;Residues: 27-31 <RNG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Remert, P.3 191-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region
A;Reference number: 138094; MUID:95121934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 116-140, 'p', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A; Cross-references: GB: M35857; NID: 9339751; PIDN: AAA63262.1; PID: 9339752
A; Cross-references: GB: M35857; NID: 9339751; PIDN: AAA63262.1; PID: 9339752
B; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Reference number: A23666; MuID: 91056048
A.Note: the list of introns is incomplete
C.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C.Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
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A; Molecule type: mRNA
A; Residues: 1-461 <SMI>
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A; Residues: 1-37 <RES>
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                                                                                                                                                                                                                                                                  (Asn) (covalent) #status
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A; Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
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R; Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A; Reference number: I48854; MuID:95178848
A; Accession: I48854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
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N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          873 GFPNCRPCVCNGR-----ADECDAHTGACLGCRDYTGGEHCER----CI-AGFH-GD 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SGGHEGHCKPWTDCTQFGF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GGPGCGP----GRILLGTGTDARCCRVHTTRC---CRDYPGEECCSEWDCMCVQPEFHCGD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FGFQCIDCASGTF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              977 GDPSKPGGRCQLCECSGNIDPTDPGACDPHTGQCLRCLHHTEGPHCGHCKP-----GF
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 125; DB 1; Length 1801;
Pred. No. 0.011;
                                                                     F;1197-1412/Region: heptad repeats
F;1445-1801/Region: heptad repeats
F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I < COOMI>
F;446-1801/Domain: I < COOMI>
F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (F;1193,1196,1800/Disulfide bonds: interchain #status predicted
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          F;1146-1190/Domain: laminin-type EGF-like homology <LE13> F;1197-1412/Domain: II <DOM2>
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26.48;
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Best Local Similarity 30.38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 SP 133
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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RESULT 148854

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R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleletc acid
A;Rosiducs: 1.287, 1LV <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: interact with cells and with other basement membrane proteins to promo C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C; Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu F;1-35/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RiHunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
Astitle: A laminin-like adhesive protein concentrated in the synaptic cleft of the Astitle: 803539; MUID:89159410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S03539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atypical <LE05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CDSGEFSAQWNREIRC -- HQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>F;36-285/Domain: VI <DOM6>
                                                                                                                                                                                                                                                                                                                                                          (NCBIP:120357)
                                                                                                                                                                                                                                                                                                                   A, Experimental source: BALB/c, liver
A, Note: sequence extracted from NCBI backbone (NCBIP:12035
C, Comment: For an alternative splice form, see PIR:A46515.
C; Comment: For an alternative splice form, see PIR:A46715.
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;989-1038/Domain: laminin-type EGF-like homology <LE10>F;1041-1095/Domain: laminin-type EGF-like homology <LE11>F;1098-1143/Domain: laminin-type EGF-like homology <LE12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;786-831/Domain: laminin-type EGF-like homology <LE06>F;788-1196/Domain: III <DOM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;880-927/Domain: laminin-type EGF-like homology <LE08> F;930-986/Domain: laminin-type EGF-like homology <LE09>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <LE01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 127.5; DB 2;
Pred. No. 0.0021;
8; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;36-285/Domain: VI < DOM6>
F;286-555/Domain: V < DOM5>
F;286-347/Domain: V < DOM5>
F;36-410/Domain: laminin-type EGF-like homology F;413-470/Domain: laminin-type EGF-like homology F;473-522/Domain: laminin-type EGF-like homology F;525-555/Domain: laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;834-877/Domain: laminin-type EGF-like homology
                                                                                                            A; Reference number: A46515; MUID: 93094586
A; Accession: A46515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laminin beta-2 chain precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%;
28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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A; Residues: 1-1801 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NKTHNAVC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Phytolacca americana (Virginian pokeweed)
Cispecies: Phytolacca americana (Virginian pokeweed)
Cispecies: Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
Ciscession: JC5559
R;Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phyto A;Reference number: JC5559; MUID:97290889
A;Reference number: JC5559
A;Reference number: JC5559
A;Reference number: JC5559
A;Residues: 1-295 cyAM>
A;Residues: 1-295 cyAM>
A;Residues: 1-295 cyAM>
A;Residues: 1-295 cyAM>
A;Residues: JC00mment: This protein is a lectin specific for N-acetylgucosamine-containing saccharid C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Reywords: glycoprotein
F;96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine A;Reference number: A46476; MUID:92105763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
                                                                                                                                                                                                                                                                                      ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000 C; Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620.626, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHPCEPGFYNEAVNYDICKQCIQCNHRSGSELKQNCIPTEDIVCQCRPGTQPRQDSSHKL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 CGITEGYCGEGCQSQC---NHQRCGKDFAGRICLNDLCCSEWG-WCGSSEAHCGQGCQSN 209
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                          1 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- PCPPGQGVQSQGKFSF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCSEWDCMCVQPEFHCGDPCCTT 63
                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 295;
                                                                                                                                                                                                             Length 271;
                                                                                                                                                                                                                                                                                      62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 CRHHPCPPGQGVQSQGKFSFGFQ-C---IDCASGTFSGGHEGHC 103
C;Keywords: growth factor receptor; transmembrane protein F;1-19/Domaln: signal sequence #status predicted <SIG> F:20-271/Product: OX40 antigen #status predicted <MAI> F;211-235/Domaln: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                             18.0%; Score 151; DB 2; 28.5%; Pred. No. 2.6e-05; ive 12; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.5%; Score 138.5; DB 2 31.7%; Pred. No. 0.00027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 CMCVQPEFHCG----DPC--CTTCRHH----
                                                                                                                                                                                                                                                                                      47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Conservative
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Matches 33; Conserv
                                                                                                                                                                                                                                                  Similarity
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A; Residues: 1-305 <TOR>
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Gaps

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GenCore version 4.5
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OM protein - protein search, using sw model

4, 2001, 16:12:11 September Run on:

; Search time 80.15 Seconds (without alignments) 130.205 Million cell updates/sec

US-09-512-363-2\_COPY\_26\_162

841 1 QRPTGGPGCGPGRLLLGTGT......FPGNKTHNAVCVPGSPPAEP 137 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

219241 Total number of hits satisfying chosen parameters: 219241 seqs, 76174552 residues

length: 0 length: 2000000000 sed 0B Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qene ox40 protein	lymphocyte activat	Ox40 homolog - hum	T-cell antigen 4-1	OX40 antigen precu	lectin-B - Virgini	B cell-associated	laminin beta-2 cha	gene murine tumour	tumor necrosis fac	tumor necrosis fac	B-cell activation	necrosi	?	hypothetical prote		insulin-like growt	MEGF6 protein - ra	laminin alpha 5 ch	fibrillin-2 precur	hypothetical prote	laminin beta-2 cha	fibrillin-2 precur	hypothetical prote		insulin-like growt	insulin receptor-r	gene shuttle craft	latent transformin
SUMMARIES	ΩI	148700	I38426	137552	B32393	S12783	JC5559	A46476	MMRTS	I48854	A35356	B38634	A60771	154182	S53869	T18975	A33837	A48805	T13954	T10053	A57278	T24272	A55677	A54105	T15651	A46016	IGHUR1	B47417	T13938	A55494
	DB							~																						
	Length		255	277	256	271	295	302	1801	459	461	474	277	435	1798	152	1371	329	1574	3635	2907	164	1797	2918	188	926	1367	540	1106	1820
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	Score	162	160.5	158.5	153	151	138.5	127.5		120.5	119		118.5	117	115	112	111	110	109	109	108	107	106	104	. 102.5	102.5	101	100	100	66
	Result No.	П	7	e	4	S.	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote adhesive ligand ep	hypothetical prote	latent transformin	nerve growth facto	MEGF2 protein - hu	thrombospondin 2 p	laminin beta-1 cha	insulin receptor-r	Doc4 protein, stre	thrombospondin 3 p	gene serrate prote	Motch B protein -	MEGF8 protein - hu	fibrillin I - bovi
T26972 A55347	T44598	A57293	3N0006	T00250	TSHUP2	MMHUB1	B36502	T14271	A57121	S16148	A49175	T00209	A55567
77	0	<b>(1)</b>	٦,	N	Н	-	~	7	~	~	~	~	C3
1111	1106	1251	416	1364	1172	1786	1268	2825	926	1408	1203	1737	2871
11.7	11.5	11.5	11.4	11.4	11.4	11.4	11.3	11.3	11.2	11.2	11.2	11.2	11.2
98 97.5	97	97	96	96	95.5	95.5	92	95	94.5	94.5	94	94	94

# ALIGNMENTS

gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000
C;Accession: I48700; I48334; S343.7
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A;Reference number: I48700; MUID:94044750
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ

A.Molecule type: mRNA A.Residues: 1-272 <RES> A.Cross-references: EMBL221674; NID:9312827; PIDN:CAA79772.1; PID:9312828 B.Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995 A.Title: Gene structure and chromosomal localization of the mouse homologue of rat OX A.Reference number: 148334; MUID:95255413

A; Accession: I48334 A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A;Residues: 1-14,'G',16-272 <RE2> A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819 C;Genetics:

A;Gene: ox40 A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1 C;Superfamily: CD27 antigen; NGF receptor repeat homology

Gaps 52; Length 272; 51; Indels / Match 19.3%; Score 162; DB 2; Local Similarity 28.3%; Pred. No. 3.5e-06; nes 45; Conservative 11; Mismatches 51; Query Match Best Local Si Matches 45;

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14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC------HPCET 65 14 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 60 ò

g

66 GFYNEAVNYDICKOCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125 61 δ q

90 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128 δ

CPPGHESPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164 126 QQ

# RESULT

lymphocyte activation-induced receptor ILA precursor - human C;Species: Homo sapiens (man)

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63 TCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Mallett, S.; Fossum, S.; Barclay, A.N.
BMBO J. 9, 1063-1068, 1990 .
A;Title: Characterization of the MRC OX40
A;Reference number: S12783; MUID:90214614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: I48879; MUID:94179805
A; Accession: I48879
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                                                                                                                                                                                                                                                                                                                                                                  T-cell antigen 4-1BB precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: B32393; I48879
R; Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86,
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                                                                                                                                         123 THNAVCVPGSPPA 135
                                                                                                                                                                                                  161 SSDAICEDRDPPA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 40; Conserv
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A; Residues: 1-271 <MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-256 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Accession: JT0752
A. Molecule type: mRNA
C. Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C. Comment: This receptor recoptor repeat homology
C. Superfamily: CD27 antigen; NGF receptor repeat homology
C. Superfamily: CD27 antigen; NGF receptor receptor; transmembrane protein
F. 1-17/Domain: signal sequence #status predicted <SIG>
F. 18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F. 18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F. 18-255/Product it ransmembrane #status predicted <ANN
F. 13-255/Binding site: phosphate (Thr) (covalent). (by casein kinase II) #status predicted
F. 242/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794
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R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment characteristic number: 137552; MUID:94170844
      C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000 C; Accession: 138426; JT0752 R; Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, Bur. J. Immunol. 24, 2219-2227, 1994 A; Title: Wolecular and biological characterization of human 4-1BB and its ligand. A; Reference number: 138426; MUID:94374434
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C;Date: 29-May_1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCSMC-EQDCKQGQELTKKG------CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g472957; PIDN:CAA53576.1; PID:g472958
                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCS----EWDCMCVQPEFHCGDP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CPPNSFSSAGG--QRICDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 160.5; DB 2; 30.9%; Pred. No. 4.4e-06; tive 12; Mismatches 52;
                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
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Gene 134, 295-298, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.1
Best Local Similarity 30.9
Matches 47; Conservative
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A; Residues: 1-255 <RES>
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Best Local Similarity
Matches 42; Conserv
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A; Residues: 1-277 <RES>
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137552
OX40 homolog - human
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A;Molecule type: mRNA
A;Residues: 1.256 <KWO>
A;Residues: 1.256 <KWO>
A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
B;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B
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                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: U02567; NID: 91117783; PIDN: AAA93113.1; PID: 9409178
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C;Accession: S12783; S08036
101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASN 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 123
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
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Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Reywords: transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: cDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547
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FT DISULFID 1890 1910 BY SIMILARITY. FT DISULFID 1913 1922 BY SIMILARITY. FT DISULFID 1925 1939 BY SIMILARITY. FT DISULFID 1989 2000 BY SIMILARITY. FT DISULFID 1991 2007 BY SIMILARITY.	DISULFID         2009         2018         BX           DISULFID         2021         2033         BY           DISULFID         2036         2043         BY           DISULFID         2038         2050         BY           DISULFID         2052         2061         BY	DISULFID 2064 2083 BY SIMILARITY. DISULFID 2086 2086 INTERCHAIN (PROBABLE DISULFID 2089 2089 INTERCHAIN (PROBABLE	CARBOHYD 17 17 N-LINKED (CARBOHYD 65 65 N-LINKED (CARROHYD 165 165 N-T-INKED)	CARBOHYD 300 N-LINKED (GLCNAC ) CARBOHYD 374 N-LINKED (GLCNAC ) CARBOHYD 402 N-LINKED (GLCNAC )	CARBOHYD 822 822 N-LINKED (GLCNAC) CARBOHYD 843 843 N-LINKED (GLCNAC) CARBOHYD 843 843 N-LINKED (GLCNAC)	CARBOHYD 1252 1252 N-LINKED (GLCNAC) CARBOHYD 1451 1451 N-LINKED (GLCNAC)	1938 2115 2128	CARBOHYD 2282 2282 N-LINKED (GLCNAC) (	atch 13.0%; Score 109; DB 1; Length 3635; cal Similarity 27.8%; Pred. No. 0.032;	Matches 44; Conservative 9; Mismatches 51; Indels 54; Gaps 10; Qy 3 PIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPG-EECCSEWDCMCVQPEFHCGDP 59	1 1946 PCGTETCDPQ	QY 60 CCTTCRHHPGPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCK 104	DD 1994 AAKGSECHPQSGQCHCQPGTTGPQCLECAPGYWGLPEKGCRRCQCPRGHCD 2044	105 PWIDCIQEGELIVEPGNKTHNAVCVPGSP 133	DD Z045 PHTGHCTCPPGLSGERCDTCSQQHQ-VPVPGKP Z076	nplete												
		LAMININ G-LIKE 2. LAMININ G-LIKE 3. LAMININ G-LIKE 4.		COLLED COLL (POTENTIAL COLLED COLL (POTENTIAL COLLED COLL ATTACHMENT SITE		BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.	BY BY BY	BY BY	BY BY		BY	BY BY	BI SIMILARIII. BY SIMILARITY. BY SIMILARITY	BY	BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.	BY BY	BY BY	BY SIMILARITY.  BY SIMILARITY.  DV CIMILARITY.	BY BY	BY	BY BY	BY	BY	BY		BY BY	BY BY	BI SIMILARITI. BY SIMILARITY.
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1749 1782 1832 1888	1989 2036 2086 2679 2679	2850 3036 3242	3428 2122 2247	2521 2556 1640	1756 222 224	246 258	281 283 318	330	353 371	383 417 419	440	464 466	497 497 510	512	555 555 557	575 587	600 602	621	1362	1393	1452	1486	1501	1532	1784 1801	1813 1832	1834	1888
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        CGPGRLLLGTGTDARCCRVHTTRC-----------------CRDYPGEE----C 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 CS--EMDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 95
                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                   13.9%; Score 117; DB 1; Length 435; 25.6%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                     66; Indels
                                                                                                                                                                    LYMPHOTOXIN-BETA RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                  Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEP 137
                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                          HSSP; P25942; 1CDF.
MIM; 600979; -
MICAFPC; PR001368; -
Pfam; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
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435 AA;
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42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ĥ
                                                              Du J., Delafontaine P.; "Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA."; Circ. Res. 76:963-972(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 187:934-939(1992).
-1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IG
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS
                                                                                                                                                                                                                                                                                                                                    Werner H., Woloschak M., Adamo M., Shen-Orr 2., Roberts C.T. Jr.,
                                                                                                                                                                                                                                                                                                                                                                       Leroith D.; "Developmental_regulation of the rat insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE OF 913-1017 FROM N.A.
MEDLINE-92412145; PUDMEd=1530648;
KUTACHI H., JODO K., Ohta M., Kawasaki T., Itoh N.;
Kutachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
"A new member of the insulin receptor family, insulin
"Acceptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASES.
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CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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                                                                                                                                                                                                                                                                                                  MEDLINE-90017496; PubMed-2477843;
TISSUE-Brain;
MEDLINE-95277910; PubMed-7758167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L29232; AAA41392.1; -. EMBL; M27293; AAA41384.1; -.
                                                                                                                                                                                                                                    1-364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; 1.
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InterPro; IPR000719;
InterPro; IPR001745;
InterPro; IPR001777;
InterPro; IPR001177;
                                                                                                                                                                                                                                SEQUENCE OF 1-364 FROM STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A33837; A33837.
HSSP; P06213; 11RK.
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WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF
ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.
SUBBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
                                                                                                                                                                                          MEMBRANDS (MAJOR COMPONIT).

-1 TISSUE SPECIFICITY: IN ADULT, HIGH LEVELS IN HEART, LUNG, AND KINDEY; LOWRE IN BRAIN, MUSCLE AND TESTIES; VERY LOW IN LIVER, GUT AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.

-1 DOMAIN: THE ALPHA HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COLLED COIL STRUCTURE.

-1 DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
-1 SIMILARITY: CONTAINS 1 LAMININ DEF-LIKE DOMAINS.
-1 SIMILARITY: CONTAINS 2 LAMININ DEF-LIKE DOMAINS.
-1 SIMILARITY: CONTAINS 5 LAMININ GF-LIKE DOMAINS.
-1 SIMILARITY: ALPHA -5 CHANIN S DOMAINS IV.
-1 SIMILARITY: ALPHA -5 CHANIN S MORE RELAFED TO DROSOPHILA ALPHA CHAIN THAN TO MAMMALIAN ALPHA CHAINS 1-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 15.
LAMININ EGF-LIKE 16 (N-TERMINAL).
LAMININ DOMAIN IV 2 (DOMAIN IV A).
ELAMININ EGF-LIKE REPEATS (DOMAIN II A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMININ N-TERMINAL (DOMAIN VI).
10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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Pfam; PF00052; laminin_EGF: 19.
Pfam; PF00054; laminin_G; 2.
Pfam; PF00055; laminin_Nterm; 1.
PROSITE; PS001022; EGF 1; 19.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01186; EGF 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U37501; AAC53430.1; -. HSSP; P02468; 1TLE.
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InterPro; IPR000034; -.
InterPro; IPR000561; -.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 --CLGSCHTPDDNTTCVACRHYYYKGVCVPACPP-----GTYRFEGWRCVDRDFCANI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 CGDLCPGTLEEKPMCEKTTINNEYNYRCWT--TNRCQKMCPSVCGKRACTE-NNECCHPE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6 x CBA; TISSUE=Lung;
MEDLINE=96081906; PubMed=7499364;
Miner J.H., Lewis R.M., Sanes J.R.;
"Molecular cloning of a novel laminin chain, alpha 5, and widespread expression in adult mouse tissues.";
J. Biol. Chem. 270:28523-28526(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 CG---PGRL------LLGTGTDARCCRVHTTRC---CRDYPGEECCSEWDCMCVQPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 FHCGDPC-----CTTCRHH-----PCPPGQGVQSQGKFSF-GFQCID---CAS- 92
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 ----GTFSGG---HEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 PNAESSDSDGFVIHDGEC---MQECPS-GFIR----NSTQSMYCIPCEGP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A5946897A41CB145 CRC64;
    CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
                                                                                                   (BY SIMILARITY). (BY SIMILARITY).
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Last annotation update)
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15-UUL-1998 (Rel. 36, Last seque
15-UUL-1998 (Rel. 36, Last annot
LAMININ ALPHA-5 CHAIN (FRAGMENT)
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Best Local Similarity 27.2
Matches 46; Conservative
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SEQUENCE FROM N.A.
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TO LAMS_MOUSE
TO C061001;
DT 01-NOV-1997
DT 15-JUL-1998
DE LAMIN ALPH
GN LAMAS.
CC HARATOLIS
CC HA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: RECEPTOR FOR TWF-ALPHA.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                          Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
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              cDNAs for two distinct murine tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR 2.
  Wong G.H., Chen E.Y., Goeddel D.V.; "Cloning and expression of cDNAs for two distinct murine tumos necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 474;
                                                                                                                                                                                       Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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462EAE398C4D6563 CRC64;
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                                                Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
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TNFR-CYS 2
TNFR-CYS 3
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                                                                                 MEDLINE-91246168; PubMed-1645445;
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Pfam; PF00020; TWRR_C6; 4.
PR031TE; PS00052; TWRR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 3.
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EMBL, M59378; AAA40463.1; -.
EMBL, U39488, AAA85021.1; -.
EMBL, X87728; CAA6618.1; -.
PIR; B38634; B38634.
HSSP; P19438; INCF.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE-91187885; Pubmed-1849278;
Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
                                                                                                                                                                                                                                                                                                                                                                           1F28967A67AEDE33 CRC64;
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(GLCNAC. . .)
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HGQAARQSCHRCTCNLLGTDP 1048
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
MEDLINE-9826553; PubMed-9605317;
Singh J., Garbbr E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L
                                                                                                                                EIRACTKOONRVCACEAGRYCAL-----KTHSGS--CROCMRLSKCGPGFGVASSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
10-MOL PECEPTOR PRECURSOR (B-CELE, SURFACE ANTIGEN CD40) (BP50) (CDW40)
(TUMOR NECROSIS FACTOR RECEPTOR 5).
                                          Gaps
                                                                                     DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- FUNCTION: RECEPTOR FOR A CYTOKINE LICAND KNOWN AS CD40L.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
-:- SIMILARITY: CONTAINS A LA-NGFR/TWFR-TYPE CYSTEINE-RICH REGION.
-:- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                80 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE-89356608; PubMed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
"A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";
                                        18;
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PROSITE; PS00652; TWFR_NGFR_1; 1.
PROSITE; PS50050; TWFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                        [2]
3D-STRUCTURE MODELING OF 24-144.
MEDLINE-97189482; PubMed-9037712;
MEDrath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional methe ligand binding domain of the human B cell receptor CD40.
Proteins 27:59-70(1997).
Pred. No. 0.00093;
                                                                                                                                                                                                                                                                                                                                              277 AA
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
30-MAY-2000 (Rel. 39, Last anno
           31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 8:1403-1410(1989).
                                        Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFRSF5 OR CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
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P25942;
                                                                                                                                107
                                        Matches
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64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CGESEFLDTWNRETHC -- - HOHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR RECEPTOR
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-I. FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IMUNE DEVELOPMENT.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. SUBCELLULAR LOCATION: A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
BC8776EC2C4A5680 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
11-OCT-2000 (Rel. 40, Last annotation with the control of the con
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27.7%; Pred. No. 0.00068;
                                   RECEPTOR
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                                                                                                                                                                                                        TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
   POTENTIAL
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179 TNKTDVVCGP 188
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Best Local Similarity
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CARBOHYD
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Nature 398:533-538(1999).

-I- FUNCTION: RECEPPOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR THE BETA.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- PTM: PHOSPHORYLATED; MINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.

-I- PTM: PHOSPHORYLATED; MINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.

-I- PTM: PHOSPHORYLATED: ON THE SIDUES.

-I- PTM: PAYERST): USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF THFR 2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93016040; PubMed-1328224; Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Liparl M.T., Goeddel D.V.; "Blochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors."
J. Biol. Chem. 265:1531-1536(1990).
[1]
SEQUENCE FROM N.A.
MEDLINE-90260639; PubMed-2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.", Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Physical mapping and genomic structure of the human TNFR2 gene.";
Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; "Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX MEDLINE-99221490; Pubmed-10206649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer
Brockhaus M.;
                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-91045991; PubMed-2172983;
Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
"A second tumor necrosis factor receptor gene product can shed
naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                            Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.
Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and partial amino acid sequence analysis of the distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-90349572; PubMed-2166946; Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorylation.";
J. Biol. Chem. 267:21172-21178(1992).
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-96299745; Pubmed-8661109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-31.
MEDLINE-90110215; PubMed-2153136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
SIMILARITY: CONTAINS A LA-NGFK/TWFR-TYPE CYSTEIRE-RICH REGION.
DATABASE: NAME-PROW, NOTE-CD FULCH C CD120b entry.
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
DATABASE: NAWE-Enbrel; NOTE-Clinical information on Enbrel;
WWW-"http://www.enbrelinfo.com/".
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 121; DB 1; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
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-> M (IN REF. 1 AND 3).
-> T (IN REF. 4).
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603B580ECD67636F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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N-LINED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
R -> P (IN REF. 4).
R -> P (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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26.38;
                                                                                                                                                      EMBL; M32315; AAA59929.1; -. EMBL; M35857; AAA63262.1; -.
                                                                                                                                                                        US2165; AAC50622.1;
US2156; AAC50622.1;
US2157; AAC50622.1;
US2158; AAC50622.1;
US2159; AAC50622.1;
US2160; AAC50622.1;
US2161; AAC50622.1;
US21621; AAC50622.1;
US2162; AAC50622.1;
                                                                                                                                                                                                                                                           AAC50622.1; J
AAC50622.1; J
AAA36755.1; -
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161
179
171
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B35010; B35010.
A23666; A23666.
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                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001368;
Pfam; PF00020; TNFR_C
                                                                                                                                                                                                                                                                                         A35356; A35356
A36007; A36007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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23
258
288
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191191;
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 -I-SUBBUILT: LAWINING.
-I-SUBBUILT: SANCH SHOWN STANCE WITH GLOBULES AT EACH END.
-I-SUBBUILT: AND LAWINING.
-I-SUBBUILT: SANCH SHOWN STANCELLULAR; FOUND IN THE BASEMENT
-I-SUBBUILT: SUBBUILT: SUBBUILT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 374:258-262(1995).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR NERVE TERMINALS.
                                57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116
                                                                                      97
 ---CRVHTTRCCRDYPGEECCSEWD-- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94319092; PubMed-8043959;
Aberdam D., Galliano M.F., Mattel M.-G., Ortonne J.P., Meneguzzi G.;
"S-laminin gene (Lams) maps to Fl band of mouse chromosome 9.";
Mamm. Genome 5:393-394(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.; "Aberrant differentiation of neuromuscular junctions in mice lacking s-laminin/laminin beta 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIANE-96278760; PubMed-8662701;
Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
Albrechtsen R., Wewer U.M.;
Structural organization of the human and mouse laminin beta2 chain
genes, and alternative splicing at the 5' end of the human
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                   -CMCVQPEFHC----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--
                                                                                                                                   98 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 133
                                                                                                                                                      LMB2_MOUSE STANDARD; PRT; 1799 AA. 061292; 062182; 01-00-1997 (Rel. 35, Created) 1-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 271:13407-13416(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-129/J;
MEDLINE-95191650; PubMed-7885444;
                                                                                                                                                                                                                                                                                                                                    LAMININ BETA-2 CHAIN PRECURSOR
LAMB2 OR S-LAM OR LAMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 348-428 FROM N.A.
 CGPG---RLLLGTGTDARC-
                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129/J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Basement membrane; Extracellular matrix; Colled coll; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LÁMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
LAMININ EGF-LIKE REPEATS (DOMAIN
LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COIL (POTENTIAL).
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LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 12.
LAMININ BGF-LIKE 13.
DOMAIN II.
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SIMILARITY.
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SIMILARITY.
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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CO
                                                                                                                                                                                                                                                                       EMBL; U43541; AAC53535.1; -.
EEML; U4564; AAC53535.1; JOINED.
EMBL; X75928; CAA53532.1; -.
HSSP; P02468; IKLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002049; -...
Pfam; PF00053; Iaminin_EGF; 13.
Pfam; PF00015; Iaminin_Nterm; 1.
PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001886; -.
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472
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1799
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InterPro; IPR000561;
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"INTERIOR TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBYONIC DEVELOPMENT & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-I- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

-I- SUBCELLULAR LOCATION: EXTRACELLULAR.

COMPONENT), S-LAMININ IS CONCENTRATED IN THE SYNAPTIC COMPONENT), S-LAMININ IS CONCENTRATED IN THE SYNAPTIC

CLEFT OF THE NEUROMOSCULAR JUNCTION.

-I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                       C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 120
                                                                                                                                                                                                                                                      62 CDSGEFSAQWNREIRC---HQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDLINE=89159410; PubMed=2922051;
Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
"A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";
Nature 338:229-234(1989).
                                                                                                                                                                                                                                  CGPGRLLLGTGTDARCCRVHTTRCCRDYPG ---- EECCSEWDCMCVQPE-FHCGDPCCTT
                                                                                                                                                .LINKED (GLCNAC. . .) (POTENTIAL). C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                              11;
    Prodrit: PSO(052; TNFR_NGFR_1; 1. PROSITE; PSO(052; TNFR_NGFR_2; 4. PROSITE; PS50050; TNFR_NGFR_2; 4. Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal. Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
                                                                                                                                                                                         Length 289;
                                                                                                                                                                                                             72; Indels
                                                   CD40L RECEPTOR. 'EXTRACELLULAR (POTENTIAL).
                                                                        POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                         DB 1;
                                                                                                                                                                                        Score 127.5; DB 1 Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1801 AA
                                                                                           4 X TNFR-CYS,
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                           32111 MW:
                                                                                                                                                                                        15.2%;
28.9%;
                                                                                                                                                                                    Query Match
Best Local Similarity 28.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
 TNFR_c6;
                                                   289
193
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216
25
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25
104
145
Pfam; PF00020;
                                                             DOMAIN
TRANSMEM
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P15800;
                                                                                                     REPEAT
REPEAT
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                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS0002; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
Glycoprotein; Basement membrane; Extracellular matrix; Colled coll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAMININ EGF-LIKE REPEATS (DOMAIN
-!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell adhesion; Repeat; Signal.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
BY SIMILARITY.
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LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
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Interpro; IPR001886; -.
Interpro; IPR02049; -.
Pfam: PF00053; laminin_EGF: 13.
Pfam: PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
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HSSP; P02468; 1KLO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
THERSFIB OR THER2 OR THEBR.
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                                                                                                                                                                                                                                      -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Waterrycha: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                             Hirano A., Brown W.C., Estes D.M.; "Cloning, expression and biological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in cattle.";
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Matches 37; Conservative
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P20333;
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15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
TUFRSFS OR CD40.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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N-LINKED (GLCNAC. ..)
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Pred. No. 0.00075;
5; Mismatches 49
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01-NOV-1997 (Rel. 35, Last sequ
15-JUL-1999 (Rel. 38, Last anno
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26.4%;
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NCBI_TaxID=9913;
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Q28203;
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                         MEDILINE-9219871; PubMed-7704935;
Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.; "Identification of OX40 ligand and preliminary characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRP-----GNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 TCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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    Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.;
"The human Ox40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW; NOTE-CD guide CD134 entry;
WWW-"http://www.ncb1.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCT
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00020; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS.
                                                                                                                  1ts activities on OX40 receptor.";
Circ. Shock 44:30-34(1994).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                    OX40L RECEPTOR
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ΜΣ
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161 SSDAICEDRDPPA 173
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InterPro; IPR001368;
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160
277 AA;
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                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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P20334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATES WITH P56-LCK.
--- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
--- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
--- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
--- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 150:771-781(1993).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY ACTIVE DURING T CELL ACTIVATION.
-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                       ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C;
MEDLINE-94179805; PubMed-8133039;
KWON B.S., Kozak C.A., Kim K.K., Pickard R.T.;
"Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducible T cell antigen 4-1BB. Analysis of expression and
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB).
TWFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL). POTENTIAL.
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PROSITE; PS50050; TWFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89184547; Pubmed-2784565;
Woon B.S., Weissman S.M.;
"CDNA sequences of two inductble T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
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MEDLINE-93139510; PubMed-7678621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Immunol. 152:2256-2262(1994).
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MGD; MGI:1101059; Tnfrsf9.
InterPro; IPR001368; -.
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                                                                                                                                               (Mouse)
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                                                                                                                                                                       Eukaryota; Metazoa;
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                          7;
                                                                                                                 102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                  65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 123
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINNEL (GLCNAC. . .) (POTENTIAL). C06465136B16E821 CRC64;
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InterPro; IPR001368; -
InterPro; IPR001368; -
InterPro; IPR00156; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                          18;
18.2%; Score 153; DB 1; Length 256; 31.5%; Pred. No. 6e-07;
                          52; Indels
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EXTRACELLULAR (POTENTIAL)
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TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (
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                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (0X40 ANTIGEN) (MRC 0X40).
                         17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
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                                                                                                                                                                                                                                                                                                                         TNFRSF4 OR TXGP1L OR OX40.
                          Conservative
                                                                                                                                                                                                                                              STANDARD;
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60
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164
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S12783; S12783.
             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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154 KDVVCGP 160
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                          40;
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P15725;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
                                                                                                                                                                             1 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD-----46
                                                                                                              6 QOPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV 58
                                                                                                                                                   47 CMCVQPEFHCG----DPC--CTTCRHH-------PCPPGQGVQSQGKFSF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_raxID=10090;
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                                       44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
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BDDLINE-93094586; PubMed-1281134;
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A., Howard M., Cockayne D.A.;
 Length 271;
                                       62; Indels
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                                                                                                                                                                                                                                                  119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163
                                                                                                                                                                                                                              84 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
18.0%; Score 151; DB 1; 28.5%; Pred. No. 9.4e-07; tive 12; Mismatches 62
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MEDLINE-92105763; PubMed-1370315;
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HSSP; P25942; ICDF.
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MGD; MGI:104512; Thfrsf4.
InterPro; IPR001368; -.
PF6am; PF00020; TWRR_G6; -.
PROSITE; PS00065; TWRR_NGFR_1; 3.
PROSITE; PS50065; TWFR_NGFR_2; 2.
PROSITE; PS50060; TWFR_2; 2.
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Copyright (c) 1993 - 2000 Compugen Ltd
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41BB_HUMAN
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CD40_BOVIN
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IG1R_RAT
IMAS_MOUSE
IMAS_MOUSE
IMB2_HUMAN
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TSP3_HUMAN
SERR_DROME
FBN1_BOVIN
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6 2 2		NCBI_TaxID=10090; [1] SPOHENCE EBOM N A	0-100;	. 6									
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2 2 2		<pre>"Cloning of mouse Ox40: a T cell T-B cell interactions."; J. Immunol. 151:5261-5271(1993).</pre>	or mor intera 1. 15;	actic 1:526	ox40: ons."; 31-527	a T	ce11 )93).	activ	ation marke	r that may	ē	arace	
2 2 2		JENCE	FROM 1	A. A.	in b Mo	: 44	2000						
2 2 2		Birkeland M.L. Barclay A.N.;	Z Z	Ç	oelanc	Z	3., G1	lbert		Jenkins N.A.,			
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POTENTIAL. OX40L RECEPTOR. EXTRACELLULAR (POTENTIAL). POTENTIAL.

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"A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor
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Immunol. Lett. 45:67-73(1995).
-1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                . .) (POTENTIAL).
                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
                                                                                                                                                                                                    ; Score 162; DB 1; Length 272;
; Pred. No. 1e-07;
11; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                   06E7BB4156F0D08E CRC64;
                                                      TNFR-CYS 2.

TNFR-CYS 3 (INCOMPLETE).

TNFR-CYS 4.

N-LINKED (GLCNAC. . .) (FACTOR A -> G (IN REF. 2).
CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS. TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (T-CELL ANTIGEN ILA) (CD137 ANTIGEN) TNFRSF9 OR ILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Immunol. 24:2219-2227(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Blood;
MEDLINE-94374434; PubMed-8088337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Blood;
MEDLINE-94085794; PubMed-8262389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95347766; Pubmed-7622190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                     MM:
                                                                                                                                                                                                          19.3%;
28.3%;
                                                                                                                                                     30153
                                                                                                                                                                                                                                               45; Conservative
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272
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103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40,
                                                                                                                                                   272 AA;
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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237
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104
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144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwarz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41BB_HUMAN
007011;
                                                                                                                CARBOHYD
                                                                                                                                                     SEQUENCE
                                                                                                                                CONFLICT
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REPEAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                       SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P43489; Q13663;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOT-2000 (Rel. 40, annotation update)
0X40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
ACTIVATED GLXCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
F3A563FE5EF00460 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.1%; Score 160.5; DB 1; Length 255; 30.9%; Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 602250; -...
Interpro; IPR01368; -...
Pfam; PF00020; TNFR.c6; 2.
PROSITE; PS00652; TNFR.NGFR.1; 1.
PROSITE; PS50050; TNFR.NGFR.2; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4-1BB LIGAND RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
DURING T CELL ACTIVATION.
LULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AA
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TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GNKTHNAVCVPG-----SPPA---EP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U03397; AAA53133.1; -. EMBL; L12964; AAA62478.2; -. HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                         -! - DATABASE: NAME-PROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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255 AA;
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Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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F;1142-1186/Domain: laminin-type EGF-like homology <LE13>

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C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jan-2000
C;Accession: A57278
R;Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A;Title: Developmental expression of fibrillin genes suggests heterogeneity of extrac A;Reference number: A57278; MUID:95263670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: Ti3954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like moti
                                                                                                                                              10;
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A; Residues: 1-1574 <NAK>
A; Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294
A; Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 DPCCTTCRHHPCPPGQGVQSQGKFSFGF------QC-ID---CASG---TFSGGHE 100
                                                                                                                                                 Gaps
                                                                                                                                                                                                 5 GGPGCGPGRLLLGTGTDARC-----CRVHTTRC--CRDYPGEECCSEWDCMCVQPEF 54
                                                                                                                                                                                                                                                                                                             55 HCGDPCC---TTCRHHPCPPGQGVQ-----SQGKFS------FGFQCIDCASG 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-creferences: GB:Li39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
C;Superfamily: unassigned EGF-related proteins; EGF homology
F;1239-1274/Domain: EGF homology <EGF1>
F;2488-2523/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                   50;
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                                                                                  Score 106; DB 2; Length 1797;
Pred. No. 0.2;
5; Mismatches 38; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 105.5; DB 2;
; Pred. No. 0.3;
11; Mismatches 40;
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26.8%;
                                                                                        14.9%;
29.5%;
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Matches 33; Conservative
                                                                                                              Best Local Similarity 29.5 Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            972 OFGDPSRPGACQ 983
                                                                                                                                                                                                                                                                                                                                                                                                                      94 TFSG-GHEGHCK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-2907 <ZHA>
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                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 CNC
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C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C; Accession A55677
R; Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattel, M.G.; Champliaud, M.F.; R; Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattel, M.G.; Champliaud, M.F.; A7Itle: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca A; Reference number: A55677; MUID:95213013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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A;Experimental source: clone T01B7
                                                                                                                                                               hypothetical protein T01B7.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Sate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24272
R:Sims, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 GCGGG----GCGCGCCCCR---PRCC------CCCRRCCTCCRT--CCCTRCCTCCR-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;410-467/Domain: laminin-type EGF-like homology <LEG03>
F;470-519/Domain: laminin-type EGF-like homology <LEG04>
F;470-519/Domain: laminin-type EGF-like homology <LEG04>
F;522-552/Domain: laminin-type EGF-like homology %LEG05>
F;783-88/Domain: laminin-type EGF-like homology <LEG05>
F;831-88/ADomain: laminin-type EGF-like homology <LEG05>
F;871-924/Domain: laminin-type EGF-like homology <LEG07>
F;927-962/Domain: laminin-type EGF-like homology <LEG09>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 164;
A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107; DB 2; Length 16
Pred. No. 0.035;
1; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:985-1034/Domain: laminin-type EGF-like homology <LEID>
F:1037-1091/Domain: laminin-type EGF-like homology <LEID>
F:1094-1139/Domain: laminin-type EGF-like homology <LEID>
                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1995
A;Reference number: 219867
A;Accession: T24272
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-164 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laminin beta-2 chain precursor (version 1) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;283-344/Domain: laminin-type EGF-like homology F;347-407/Domain: laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 PCCCGCGC-----GCGCCGCGGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 PCPPGQGVQSQGKFSFGFQCIDCASG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.0%;
Best Local Similarity 34.9%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: X79683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-1797 <WEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP:T01B7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues:
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õ g ò QQ 9,

C;Genetics: A;Gene: MEGF6

œ % Query Match
14.8%; Score 105; DB 2; Length 1574;
Best Local Similarity 28.8%; Pred. No. 0.22;
Matches 34; Conservative 8; Mismatches 36; Indels 40; Gaps QY

g ò

Search completed: September 4, 2001, 16:12:12 Job time: 1109 sec

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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287./LV' cRL>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A;Reference number: A46476; MUID:92105763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: sequence extracted from NCBÍ backbone (NCBIN:75206, NCBIP:75207)
A; Note: Ihis translation is not annotated in GenBank entry MUSCD40A, release 113.
R; Grimaldi, J. C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Co J. Immunol. 149, 3921-3926, 1992
J. Immunol. 149, 3921-3926, 1992
A; Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A; Reference number: A46515; MUID:93094586
A; Accession: A46515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      873 GFPNCRPCVCNGR-----ADECDAHTGACLGCRDYTGGEHCER----CI-AGFH-GD 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919 PRLPYGGOCRPCPEGPG--SQRHFATSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHF 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 PCCT---TCRHHPCPPGQGVQSQGKFS--------FGFQCIDCASGTF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GGPGCGP----GRLLLGTGTDARCCRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     977 GDPSKPGGRCQLCECSGNIDPTDPGACDPHTGQCLRCLHHTEGPHCGHCRP 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SGGHEGHCKP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B cell-associated surface molecule CD40, long splice form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 122; DB 1; Length 1801; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1562/Binding site: carbohydrate (
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: BALB/c, liver
A; Note: sequence extracted from NCBI backbone (NCBIP:120357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: For an alternative splice form, see PIR:A46515. C;Comment: For an alternative splice form, see PIR:A46476.
                                                                                                                                                                                                                                                                                                F;1041-1095/Domain: laminin-type EGF-like homology <LEI1>F;1098-1143/Domain: laminin-type EGF-like homology <LEI2>F;1146-1190/Domain: laminin-type EGF-like homology <LEI3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat homology
                                                                                                                            F:834-877/Domain: laminin-type EGF-like homology <LE07>F:880-927/Domain: laminin-type EGF-like homology <LE08>F:930-986/Domain: laminin-type EGF-like homology <LE09>F:989-1038/Domain: laminin-type EGF-like homology <LE10>
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                                                       laminin-type EGF-like homology <LE06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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A;Molecule type: mrs
A;Residues: 1-305 <TOR>
A;Residues: 1-305 <TOR>
A;Cross-references: GB:M83312; NID:g1553058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: CD27 antigen; NGF receptor
Keywords: alternative splicing; transmem
                                                                                                                                                                                                                                                                                                                                                                                                                         F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1446-1801/Region: heptad repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 17.2%;
1 Similarity 27.5%;
47; Conservative
                                                                                                   F;788-1196/Domain: III <DOM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <DOM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
137552
137552
137552
CX40 homolog - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: 13755
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Bur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment chromosomal chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laminin beta-2 chain precursor - rat
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Decies: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neurch A;Reference number: S03539; MUID:89159410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: interact with cells and with other basement membrane proteins to promote
                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g472957; PIDN:CAA53576.1; PID:g472958
                                                                                                                                                                       9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 59
                                                                                                                                                                                                                                                     48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;473-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
                                                                                                                                                                                                                                                                                                                                                                                           60 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 123.5; DB 2; Length
Pred. No. 0.0022;
5; Mismatches 60; Indels
                                                                                              41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA535
C;Superfamily: CD27 antigen; NGF receptor repeat homology
    DB 2;
    Score 135.5; DB 2
Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                      9; Mismatches
19.1%;
32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%;
31.5%;
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Matches 35; Conservative
                                                                                          Conservative
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A; Residues: 1-1801 <HUN>
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-277 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: 137552
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                                                                                      37;
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R;Stamenkovic, I;Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor recept A;Reference number: S04460; MUID:89356608
A;Molecule control of the nerve growth factor recept A;Reference number: S04460; MUID:89356608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 20q12-20q13.2
C; Superfamily: CD27 antigen: NGF receptor repeat homology
C; Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F; 1-20, Domain: signal sequence #status predicted <SIG>
F; 21-27, Product: B-cell activation protein CD40 #status experimental <MAT>
F; 21-193, Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851
R; Braesch Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 198
A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-A; Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell activation protein CD40 precursor - human
NiAlternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Species: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   870 GFPSCRP-----CVCNGHADECNTHTGACLGCRDHTGGEHCER----CI-AGF 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GGPGCGPGRLLLGTGTDARC-----CRVHTTRC--CRDYPGEECCSEWDCMCVQPEF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 HCGDPCCT---TCRHHPCPPGQGVQ-----SQGKFS------FGFQCIDCASG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:194-215/Domain: transmembrane #status predicted <TMM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         972 HFGDPSRPGGRCQLCECSGNIDPMDPDACDPHTGQCLRCLHHTEGPHCAHCKP 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SGGHEGHCKP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 112; DB 2; Length 1798;
Pred. No. 0.065;
5; Mismatches 35; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDC 109
                      F;783-828/Domain: laminin-type EGF-like homology <LED6>F;831-874/Domain: laminin-type EGF-like homology <LED7>F;877-924/Domain: laminin-type EGF-like homology <LED7>F;977-934/Domain: laminin-type EGF-like homology <LED8>F;927-983/Domain: laminin-type EGF-like homology <LED9>F;1038-1092/Domain: laminin-type EGF-like homology <LEID>F;1038-1140/Domain: laminin-type EGF-like homology <LEID>F;1043-1187/Domain: laminin-type EGF-like homology <LEID>F;1043-1187/Domain: laminin-type EGF-like homology <LEID>F;1043-1187/Domain: laminin-type EGF-like homology <LEID>F;1143-1187/Domain: laminin-type EGF-like homology <LEID>F;1143-1187/Domain: laminin-type EGF-like homology <LEID3>F;1143-1187/Domain: laminin-type EGF-like homology <LEID3>F;1143-1187/Domain: laminin-type EGF-like homology <LEID3>F;1143-1187/Domain: laminin-type EGF-like homology <LEID3>F;1143-1187/Domain: laminin-type EGF-like homology <LED3>F;1143-1187/Domain: laminin-type EGF-like <LED3-F;1143-1187/Domain: laminin-type EGF-like <LED3-F;1143-1187/Domain: laminin-type EGF-like <LED3-F;1143-1187/Domain: laminin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 108.5; DB 2; 29.4%; Pred. No. 0.037;
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A;Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%;
24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 29.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A60771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matrix Biol. 14, 489-497, 1994
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss
A;Reference number: 553869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                   ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-152 < WILL>
A; Residues: 1-152 < WILL>
A; Cross-references: EMBL:249886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:C06A1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laminin beta-2 chain precursor (version 2) - human
N.Alternate names: s-laminin
C.Species: Homo sapiens (man)
C.Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
C.Accession: §53869
                                                                                                                                                                                                                            62 CDSGEFSAQWNREIRC---HQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                   9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 63
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F;283-344/Domain: laminin-type EGF-like homology <LE01>
F;347-407/Domain: laminin-type EGF-like homology <LE02>
F;410-467/Domain: laminin-type EGF-like homology <LE03>
F;410-519/Domain: laminin-type EGF-like homology <LE03>
F;522-552/Domain: laminin-type EGF-like homology status atypical <LE05>
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A;Map position: 3p21.3-3p21.2
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 112; DB 2; Length 152;
Pred. No. 0.013;
0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSC 167
                                                                                                                                                                                                                                                                                                                                           64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDC 109
                                                                               Indels
0.0088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C06A1.6 - Caenorhabditis elegans
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, June 1995
A; Reference number: 219054
A; Accession: T18975
                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 PCCCGCGC-----GCGCCGCGGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone C06Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%;
illarity 34.9%;
Conservative
                                   ilarity 31.2%;
Conservative
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A; Residues: 1-1798 <IIV>
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Best Local Similarity
Matches 30; Conserv
                                       Best Local Similarity
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                                                                                   Matches
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GenCore version 4.5
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OM protein - protein search, using sw model

September Run on:

4, 2001, 16:12:11:; Search time 80.15 Seconds (without alignments) 108.346 Million cell updates/sec

US-09-512-363-2\_COPY\_26\_139 711

QRPTGGPGCGPGRLLLGTGT.......FSGGHEGHCKPWTDCTQFGF 114 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

pirl:\* pir2:\* pir3:\*

# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## MEGF6 protein - ra fibrillin-2 precur hypothetical prote laminin alpha 5 ch hypothetical prote laminin beta-2 cha B-cell activation lymphocyte activat 0x40 homolog - hum laminin beta-2 cha ypothetical prote aminin beta-2 cha ibrillin-2 precur atent transformin aminin beta-1 cha adhesive ligand ep .nsulin receptor-r cumor necrosis fac nsulin receptor-r agglutinin isolect ectin-B - Virgini -cell antigen 4-1 B cell-associated gene ox40 protein spidermal growth Notch B protein SUMMARIES \$12783 B32393 JC5559 I38426 I37552 MMRTS A46476 S53869 T13954 A54105 15651 10053 Query Match Length DB 540 1820 1786 435 1268 1203 212 644 644 1786 2907 1574 2918 3635 9999 996677 9999 94656 9999 9466 9999 9466 9999 9466 105.5 105 103.5 102.5 98 Score 140 138.5 135.5 123.5 116.5 112 112 108.5 Result No.

7;

Gaps

52;

RESULT 2 \$12783 OX40 antigen precursor - rat N;Alternate names: nerve growth factor receptor homolog

aminin beta-1 cha nsulin-like growt

126 CPPGHFSPGNNQACKPWTNCTLSG 149

CASGTFSGGHEGHCKPWTDCTQFG 113

90

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apolipoprotein E r insulin-like growt MFGF8 profesin - hu	orgelin - mouse agglutinin isolect intrinsic factor-B	epidermal growth f latent transformin tenasoln-x precurs ultra high-sulfur	lectin precursor - probable tenascin hypothetical prote Doc4 protein, stre	high sulfur protei cartilage oligomer
JE0237 A33837	142214 A28401 T08618	A53183 A57293 A40701 S18946	LNR2 T09070 T26972 T14271	JC6547 A44315
999	000	2211	- 0 0 0	0 0
996 1371	2910 186 3623	1210 1251 3566 169	227 4006 1111 2825	188 755
13.0	12.9 12.9 12.9	12.7	12.7	12.5 12.5
92.5	91.5 91.5	90.5 90.5 90.5	90 90 99.5	6 8 6 8
30 31	1 E E E	3 8 3 4 6 3 8 4 6	4 4 4 0 1 2 6	44

## ALIGNMENTS

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Grand ox40 protein - mouse

N.Alternate names: Ox40 antigen
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C.Accession: I48700; I48334; S34377
E.Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
J. Inmunol. 151, 5261-5271, 1993
A.Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-272 <RES>
A; Cross-references: EMBL:221674; NID:9312827; PIDN:CAA79772.1; PID:9312828
A; Cross-references: EMBL:221674; NID:912827; D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A; Reference number: 148334; MUID:95255413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GFYNEAVNYDICKOCTOCNHRSGSELKONCTPIODIVCRCRPGTOPRODSGYKLGVDCVP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CPPGQGVQSQGKFSFGFQCID 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 272;
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 20.1%; Score 143; DB 2; Local Similarity 27.8%; Pred. No. 5.7e-05; nes 40; Conservative 8; Mismatches 44;
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                     A; Accession: I48700
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Best Local S
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A; Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Ph A; Reference number: JC5559; MUID:97290889
A; Accession: JC5559
A; Molecule type: protein
A; Residues: 1-295 < YAM>A; Residues: 1-295 < YAM>A; Experimental source: root
C; Comment: This protein is a lectin specific for N-acetylgucosamine-containing saccha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment: This protein is a lectin specific for N-acetylgucosamine-containing saccha; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocyte activation-induced receptor ILA precursor - human C;Species: Homo sapiens (man) C;Date: 29-May-1998 #text_change Ol-Dec-2000 C;Dates: 29-May-1998 #text_change Ol-Dec-2000 C;Accession: I38426; JT0752 Erevision 29-May-1998 #text_change Ol-Dec-2000 Erevision, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, Eur. J. Immunol. 24, 2219-2227, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Molecular and biological characterization of human 4-1BB and its ligand. A;Reference number: 138426; MUID:94374434
                                                                                                                                                                                                                                                                        C;Species: Phytolacca americana (Virginian pokeweed)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U03397; NID:9571320; PIDN:AAA53133.1; PID:9571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 295;
                                                                     102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDG 143
                                                                                                                                                                                                                                                                                                                                    C; Accession: JC5559
R; Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                          65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 CRHHPCPPGQGVQSQGKFSFGFQ-C---IDCASGTFSGGHEGHC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-255 <RES>
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C:Special antigen 4-1BB precursor - mouse
C:Special antigen 4-1BB precursor - mouse
C:Special antigen 4-1BB precursor - mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
R:Roor, B.S.; Weissman, S.M. 86, 1963-1967, 1989
R:Roor, Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: Capanic of two inducible T-cell genes.
A;Reference number: A32393; MUID:99184547
A;References: GB:J04492; NID:9201121; PIDN:AAA40167.1; PID:9201122
A;Cross-references: GB:J04492; NID:9201121; PIDN:AAA40167.1; PID:9201122
A;Cross-references: GB:J04492; NID:94179805
A;Reference number: 148879; MUID:94179805
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC Ox40 antigen of activated CD4 positive T ly
A;Reference number: S12783; MUID:90214614
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 AAMLA
A;Residues: 1-271 AAMLA
A;Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted ASMT>
F;20-271/Froduct: Ox40 antigen #status predicted ATM>
F;211-235/Domain: transmembrane #status predicted <TMM>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ORPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----- 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
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C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Reywords: transmembrane protein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-256/Product: 4-1BB protein #status predicted <MAT>
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; Pred. No. 9.6e-05;
15; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 141; DB 2;
Pred. No. 8.3e-05;
9; Mismatches 53
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32.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: BASAL MEMBRANE OF THE UPPER ALIMENTARY TRACT AND URINARY AND NASAL EPITHELIA, SALIVARY GLANDS AND TEETH (BOTH VARIANTS). ISOFORM A IS PREDOMINANTLY EXPRESSED IN SKIN, HAIR FOLLICLES AND DEVELOPING NEURONS OF THE TRIGEMINAL GANGLION. ISOFORM B WAS FOUND IN BRONCHI, ALVEOLI, STOMACH, INTESTINAL CRYPTS, WHISKER PADS, CNS, TELENCEPHALIC NEUROECTOBEM, THALAMUS, BATHKE'S POUCH, AND PERLYENTRICULAR SUBERENDYMAL GERMINAL LAYER. DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
SEQUENCE FROM N.A.
STRAIN-BALBAC; TISSUE-Lung;
STRAIN-BALBAC; TISSUE-Lung;
BEDLINE-95394948; PubMed-7655604;
Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
"Cloning and complete primary structure of the mouse laminin alpha 3 chain. Distinct expression pattern of the laminin alpha 38 phain isoforms.";
3B chain isoforms.";
J. Biol. Chem. 270:21820-21826(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANES (MAJOR COMPONENT).
ALTERNATIVE FRODUCTS: THE TWO ISOFORMS A AND B, WHICH DIFFER IN THEIR N-TERMINAL ARE DERIVED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF THE LARGER ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE ALPHA HELICAL DOMAINS I AND II ARE THOUGHT TO INW WITH OTHER LAMININ CHAINS TO FORM A COILED COLL STRUCTURE. DOMAIN: DOMAINS IV AND G ARE GLOBULAR.
SIMILARITY: CONTAINS 6.5 LAMININ BGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV' IS NOT SIMILARITY: CONTAINS 1 LAMININ GOMAIN IV (DOMAIN IV' IS NOT SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                           Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.
Meneguzzi G.;
                                                                                                                                                                                                                                                Aberdam D., Galliano M.-F., Mattel M.-G., Pisani-Spadafora A., Ortonne J.-P., Meneguzzi G.; "Assignment of mouse nicein genes to chromosomes 1 and 18."; Mamm. Genome 5:229-233(1994).
                                                                                                                                                     Aberdam D.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           TISSUE-Lung;
MEDLINE-94363405; PubMed-8081888;
                                                                                                                                                                                                                  TISSUE-Lung;
MEDLINE-94281750; Pubmed-8012114;
MEDLINE-94281750; Pubmed-8012114;
                                                                                                                                                                                                     SEQUENCE OF 1052-1770 FROM N.A.
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1052-1770 FROM N.A.
                                                                                                                                        REVISIONS.
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LAMININ DOMAIN IV (DOMAIN IV A).
3 X LAMININ EGF-LIKE REPEATS (DOMAIN III
                                                                                Pfam; PF00052; laminin_B; 1.
Pfam; PF00053; laminin_EGF; 4.
Pfam; PF00054; laminin_G; 3.
PROSITE; PS00025; EGF_1; 4.
PROSITE; PS01248; LAMININ_TYPE_EGF; 4.
PROSITE; PS01248; LAMININ_TYPE_EGF; 4.
Calycoprotein; Basement membrane; Extracellular matrix; Coiled coll; Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
Alternative splicing.
                                                                                                                                                                                                                                                                         LAMININ EGF-LIKE 4 (C-TERMINAL).
LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 7 (INCOMPLETE).
DOMAIN II AND I (HEPTAT REPEATS).
5 X LAMININ G-LIKE 1.
LAMININ G-LIKE 1.
                                                                                                                                                                                                                                                                                                                                 LAMININ G-LIKE 1.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
CALLED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                               LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4 (N-TERMINAL).
                                                                                                                                                                                               DOMAIN III B.
3.5 X LAMININ EGF-LIKE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                               LAMININ ALPHA-3 CHAIN
        . . .
     EMBL; X84014; CAA58837.1;
EMBL; X84013; CAA58836.1;
EMBL; L20478; AAA68091.1;
HSSP; P02468; ITLE.
MGD; MGI:99909; Lama3.
InterPro; IPR00034;
InterPro; IPR000561;
InterPro; IPR002049;
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DOMAIN
  10;
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN ISOPORM A).
MISSING (IN ISOPORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHLVEMCACPPDYTGDSC -> MLPAVRWSAWSTGWLWIFG
                                                                                                    AALGOCLGYGSEQQRVAFLQRPSQNHLQASYMELRPS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANES (MAJOR COMPONENT).
TISSUE SPECIFICITY: IN ADULT, HIGH LEVELS IN HEART, LUNG, AND
KIDNEY; LOWER IN BRAIN, MUSCLE AND TESTIS; VERY LOW IN LIVER, GUT
                                                                                                                                                                                            864 RLTLGEVGLEEASDTGSGPRAHLVEMCACPPDYTGDSCOGCRPGYYWDNKSLPVGRCVPC 923
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CSTRAIN-CSTRAIN-6X TEASUB-Lung;
STRAIN-CSTRAIN-6X TEASUB-149334;
MIDDILINE-96081906; PubMed-7499334;
Miner J.H., Lewis R.M., Sanes J.R.;
"Molecular cloning of a novel laminin chain, alpha 5, and widespread expression in adult mouse tissues.";
J. Biol. Chem. 270:28523-28526(1995).
                                                                                                                                                             Gaps
                                                                                                                                                                            13 RLLLG------TGTDARCCRVHTTRCCRDYPGEEC--CSE---WD-----C 47
                                                                                                                                                                                                            .----- PCP----- 70
                                                                                                                                                                                                                                                      71 -PGQGVQSQGKFSF-GFQCIDCASGTF-----SGGHEGHCKPWT-DC 109
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                            81;
                                                                                                                                            Score 99.5; DB 1; Length 2569; Pred. No. 0.086;
                                                                                                                                                           47; Indels
                                                                                                                   40D4306BEF340DBC CRC64
                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
LAMININ ALPHA-5 CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                     PRT; 3635 AA
                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                            48 MCVQPEFHC -- GDPCCTTCRHH----------
                                                                                                          ISOFORM A)
                                                                                                                                           14.08;
24.78;
                                                                                                                    2569 AA; 282159
                                                                                                                                                   Best_Local Similarity 24.7
Matches 44; Conservative
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1986
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Q61001:
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VARSPLIC
VARSPLIC
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AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.

-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COLLED COIL STRUCTURE.
-1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
-1- SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-1- SIMILARITY: CONTAINS 21.5 LAMININ BGF-LIKE DOMAINS.
-1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
-1- SIMILARITY: ALPHA-5 CHAIN IS MORE RELATED TO DROSOPHILA ALPHA CHAIN THAN TO MAMMALIAN ALPHA CHAINS 1-4.
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LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE REPEATS (DOMAIN IT 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAMININ N-TERMINAL (DOMAIN VI).
10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOMAIN IV A).
KE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Basement membrane; Extracellular matrix; Coiled coll; Laminin EGF-like domain; Cell adhesion; Repeat.

NON_TER 1 1 1 LAMININ N-TERMINAL (DOMAIN VI).
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LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 15.
LAMININ DOMAIN IV 2 (DOMAIN IV A).
6.5 X LAMININ EGF-LIKE 16 (C-TERMINAL).
LAMININ EGF-LIKE 17.
LAMININ EGF-LIKE 17.
LAMININ EGF-LIKE 17.
LAMININ EGF-LIKE 17.
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N EGF-LIKE 19.
N EGF-LIKE 20.
N EGF-LIKE 21.
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LAMININ EGF-LIKE 20
LAMININ EGF-LIKE 21
LAMININ EGF-LIKE 21
LAMININ EGF-LIKE 22
DOMAIN II AND I.
5 X LAMININ G-LIKE
LAMININ G-LIKE
LAMININ G-LIKE 2.
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InterPro: IPR002049; -.
Pfam; PF00052; laminin_B; 1.
Pfam; PF00053; laminin_B; 1.
Pfam; PF00054; laminin_G; 2.
Pfam; PF00055; laminin_Nerm; 1.
PROSITE; PS00022; EGF_1; 19.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U37501; AAC53430.1; -. HSSP; P02468; 1TLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:105382; Lama5.
InterPro; IPR000034; -.
InterPro; IPR000561; -.
InterPro; IPR001791; -.
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Nature 352:330-334(1991)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...) (1
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RA MEDILINE-9415110; bubwed-1870105;

Zhang H. Apfeltrone S. D., Hu W. Davis E.C., Sanguinet C.,

Zhang H. Apfeltrone S. D., Hu W. Davis E.C., Sanguinet C.,

Zhang H. Apfeltrone S. D., Hu W. Davis E.C., Sanguinet C.,

R. Danddo J. Wecham R.P. Manies F. E.

R. J. Call Bill. 124.85-691(1994).

R. MEDILINE-90194557; bubwed-185206;

R. MEDILINE-90194559; bubwed-185206;

R. MEDILINE-90195959; bubwed-185206;

R. MEDILINE-901945959; bubwed-185206;

R. MEDILINE-90194957; bubwed-185206;

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R. MEDILINE-90194969; bubwed-185206;

R. MEDILINE-90194969; bubwed-185206;

R. MEDILINE-901949; bubwed-185206;

R. MEDILINE-901949;
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æ ---QC-ID---CASG---TFSGGHE 100 ---RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG :|| :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| EPC------QPCPAKNSAEFHGLCSSGVGITVDGRDINECALDPDICANGICENLRGSYR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1] Length 2911; 

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DD.  12.  13.  14.43.  16.1um-binding; Glycoprotein; EGF-like domain; potentia.  17.443.  18.43.  19.1um-binding; Glycoprotein; EGF-like domain; potentia.  19.1um-binding.  10.1um-binding.	EGF-LIKE 9, TGFP-1X: TGFP-1X: TGFP-1X: TGFP-1X: TGFP-1X: TGFP-1X: TGF-LIKE 13 EGF-LIKE 14 TGF-LIKE 15 EGF-LIKE 25 EGF-LIKE 27 EGF-LIKE 27 EGF-LIKE 27 EGF-LIKE 27 EGF-LIKE 27 EGF-LIKE 31 EGF-LIKE 41	BY S1
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 -i- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_LGF; 13.
PRINTS; PR00011; EGFLAMININ.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
LAMININ EGF-LIKE 5 (INCOMPLETE).
BANININ DOMAIN IV.
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LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 11.
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EMBL; Z68156; CAA92279.1; JOINED.
EMBL; X79683; CAA56130.1; -.
EMBL; S77512; AAB34682.2; -.
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   THE HUMBEL TABLILLIA DELGA. CHAIRIN (S-IGHILID): SLUCLURE, SEPPESSION IN FETAL LISSUES and Chromosomal assignment of the LAMBE gene.";

MATLIX BIOL. 14:489-497(1995).

-!-FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING MITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-!- SUBGUIT: LAMININ IS A COMPLEX GLAVORPOTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

--- COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

--- THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ), LAMININ-4

--- SUBCELLULAR LOCATION: EXTRACELLULAR.

--- SUBCELLULAR LOCATION: EXTRACELLULAR.

--- TISSUES SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT). S-LAMININ IS CONCENFRATED IN THE SYNAPTIC

--- DOMAIN: THE ALPHA HELICAL DOMAINS I AND '11 ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COLL STRUCTURE.

--- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

--- SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilvanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
Sariola H., Tryggvason K.;
"The human laminin beta 2 chain (S-laminin): structure, expression in
                                                                                                                                                                                                                                                                                                     58 DPCCTTCRHHPCPPGQGVQSQGKFSFGF------QC-ID---CASG---TFSGGHE 100
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                9 CGPGRLLLGTGTDARCC-----RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG 57
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=9213013; PubMed=7698745;
WEDLINE=9213013; PubMed=7698745;
Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G., Champliaud M.F., Burgeson R.E., Albrechtsen R.;
"Human beta 2 chain of laminin (formerly S chain): cDNA cloning, chromosomal localization, and expression in carcinomas.";
Genonics 24:33-252(1994).
                                                                                                                                                                                               39;
                                                                                                                                                            Length 2907;
                                                                                                                                                                                               Indels
                                                                                                                                                                                               40;
                                                                                                                                                            DB 1;
                                                                                                                                                          Score 105.5; DB Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).
                              SIMILARITY.
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01-007-1996 (Rel. 34, Created)
10-007-1996 (Rel. 34, Last seno
01-007-2000 (Rel. 40, Last and
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/C: TISSUE-Liver;
MEDLINE-93094586; Pubmed-1281194;
Grimaldd J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
"Genomic structure and chromosomal mapping of the murine CD40 gene.";
                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .) (POTENTIAL)
                                                                                                    MEDLINE-92105763; PubMed-1370315;
TOTRES R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA
species of murine CD40 upon B lymphocyte activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROMITY PS00652: TWER_NGFR_1; 1.
PROSITE; PS0050; TWFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
STGNAL, 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 149:3921-3926(1992).
-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
                                                                                                                                                                                                        STRAIN-BALB/C;
Torres R.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                Immunol. 148:620-626(1992).
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InterPro; IPR001368; -.
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RSF5 OR CD40. musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A46476; A46476.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145
153
289 AA;
                                                                                      SEQUENCE FROM N.A.
                                                        NCBI_TaxID=10090;
                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CGKGEFLSTWNREKYC---HEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQ-HCTSHTCE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 62
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                               Immunology 90:294-300(1997).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-97281523; PubMed-9135560; Hirano A., Brown W.C., Estes D.M.; "Cloning, expression and biological function of the bovine CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 TCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 269;
                                                                                                                                                                                                                                                                                                                      homologue: role in B-lymphocyte growth and differentiation
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  746903F30F95F387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110.5; DB 1;
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD40L RECEPTOR.
                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 X TNFR-CYS.
                                                                                269
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TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GI
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                                                                                                          (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 38, Last anno
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29.8%;
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                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193
215
>269
187
                                                                                                                                                                 TNFRSF5 OR CD40.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
269
269 AA;
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                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                         01-NOV-1997
01-NOV-1997
                                                                               CD40_BOVIN
Q28203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
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CARBOHYD
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SEQUENCE
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                                                                  CD40_BOVIN
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5

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Gaps

11;

58; Indels

16.4%; Score 116.5; DB 1 31.2%; Pred. No. 0.00048; tive 6; Mismatches 58

1 Similarity 31.2%; 34; Conservative

Query Match Best Local

Matches

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DB 1; Length 289;

CDSGEFSAQWNREIRC---HQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118

64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDC 109

9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 63

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98266353; PubMed-905317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Zheng J., Naismith J.H., Thomas D.;
The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
I- SIMELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
I- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
I- SIMILARITY: CONTAINS A LA-NGER/TNEF TYPE CYSTEINE-RICH REGION.
I- DATABASE: NAME-PROW: NOTE-CD guide CD40 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
TUMOR NECROSIS FACTOR RECEPTOR 5).
                                                                                                                                                                                                                                                                                                    model of
                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nin, Projection (PRO) (1988) -. Pfam: PF00020; TWFR_c6; 4. PROSITE; PS00652; TWFR_NGFR_1; 1. PROSITE; PS50050; TWFR_NGFR_2; 4. Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                 "Construction and analysis of a detailed three-dimensional m
the ligand binding domain of the human B cell receptor CD40.
Proteins 27:59-70(1997).
                                                                                                                                                                                                       Stamenkovic I., Clark E.A., Seed B.;

*A B-Inmphocyte activation molecule related to the nerve factor receptor and induced by cytokines in carcinomas.";

EMBO J. 8:14003-1410(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD40L RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                     [3]
3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                 277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                              MEDLINE=89356608; PubMed=2475341;
                                                                                                                                                                                                                                                                3D-STRUCTURE MODELING OF 24-144.
MEDLINE=97189482; PubMed=9037712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60592; CAA43045.1; -.
                                STANDARD;
                                                                                                                                                                                                                                                                                      Bajorath J., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
277
193
215
215
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277
187
60
60
103
1187
37
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MIM; 109535; -.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=9606;
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20
20
216
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25
61
104
145
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SIGNAL
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                              CD40_HUMAN P25942;
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TRANSMEM
DOMAIN
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILIN-1-CONTAINING MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.

-I- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118
                                                                                                                                                                                                                                                                                                                                                                                   11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         9 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95263670; PubMed-7744963;
Zhang H., Hu W., Ramirez F.;
"Developmental expression of fibrillin genes suggests heterogeneity of extracellular microfibrils.";
J. Cell Biol. 129:1165-1176(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 210-317 FROM N.A.
MEDLINE-94140368; PubMed-8307578;
Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
Francke U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Fibrillin genes map to regions of conserved mouse/human synteny on mouse chromosomes 2 and 18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                                                                                                                                        15.3%; Score 108.5; DB 1; Length 277; 29.4%; Pred. No. 0.0025; Live 8; Mismatches 58; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: CONTAINS. 7 TGF-BETA BINDING PROTEIN DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FENZ_MOUSE STANDARD; PRT; 2907 AA. 061555; Q63957; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) FIBRILLIN 2 PRECURSOR.
                                                                                                                                                                                                                                               MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L39790; AAA74908.1; -. EMBL; S69359; AAC60685.1; -.
51
77
77
1103
1119
1116
1143
1153
30619
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                                                                                                                                                                                                                                                                                                                              Query Match 15.39
Best Local Similarity 29.49
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:95490; Fbn2.
InterPro; IPR000152; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
38
41
62
83
105
111
125
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180
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DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                               SEQUENCE
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10;

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NOAKES P.G., GAUTAM M., MUDD J., Sanes J.R., Merlie J.P.;
"Aberrant differentiation of neuromuscular junctions in mice lacking
s-laminin/laminin beta 2.";
Nature 374.258-262(1995).
-I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONE DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-I- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
NERVE TERMINALS.
-I- SUBBUIT: LAMININ-1S A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALCHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
                                                                                                                                                                                                                                                          919 PRLPYGGQCRPCPCPEGPG--SQRHFATSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHF 976
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Lung;
MEDLINE-94319092; PubMed-8043859;
Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
"S-laminin gene (Lams) maps to Fl band of mouse chromosome 9.";
Mamm. Genome 5:393-394(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129.75;
MEDLINE-962760; PubMed-8662701;
MEDLINE-96210 B., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
Albrechtsen R., Wewer U.M.;
Structural organization of the human and mouse laminin beta2 chain
genes, and alternative splicing at the 5' end of the human
transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                    5 GGPGCGP----GRLLLGTGTDARCCRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGD
                                                                                                                                                                                                                                            ------FGFQCIDCASGTF
             (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
CRC64;
    (POTENTIAL)
                                                                                                                                                         86;
                                                                                                                                                                                                                                                                                                                   977 GDPSKPGGRCQLCECSGNIDPTDPGACDPHTGQCLRCLHHTEGPHCGHCKP 1027
                                                                                                                           Score 122; DB 1; Length 1801; Pred. No. 0.0006; 3; Mismatches 35; Indels 80
                                                                                                                                                                                                                                                                                                   -----SGGHEGHCKP 105
 N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (MKN)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                            59 PCCT---TCRHHPCPPGQGVQSQGKFS----TCRHHPCPPGQGVQSQGKFS------
                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1799 AA
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MEDLINE-95191650; PubMed-7885444;
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ID LMB2_MOUSE STANDARD; E

AC 061292; 062182;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last seq

DT 15-JUL-1999 (Rel. 38, Last annoverset)
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LAMININ EGF-LIKE 5 (INCOMPLETE).
R X LAMININ EGF-LIKE REPEATS (DOMAIN II).
 LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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RESULT 8
CD40_MOUSE
TD CD40_MOUSE STANDARD; PRT; 289 AA.

D CD40_MOUSE STANDARD; PRT; 289 AA.

D 27512;
DT 01-AUG-1992 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DF CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (RP50) (CDW40).
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                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Pram; PF00053; laminin_EGF; 13.
Pram; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
PROSITE; PS01022; EGF_1, 10.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
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LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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EMBL; U4C824; AAC53535.1; JOINED.
EMBL; X75528; CAA53532.1; -.
HSSP; P02468; IKLO.
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InterPro; IPR000561; -.
InterPro; IPR001886; -.
InterPro; IPR002049; -.
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MEDLINE-94085794; PubMed-8262389;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G., "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                47 CPPSTFSSIGGQPNCNICRV----CAGYFRFKKFCSSTHNAECECIE-GFHCLGPQCTRC 101
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           9 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 64
                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-02-1995 (Rel. 31, Last sequence update)
01-02-2000 (Rel. 40, Last annotation update)
4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
(T-CELL ANTIGEN ILA) (CDI37 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 -EKDCRPGQELTKQG------CKTCSLGTFNDQNGTGVCRPWTNCSLDG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                      41; Indels
                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                          EMBL; U02567; AAA93113.1; -.
PIR; B32393; B32393.
HSSP; P25942; LCDF.
MGD; MGI:1101059; Thfrsf9.
InterPro; IPR001368; -.
Pfam; PF00020; TNFR_G6; 1.
PROSITE; PS00652; TNFR_NGF_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NGG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                          4-1BB LIGAND RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                              19.7%; Score 140; DB 1; 32.7%; Pred. No. 3.3e-06; Live 15; Mismatches 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Immunol. 24:2219-2227(1994)
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MEDLINE-94374434; PubMed-8088337;
                                                                                                                                                                                                                                                                                                                                                27598 MW;
                                                                                                 EMBL; J04492; AAA40167.1; -.
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Matches 36; Conserv
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                        member of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA
                                                                                                                                                                                                                                                                                                                                                     "Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (POTENTIAL)
LINKED (GLCNAC. . .) (POTENTIAL)
F3A563FE5EF00460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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                                                                                                                                                                                                                                                                                     Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.1%; Score 135.5; DB 1; Length 255; 32.5%; Pred. No. 8.3e-06;
Schwarz H., Tuckwell J., Lotz M.;
"A receptor induced by lymphocyte activation (ILA): a new me
the human nerve-growth-factor/tumor-necrosis-factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- DATABASE: NAME-PROW; NOTE-CD guide CDw137 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm"
                                                                                                                                                                                          Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; buzzou;
Interpro; IPR001368; -.
Pram; PF00020; TURR_C6; 2.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-1BB LIGAND RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
N-LINKED (GLCN/
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                                                                                                                                                                                                                                                               TISSUE-Blood;
MEDLINE-95347766; Pubmed-7622190;
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
255
213
2213
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149
                                                                                          Gene 134:295-298(1993)
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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187
214
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255 2
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REVISION TO 107
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                                                                                                                                                                    Schwarz H.;
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46 CRP----GNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCT 100

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                                                                                                                                                                                                                                                                                                     MEDLINE=94170844; PubMed=7510240; MEDLINE=94170844; PubMed=7510240; Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.; "The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen."; Eur. J. Immunol. 24:677-683(1994).
                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                        ol-nuy-1995 (Rel. 32, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECUESOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_2; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS. TNFR-CYS.
277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X75962; CAA53576.1; -.
EMBL; S76792; AAB33944.1; ALT_INIT.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-95219871; Pubmed-7704935;
            P43489; 013663;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
01-OCT-2000 (Rel. 40, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29340 MW;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001368;
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160
277 AA;
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REPEAT
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THE ADMINIT: LAMININ IS A COMPURED.

C. 1. SUBUNIT: LAMININ IS A COMPURED.

C. TO EACH OTHER BY LOSULEIDE GALAN, BETA, GAMMA), WHICH ARE BOUND

C. TO EACH OTHER BY DISULEIDE BONDS INTO A GROSS-SHARED MOLECULE

COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

THE BETA-2 CHAIN IS SUBUNIT OF LAMININ-3 (S-LAMININ-4

C. S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

C. I- SUBCELLULAR LOCATION: EXTRACELLULAR.

C. I- SUBCELLULAR LOCATION: EXTRACELLULAR.

C. CALET OF THE NUSTROWISCULAR JUNCTION.

C. CLET OF THE NUSTROWISCULAR JUNCTION.

C. I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT

WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

C. I- DOMAIN: DOMAINS VI AMD IV ARE GLOBULAR.

C. I- SIMILARITY: CONTAINS 1.2.5 LAMININ DOMAIN (DOMAIN VI).

C. I- SIMILARITY: CONTAINS 1.1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;

"A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";

Nature 338.229-234(1989).

-I. FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DUBING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00053; laminin_BGF; 13.
Pfam; PF00055; laminin_LBGF; 13.
Pfam; PF00055; laminin_LBGF; 13.
PRINTS; PR0001; EGFLANIN.
PROSITE; PS00186; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01186; LAMININ_TYPE_EGF; 12.
PROSITE; PS01146; LAMININ_TYPE_EGF; 12.
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UDL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
  63 TCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFG 113
                        101 ATQDTVCRCRAGTQPLDSYRPGVDCAPCPPGHFSPGDNQACKPWTNCTLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAMININ BETA-2 CHAIN.
                                                                                                                                                  PRT; 1801 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89159410; PubMed-2922051;
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                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P02468; 1KLO.
InterPro; IPR000561; -.
InterPro; IPR001886; -.
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116
                                                                                                                                                LMB2_RAT
P15800;
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                                                                                                                              LMB2_RAT
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4

60; Indels 11; Gaps

CGPGRLLLGTGTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQPEFHCGD----PCCT 62

/ Match 17.4%; Score 123.5; DB 1; Length 277; Local Similarity 31.5%; Pred. No. 0.00011; nes 35; Conservative 5; Mismatches 60; Indels 11

Query Match

Best Loca Matches

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September Run on:

4, 2001, 16:15:22; Search time 43.78 Seconds (without alignments) 89.199 Million cell updates/sec

US-09-512-363-2\_COPY\_26\_139
711
QRPTGGPGGCPGRLLLGTGT......FSGGHEGHCKPWTDCTQFGF 114 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	L mus	P15725 rattus norv		Q07011 homo sapien	homo	rattu	Q61292 mus musculu	P27512 mus musculu		homo	mus m	homo	homod	mus n		Q16787 homo sapien	rattn	рошо	homo	homod	horde	_			Q95209 o sortilin-		рошо	1 homo s	oryza		P35444 rattus norv	drosophil	P10968 triticum ae
SUMMARIES	ID	OX40_MOUSE	OX40_RAT	41BB_MOUSE	41BB_HUMAN	OX40_HUMAN	LMB2_RAT	LMB2_MOUSE	CD40_MOUSE	CD40_BOVIN	CD40_HUMAN	FBN2_MOUSE	LMB2_HUMAN	FBN2_HUMAN	LMA3_MOUSE	LMA5_MOUSE	LMA3_HUMAN	IRR_RAT	LMB1_HUMAN	TNRC_HUMAN	IRR_HUMAN	AGI_HORVU	LMB1_MOUSE	IGIR_RAT	AGI3_WHEAT	SORL_RABIT	EGFR_MOUSE	TENX_HUMAN	KRUA_HUMAN	AGI_ORYSA	MCS_HUMAN	COMP_RAT	ITBX_DROME	AGI1_WHEAT
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ď	Query Match	20	σ	σ	φ.	7	7	16.5	ė.	S.	'n.	4.	4	4	4.	<u>.</u>	٠ ش	e,					٠	•	12.	12.	12.	12.	12.	12.	12.	-	12.	-
	Score	H	141	140	135.5	123.5	122	117	116.5	110.5	108.5	105.5	104	103.5	99.5	σ	7	9	95.5	4	マ	ς.	<u>.</u>	92.5	-	91	90.5	90.5	90	90	80	83	68	88.5
	Result No.	ч	7	m	4	S	9	7	80	o i	. 10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33

P98167 bos taurus P37889 mus musculu P08069 homo sapien P10040 drosophila P47798 drosophila P31695 mus musculu P98133 bos taurus P35555 homo sapien P20333 homo sapien P2033 homo sapien P22034 homo sapien Q05895 mus musculu P22064 homo sapien	S	RESULT 1  OX40_MOUSE STANDARD; PRT: 272 AA.  AC 47741.  OX40_MOUSE STANDARD; PRT: 272 AA.  AC 47741.  O1-TERB 1996 (Rel. 33, Created)  DT 01-TERB 1996 (Rel. 34) Created)  DT 01-TERB 1996 (Rel. 36) Last sequence update)  SERVINGER OF TAXEN DE CONTROL OR OX40.  AND MINISTRA CREEPTOR PRECUPENS (OX40 ANTIGEN).  THERST OCT 2000 (Rel. 36) Last sequence update)  SEQUENCE FOR WAS DEADLY OR OX40.  AND MINISTRA CREEPTOR PRECUPENS (OX40 ANTIGEN).  AND MINISTRA CREATED OR OX40.  AND MINISTRA CREATED OX OX40.  AND MINISTRA CREATED OX OX40.  AND MINISTRA CREATED OX OX40.  AND MINISTRA CREATED OX40.  AND MINISTRA
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SSPO_BOVIN FBL2_MOUSE IGIR_HUMAN GSTC_BOROME STC_DROME NTC4_MOUSE FBN1_BOVIN FBN1_BOVIN TNR2_HUMAN TSP3_MOUSE TGFB_HUMAN	ALIG	PRT;  () ) () ) () () () () () () () () () (
		Star See to Cotton of Cott
867 1367 2139 11106 1106 12871 2871 4671 956 1394 2215		DARD;  13, Cr.  133, Car.  140, Lau.  140, Lau.  1527;  11-527;  1
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44444444444444444444444444444444444444		RESULT 1  OX40_MOUSE  DO OX40_MOUSE  DO OX40_C  DT 01-FEB  DX 040_C  MAMMADIN  NO NCBL_T  RN NCBL_T  RN SEQUEN  RX Calder  RY Gene  RY R
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                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90214614; PubMed-2157591;
Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive I Jumphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                      14 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC------HPCET 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 -----CTTCRHHP-----CTTCRHD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 3:1003-12004(1530).
-I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                            . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                 52;
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PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                  Score 143; DB 1; Length 272;
Pred. No. 1.8e-06;
8; Mismatches 44; Indels
                                                                                                                                                                                                    A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE)
TNFR-CYS 4.
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (0X40 ANTIGEN) (MRC 0X40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 CPPGHFSPGNNQACKPWTNCTLSG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 CASGIFSGGHEGHCKPWIDCTQFG 113
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27.8%;
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30153
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103
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InterPro; IPR001368;
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Best Local Similarity
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01-APR-1990
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P15725;
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CONFLICT
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  DOMAIN
DOMAIN
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REPEAT
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-i- TISSUE SPECTFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
-i- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                      59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL 118
                                                                                                                                                                                                                                                              1 ORPIGGPGCGPGKLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----- 46
                                                                                                                                                                                                                                                                                        6 QOPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV 58
                                                                                                                                                                                                                                                                                                                         -----PCPPGQGVQSQGKFSF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVE DURING T CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Immunol. 150:771-781(1993).
-1- FUNGTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.; Genomic organization and chromosomal localization of the T-cell
                                                                                                                                      -LINKED (GLCNAC. . .) (POTENTIAL). C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Inducible T cell antigen 4-1BB. Analysis of expression and
                                                                                                                                                                                                 Length 271;
                                                                                                                                                                                                  Score 141; DB 1; Length 27
Pred. No. 2.8e-06;
9; Mismatches 53; Indels
OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB)
TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
                                                                                                        TNFR-CYS 3 (INCOMPLETE). TNFR-CYS 4.
                                          CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION, AND SEQUENCE OF 25-29.
MEDLINE-93139510; Pubmed-7678621;
                                                                                                                                                                                                                                                                                                                                                                                    84 GFQCIDCASGIFSGGHEGHCKPWIDCTQFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                  119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSG 148
                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                         47 CMCVQPEFHCG----DPC--CTTCRHH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C;
MEDLINE-94179805; PubMed-8133039;
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MEDLINE=89184547; PubMed=2784565;
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29895 MW;
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ilarity 29.3%;
Conservative 9
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 271
210
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271
164
60
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123
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                                                                                                                                                                                                 Query Match
Best Local S:
Matches 44;
 CHAIN
DOMAIN
TRANSMEM
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197 INNEYNYRCWT--TNRCQKMCPSVCGKRACTE-NNECCHPE--CLGSCHTPDDNTTCVAC 251
                                               130 PWTDCTQFGFLTVFPGNKTHNAVCVPGSPP 159
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Search completed: September 4, 2001, 16:12:16 Job time: 1113 sec

304 -MQECPS-GFIR----NSTQSMYCIPCEGP: 327

region

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A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
R;Residues: 23-40;65-69;136-141;300-306 <LOE>
T; Engelmann, H.; Novick, D.; Mallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A;Reference number: A35010; MUID:90110215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30 Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of CDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885
       A;Title: Purification and partial amino acid sequence analysis of two distinct tumor A;Reference number: A23666; MUID:91056048
A;Accession: A23666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P:,Kemper, O.; Wallach, D.
Gene 150, 381:386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5'
A;Reference number: 138094; MUID:95121934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 -CMCVQPEFHC-----GDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSG-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Note: the list of introns is incomplete
(S. Superfamily: tunor necrosis factor receptor type 2; NGF receptor repea
(S. Superfamily: tunor necrosis factor receptor; transmembrane protein
(S. Reywords: duplication; glyoprotein; receptor; transmembrane protein
(S. 1-22/Domain: signal sequence #status predicted <SIG>
(S. 1-24/Pomain: signal sequence #status predicted <SIG>
(S. 1-27/Domain: NGF receptor repeat homology <NG1>
(S. 1-19/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;120-162/Domain: NGF receptor repeat homology <NG3> F;164-201/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                             A; Status: preliminary
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tunor necrosis factor receptor 2 precursor [validated] - human

N. Alectrate names 75 % tunor necrosis factor receptor; TNF receptor type 2

C. Species: How sapiens (man)

A. Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A. Recension: A3536, MAG/TS, A48416, A3607; A32665; B35010; ISB034

A. Status: preliminary

A. Molecule Type im RNA

A. Residues: 1-61 C. SMI

A. Residues: 1
                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            837 GALSSICEKTSGOCLCRTGAFGLRCDRCQRGQWGFPSCRP-------CVCNGHAD 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 -CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQ-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885 ECNTHIGACLGCRDHIGGEHCER----CI-AGFH-GDPRLPYGGOCRPCPEGPGSORH 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::|
939 FATSCHQDEYSQQIVCHCRAGYTGLRCEACAPGHFGDPSRPGGRCQLCECSGNIDPMDPD 998
                                                                                                                                                                                                                                                                                                                                                                                     8 GAFRALC----GLALLCALSLGQR------PTGGPGCGPGRLLLGTGTDARC----- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 999 ACDPHTGOCLRCLHHTEGPHCAHCKP-----GFHGQAARQSCHRCTCNLLGTNPQQ 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPPAE 161
                                                                                                                                                                                                                                    Length 1798;
F;986-1035/Domain: laminin-type EGF-like homology <LE10> $1038-1092/Yomain: laminin-type EGF-like homology <LE11> F;1095-1140/Yomain: laminin-type EGF-like homology <LE12> F;1143-1187/Domain: laminin-type EGF-like homology <LE12>
                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                            Query Match 12.2%; Score 119.5; DB 2; Best Local Similarity 23.9%; Pred. No. 0.051; Matches 57; Conservative 10; Mismatches 62;
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F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Braesch-Andersen, S.; Paulle, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 c8RA>
A;Experimental source: Burkitt lymphoma cell line Raji
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() Superfamily: CD27 antigen; NGF receptor repeat homology

() Superfamily: CD27 antigen; NGF receptor repeat homology

() Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein

() F;1-20/Domain: signal sequence #status predicted <SIG>
() F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
() F;21-19/Domain: extracellular #status predicted <EXT>
() F;194-215/Domain: intracellular #status predicted <CYT>
() F;216-277/Domain: intracellular #status predicted <CYT>
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A;Reference number: A40254; MUID:91246168
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Embo J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608
                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1.474 <GOO>
A; Cross-references: GB.M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R; Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A; Description: Characterization of the promoter region of the murine p75-TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type 2; NGF receptor repeat homology
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C.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homole
C.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homole
F.1-22/Domain: signal sequence #status predicted <SIG>
F.23-474/Product: tumor necrosis factor receptor type 2 *status predicted <MAT>
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A60771
A60777
N.Alternate names: B-cell surface antigen Bp50
C.Species: Homo sapiens (man)
C.Date: 03.Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C.Sacession: S04460; A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 EIRACTKOONRVCACEAGRYCAL-----KTHSGS--CROCMRLSKCGPGFGVASSR 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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Local Similarity 31.0%;
les 36; Conservative
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A; Accession: S54816
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-22 <KIS>
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A; Molecule type: mRNA
A; Residues: 1-277 <STA>
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insulin-like growth factor I receptor precursor - rat
N;Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I be
C;Species: Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D. Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989
A;Title: Developmental regulation of the rat insulin-like growth factor I receptor ge A;Reference number: A33837; MUID:90017496
A;References number: A33837
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A; Residues: 913-984, PY', 987-1017 < KUR>
A; Cross-references: GB-D12679; NID:q220918; PIDN:BAA20983.1; PID:g4433359
C; Superfamily: insulin receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor; kinase-related transforming protein; transme
F;1-30/Domain: signal sequence #status predicted < SIG>
F;1-47/Product: insulin-like growth factor I alpha chain #status predicted < IGB>
F;937-959/Domain: transmembrane #status predicted < TMM>
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Blochem. Blophys. Res. Commun. 187, 934-939, 1992
A;Title: A new member of the insulin receptor family, insulin receptor-related recept
A;Reference number: PC1130; MUID:92412145
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                                                                                                                                                                                                                                                                                                         89 C-RHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                                                                                                                                                                                                                   119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 GAIRIEKNADLCYLSTIDWSLILDAVSNNYIVGNKPP--KECGDLCPGTLEEKPMCEKTT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --CTTC 89
                                                                                                                                                    34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- 40
                                                                                                                                                                                                       62 CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
                                                                              11;
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Length 277;
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GAFRA-----LCGLA-----LLCALS----LGQRPTGGPGCG---PGRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 LGTGTDARCCRVHTTRC---CRDYPGEECCSEWDCMCVQPEFHCGDPC--
Query Match 12.1%; Score 118.5; DB 2; Best Local Similarity 27.7%; Pred. No. 0.018; Matches 36; Conservative 10; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.8%; Score 115.5; DB Best Local Similarity 27.1%; Pred. No. 0.087; Matches 57; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
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A;Cross-references: GB:M27293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;971-974/Region: GPXY motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;978-981/Region: NPXY motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          =
                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 NKTHNAVCVP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TNKTDVVCGP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1371 <PED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: JC2461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        v;Molecule type:
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A)Cross-references: GB: M83312; NID:g1553058
A)Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A)Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
B)Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
B)Crimaldi J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay J. Immunol. 149, 3921-3926, 1992
A)Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A)Reference number: A46515; MUID:93094586
A)Accession: A46515
A)Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1.1801 <HUN>
A; Residues: 1.1801 <HUN>
A; C. CAR34561.1; PID:g57251
C; Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: interact with cells and with other basement membrane proteins to promo C; Superfamily: laminin beta-1 chain; laminin-type EGF-11ke homology C; Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu F; 1-35, Domain: signal sequence #status predicted <SIC>
F; 36-1801, Product: laminin beta-2 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: nucieic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin beta-2 chain precursor - rat

N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-bec-1999
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the A;Reference number: S03539; MUID:89159410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 CHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;413-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology *status atypical <LE05>
F;555-784/Domain: laminin-type EGF-like homology *status atypical <LE05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 -------RVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Experimental source: BALB/c, 11ver
A:Note: sequence extracted from NCBI backbone (NCBIP:120357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigon; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%; Score 135.5; DB 2; 26.1%; Pred. No. 0.00091; tive 10; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCGL - - ALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCC - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;286-555/Domain: V <DOM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 NKTHNAVC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Phytc
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Cispecies: Phytolacca memicana (Virginian pokewed)
Cispecies: Phytolacca memicana (Virginian pokewed)
Cispecies: Division 105599197 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
Cispecies: USECESSION 1055919889
A.Y. He amino acid sequence of mitogenic lectin-B from the roots of pokeweed (A. Reference number: US5559; MUID:97290889
A. Rocession: US559; MUID:97290889
A. Rocession: US559
A. Rocession: US55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jo
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A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Dete: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
J: Immunol. 148, 620-626, 1992
J: Immunol. 148, 620-626, 1992
A;Tute: Differential increase of an alternatively polyadenylated mRNA species of A;Reference number: A46476; MUID:92105763
A;Reference number: A46476
A;Status: preliminary
A;Molecule type: mRNA
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 SEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ-C---IDCASGTFSGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         26 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT----RCCRD-YPGEECCSEWD----
                                                                                                                                                                                                                                                  Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
14.2%; Score 139; DB 2; 28.8%; Pred. No. 0.00047; Live 18; Mismatches 41;
                                                                                                                                                                                                                                              15.4%; Score 151; DB 2; 28.5%; Pred. No. 5.2e-05; Live 12; Mismatches 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 CMCVQPEFHCG----DPC--CTTCRHH----
                                                                                                                                                                                                                                                                                    Local Similarity 28.59 tes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 28.8
mes 36; Conservative
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                                                                                                                                                                                                                                              Query Match
Best Local Si
Matches 47;
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Best Local Si
Matches 36;
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--SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Scor
30.3%; Pred
ative 11; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.3%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laminin-type
laminin-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laminin beta-2 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;522-552/Domain: laminin-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: s-laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S53869
A; Accession: S53869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1798 <IIV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S53869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;783-828/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;831-874/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: LAMB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||
SP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Homo sapiens (man)
C; Date: 24 May-1996 #sequence_revision 24 May-1996 #text_change 17-Mar-2000
C; Accession: 154182
C; Accession: 154182
R; Baens, M; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequent A; Reference number: 154182; MUID: 93252381
A; Accession: 154182
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                         F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Gross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892 HTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SQRHFA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840 GALSALCEGTSGOCLCRTGAFGLRCDHCORGOWGFPNCRPCVCNGR-----ADECDA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 HTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQGKFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CPP-----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 GAFRALC-GLALLCALSLG-----QRPTGG-PGCGP----GRLLLGTGTDARCCRV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944 TSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDPGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1004 DPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTCNLLGTDP 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 134.5; DB 1; Length 1801;
Pred. No. 0.0035;
6; Mismatches 60; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 435;
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                                                F.834-877/Domain: laminin-type EGF-like homology <LE07>
F.886-927/Domain: laminin-type EGF-like homology <LE08>
F.9810-986/Domain: laminin-type EGF-like homology <LE08>
F.9810-1038/Domain: laminin-type EGF-like homology <LE10>
F.1041-1095/Domain: laminin-type EGF-like homology <LE11>
F.108-1143/Domain: laminin-type EGF-like homology <LE11>
F.1146-1190/Domain: laminin-type EGF-like homology <LE12>
F.1141/Negion: laminin-type EGF-like homology <LE13>
F.1197-1412/Negion: heptad repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor receptor 2-related protein - human
F;786-831/Domain: laminin-type EGF-like homology <LE06>F;788-1196/Domain: III <DOM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 121; DB 2; ilarity 26.1%; Pred. No. 0.015; Conservative 12; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FGFQCIDCASGTF-----
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                                                                                                                                                                                                                                                                                                                          F;1446-1801/Region: heptad repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.7%;
Best Local Similarity 26.9%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                               F;1413-1445/Domain: alpha <ALP>
                                                                                                                                                                                                                                                                                                                                                   F;1446-1801/Domain: I <DOM1>
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Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-435 <RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 -----
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Matrix Biol. 14, 489-497, 1994
A.Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule_type: mRNÄ
A;Residues: 1-459 FRES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer F;1-32/Domain: signal sequence #status predicted <SIG> F;3-1798/Product: laminin beta-2 chain #status predicted <MAT> F;33-1798/Product: laminin beta-2 chain #status predicted <MAT> F;347-407/Domain: laminin-type EGF-like homology <LE01> F;347-407/Domain: laminin-type EGF-like homology <LE02> F;410-467/Domain: laminin-type EGF-like homology <LE03>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
9
                                                                                                                                                                                                                                                                                C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allellc variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848
                                                                                                                                                                                             gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVQSQGKFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 RTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGS--CRQCMRLSKCGPGF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology <LE04>
homology #status atypical <LE05>
homology <LE06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCCRVHTTRCCRDYPGEECCSEWD---CMCVQPEF----HCGDPCCTTC-RHHPCPPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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A;Map position: 3p21.3-3p21.2
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
176 QNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC---KNPLEPL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <LE07><LE08><LE09>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 120.5; DB 2;
Pred. No. 0.017;
1; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (version 2) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
homology
homology
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EGF-like |
EGF-like |
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4, 2001, 16:12:15; Search time 80.15 Seconds
(without alignments)
155.866 Million cell updates/sec
4.5
Compugen Ltd.
version 4
- 2000 (
                                                                     OM protein - protein search, using sw model
GenCore
Copyright (c) 1993
                                                                                                         September
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Run on:

1 MAQHGAMGAFRALCGLALLC......GNKTHNAVCVPGSPPAEPLG 164 US-09-512-363-2\_COPY\_1\_164 979 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	gene ox40 protein	homol	lymphocyte activat	T-cell antigen 4-1	tigen pr	lectin-B - Virgini	B cell-associated	laminin beta-2 cha	tumor necrosis fac	gene murine tumour	laminin beta-2 cha	m	tumor necrosis fac	B-cell activation	insulin-like growt	insulin-like growt	•	hypothetical prote		EGF repeat transme	fibrillin-2 precur	hypothetical prote	Notch-1 protein -	MEGF6 protein - ra	laminin alpha 5 ch	fibrillin-2 precur	hypothetical prote	-	က
	QI	148700	137552	I38426	B32393	S12783	JC5559	A46476	MMRTS	154182	I48854	S53869	A35356	B38634	A60771	A33837	A48805	A55677	T18975	T26972	T30176	A57278	T24272	A46019	T13954	T10053	A54105	T15651	TSHUP2	A46016
	DB	7	~	7	~	7	7	~	Н	7	7	~	Н	~	~	~	C3	7	~	~	~	~	7	~	~	N	~	~	٦	7
	Length	272	277	255	256	271	295	305	1801	435	459	1798	461	474	277	1371	329	1797	152	1111	1687	2907	164	2531	1574	3635	2918	188	1172	926
	Query	6.5	6.5	6.4	5.6	•	4.2	3.8	3.7	•				2.5		1.8	•	11.5		•		•		1.2	1.1	•	6.0	0.7	٠.	0.5
æ	Maa		Н	-	-	Н	-	-	Н	Н	Н	Н	٦	Н	-	Н	Н	Н	Н	-	-	-	٦		-	٦	٦		_	-
	Score	162	162	160.5	153	151	139	135.5	134.5	121	120.5	119.5	119	119	118.5	115.5	₹.	112.5	112	111	110.5	110.5	109.5	109.5	109	109	106.5	105	105	102.5
	Result No.	1	7	Э	4	ഗ	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

30 102 10.4 186 2 A28401 31 101.5 10.4 1367 1 IGHUR1 32 101.5 10.4 2318 2 S45306 34 100.5 10.3 4543 1 A53102 35 100.5 10.3 2531 2 S18188 36 100 10.2 540 2 B47417 37 100 10.2 956 2 B47417 39 99.5 10.2 1106 2 T13938 40 99.5 10.1 227 1 LNEZ 40 99.5 10.1 227 1 AEWT2 41 98.5 10.1 2139 2 A55494 43 98.5 10.1 2139 2 A35672	agglutinin isolect	insulin-like growt	notch 3 protein -	alpha-2-macroglobu	MEGF8 protein - hu	notch protein homo	Insulin receptor-r	apolipoprotein E r	gene shuttle craft	ultra high-sulfur.	lectin precursor .	agglutinin isolect	latent transformin	alpha-2-macroglobu	cartilage oligomer	crumbs protein - f
444mmmgggggggggggggggggggggggggggggggg	A28401	IGHUR1	S45306	A53102	T00209	S18188	B47417	JE0237	T1.3938	S18946	LNRZ	AEWT2	A55494	S02392	A44315	A35672
444mmmgggggggggggggggggggggggggggggggg	7	Н	~	Н	~	~	~	~	~	-	Н	Н	~	Н	~	7
•	186	1367	2318	4543	1737	2531	540	966	1106	169	227	213	1820	4544	755	2139
30 101.5 33 101.5 33 101.5 33 101.5 33 100.5 33 100.5 33 100.5 34 100 39 99.5 44 99.5 44 98.5	10.4	10.4	10.4	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.1	10.1	10.1
0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	102	101.5	101.5	101	100.5	100.5	100	100	100	99.5	99.5	66	66	66	98.5	98.5
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Greenstenate names: OX40 antigen

N.Alternate names: OX40 antigen

N.Alternate names: OX40 antigen

N.Alternate names: OX40 antigen

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house name)

C.Saccession: 148700; 148334; 534377

R.Salderhead; D.M.; Bulhaman, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.

R.Stalderhead; D.M.; Bulhaman, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.

A.Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell

A.Status: translated from GB/EMBL/DDBJ

A.Scession: 148700

A.Status: translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Residues: 1-272 <RES>
A.Cross-references: EMBL: 221674; NID: 9312827; PIDN: CAA79772.1; PID: 9312828

R.Strkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.

Eur. J. Immunol. 25, 926-930, 1995

A.Title: Gene structure and chromosomal localization of the mouse homologue of rat OX

A.Reference number: 148334; MUID: 95255413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosaldues: 1-14,'G', 16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 ------CTTCRHHP----CPGGCVQSQGKFSFGFQCID 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC------HPCET 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 LILIGIGIDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.5%; Score 162; DB 2; Length 27 ilarity 28.3%; Pred. No. 7.3e-06; Conservative 11; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: 0x40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Оp
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7;

126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164

137552 OX40 homolog - human C;Species: Homo sapiens (man)

RESULT

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R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Wallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
EMBO J. 9, 1063-1068, 1990
A;Fitle: Characterization of the MRC OX40 antigen of activated CD4 positive
A;Reference number: S12783; MUID:90214614
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U02567; NID:91117783; PIDN:AAA93113.1; PID:9409178
                                                102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
             85 CCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 RHHPCPPGOGVOSOGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831 C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN: AAA40167.1; PID: 9201122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Reywords: transmembrane protein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-256/Product: 4-1BB protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: cDNA sequence of two inducible T-cell genes A;Reference number: A32393; MUID:89184547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.6%; Score 153; DB 2; 31.5%; Pred. No. 3.5e-05; tive 17; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
                                                                                                                                                --SPPA---EP 162
                                                                                                                                                                                                              150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: B32393
A,Molecule type: mRNA
A,Residues: 1-256 cKWO>
A,Cross-references: GB:J04492; NID:g201121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: I48879; MUID:94179805
A; Accession: I48879
                                                                                                                                                                                                                                                                                                                                                                                      T-cell antigen 4-1BB precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 31.5%
Matches 40; Conservative
                                                                                                                                            GNKTHNAVCVPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: B32393; I48879
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A; Residues: 1-271 <MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-256 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 HNAVCVP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 KDVVCGP 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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A. Molecule type: mRNA
A. Residues: 1-106, fr., 108-255 <SCH>
A. Molecule type: mRNA
A. Residues: 1-106, fr., 108-255 <SCH>
A. Molecule type: mRNA
A. Residues: 1-106, fr., 108-255 <SCH>
C. Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C. Comment: This receptor recoptor repeat homology
C. Superfamily: CD27 antigen: NGF receptor repeat homology
C. Reywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F.11-17/Domain: signal sequence #status predicted <SIGN
F.187-23.7Domain: transmembrane #status predicted <FMAT>
F.187-23.7Domain: transmembrane #status predicted <FMAT>
F.187-23.7Domain: glycoprotein; phosphate (Abn) (Covalent) #status predicted
F.234,235/Binding site: phosphate (Thr) (Covalent) (by casein kinase II) #status predicted
F.242/Binding site: phosphate (Ser) (covalent) (by protein kinase I) #status predicted
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C; Accession: 137552
R; Latza. U; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Bur. J. Immunol. 24, 677-683, 1994
A; Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment A; Reference number: 137552; MUID: 94170844
A; Accession: 137552; MUID: 94170844
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-277 cRES>
A; Cross-references: EMBL: X75962; NID: 9472957; PIDN: CAA53576.1; PID: 9472958
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.J.; Falk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C;Accession: 138426, JT0752
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molecular and biological characterization of human 4-IBB and its ligand. A;Reference number: 138426 MUID:94374434
A;Accession: I38426 MUID:94374434
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-255 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GARRLGRGPCAALLLLGLGLGTTTTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMGAFRALCGLALLCALSLG-----QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.5%; Score 162; DB 2;
llarity 29.7%; Pred. No. 7.4e-06;
Conservative 11; Mismatches 92.
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Best Local Similarity
Matches 47; Conserva
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nes 51; Conserv
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Best Local S.
Matches 51
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7;

Gaps

18;

positive T lymphoc

13;

Gaps

65; Indels 107;

884

Length 1798;

DB 1;

11.4%; Score 111.5;

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---SQGKFS------FGFQCIDCASGTF------120
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ATSCHQDEYSQQIVCHCRAGYTGLRCEACAPGHFGDPSRPGGRCQLCECSGNIDPMDPDA 999
                                                                GAFRALC ---- GLALLCALSLGQR ----- PTGGPGCGPGRLLLGTGTDARC ---- 49
                                                                                                                                                                                                                                                                                                         1000 CDPHTGQCLRCLHHTEGPHCAHCKP-----GFHGQAARQSCHRCTCNLLGTNPQQ 1049
                                                                                                                                                                                                                                                                                        -----SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPPAE 161
                                                                                     Pred. No. 0.018;
   23.2%; Pred. ....
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       Best Local Similarity 23.2° Matches 55; Conservative
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-> A (IN REF. 2).
9555CF5B24850CB7 CRC64;
LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 9.

LAMININ EGF-LIKE 9.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 13.

DOMAIN II.

COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

BY SINILARITY.

BY SINILARI
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CONFLICT
SEQUENCE
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TISSUE-Brain;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CGESEFLDTWNRETHC --- HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88
                             -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
-i- SIMILARITY: CONTAINS A LA-NGFRYTHRF-TYPE CYSTEINE-RICH REGION.
-i- DATABASE: NAME-PROW, NOTE-CD guide CD40 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                             InterPro; IPR001368; -.
Pfam; PF00020; TNFR_C6; 4.
PROSITE; PS0652; TNFR_L1; 1.
PROSITE; PS50050; TNFR_USFR_1; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 277;
with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
                                                                                                                                                                                                                                                                                     CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL). 4 X INFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 118.5; DB 1; 27.7%; Pred. No. 0.0011; tive 10; Mismatches 73;
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01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                      TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 TNKTDVVCGP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AA;
                                                                                                                                                                                                                                                                   3D-structure.
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MIM; 109535;
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P24062;
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Matches
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-!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
TYROSINE-PROTEIN KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBGUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                  Du J., Delafontaine P.; "Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA."; Circ. Res. 76:963-972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Developmental regulation of the rat insulin-like growth factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
01-OCT-2000 (Rel. 40, Last annotation update)
:NSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0109; TYRKINASE.
PROSTIE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSTIE; PSO0109; PROTEIN_KINASE_TYR; 1.
PROSTIE; PSO0239; RECEPTOR_YPR_KIN_II; 1.
PROSTIE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
"A new member of the insulin receptor family, insulin
receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90017496; PubMed-2477843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 913-1017 FROM N.A. MEDLINE-92412145; PubMed-1530648;
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95277910; PubMed-7758167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR002174; -...
Pfam; PF00757; Furin-like; 1..
Pfam; PF01030; Recep_L_domain;
Pfam; PF000041; fn3; 2..
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN TYROSINE PHOSPHATE.
                                                                                                                Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L29232; AAA41392.1; -. EMBL; M27293; AAA41384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-364 FROM N.A.
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Interpro; IPR001777; ...
Interpro; IPR002011; ...
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HSSP; P06213; 11RK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAFRA-----LCGLA-----LLCALS----LGQRPTGGPGCG---PGRL-----L 40
                                                                                 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                       INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGTGTDARCCRVHTTRC---CRDYPGEECCSEWDCMCVQPEFHCGDPC-----CTTC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.8%; Score 115.5; DB 1; Length 1370; 27.1%; Pred. No. 0.0066; tive 22; Mismatches 52; Indels 79;
Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal. SIGNAL 1 30 POTENTIAL.
                                                                                                                                                                                                                                                                                                          (BY
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                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                              CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                             ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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THE BETA-2 CHAINING TO CELLS UND A HIGH AFFINITY RECEPTOR, LAMINING TO CELLS UITS BIOL 14:489-497(1995).

11. FUNCTION: BINDING TO CELLS UIA A HIGH AFFINITY RECEPTOR, LAMINING TO CELLS UITS BIOL TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYCONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

12. SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLVEPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

12. CAMENSING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

13. SUBCELLULAR LOCATION: EXTRACELLULAR.

14. SUBCELLULAR LOCATION: EXTRACELLULAR.

15. CHENT OF THE NEUROMUSCULAR JUNCTION.

16. CHENT OF THE NEUROMUSCULAR JUNCTION.

17. DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO PORM A COILED COIL STRUCTURE.

15. DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

16. SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAINS VI .

17. SIMILARITY: CONTAINS 1 LAMININ BOMAINS.

18. SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          Livanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
Sariola H., Tryggvason K.;
"The human laminin beta 2 chain (S-laminin): structure, expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01186; EGF_2; 2. PROSITE; PS01186; EGF_2; 12. PROSITE; PS01248; LAMININ_TYPE_EGF; 12. Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
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Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattel M.-G., Champlaud M.F., Burgeson R.E., Albrechtsen R.; Human beta 2 chain of laminin (formerly S chain): chromosomal localizatelland, and expression in carcinomas.";
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N BGF-LIKE 2.
N BGF-LIKE 3.
N BGF-LIKE 4.
N BGF-LIKE 5 (INCOMPLETE).
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LAMININ EGF-LIKE 6.
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EMBL; Z68156; CAA92279.1; JOINED.
EMBL; X79683; CAA56130.1; --
EMBL; S77512; AAB34682.2; --
HSSP; P02468; IKLO.
                                                                                                                          MEDLINE-95316263; PubMed-7795887;
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Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
PROSITE; PS00022; EGF_1; 10.
                                                                       Genomics 24:243-252(1994).
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SEQUENCE FROM N.A.
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- SUBCELLULAR LOCATION : TYPE I MEMBRANE PROTEIN

- I- SUBCELLULAR LOCATION : TYPE I MEMBRANE PROTEIN

- I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.
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MEDILINE-90110215; PubMed-2153136;
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE=93016040; PubMed=1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   `.
X
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy F. Dower S.K., Cosman D., Goodwin R.G.; A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins."; Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                             "Physical mapping and genomic structure of the human TNFR2 gene."; genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; "Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                                                                                                                                                    Beltinger C.P., White P.S., Maris J.M., Sulman B.P., Jensen S.J., Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
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Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer
Brockhaus M.;
                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE-91045991; PubMed-2172983;
MEDILINE-91045991; PubMed-2172983;
KOHOO T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
"A second tumor necrosis factor receptor gene product can shed
naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
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distinct tumor necrosis factor receptors from HL60 cells.";
J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
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J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96299745; Pubmed-8661109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ringold G.M.;
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R > P (IN REF. 4).
R -> M (IN REF. 4).
R -> M (IN REF. 4).
WWW="http://www.ncbl.nlm.nih.gov/prow/cd/cd120b.htm".
DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
WWW="http://www.enbrelinfo.com/".
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                       JOINED
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                                                                                                                                                                                                                                                                                   U52158; AAC50622.1; U52159; AAC50622.1; U52160; AAC50622.1; U52161; AAC50622.1; U52161; AAC50622.1; U
                                                                                                                                                                                                 EMBL; M32315; AAA59929.1;
EMBL; M35857; AAA63262.1;
                                                                                                                                                                                                                                                  AAC50622.1;
AAC50622.1;
                                                                                                                                                                                                                                                                                                                                                                                     AAC50622.1;
AAA36755.1;
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PIR, A36007, A36007.
PIR, A36475, A36475.
PIR, B35010, B35010.
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PDB; 1CA9; 12-APR-99
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U52164;
M55994;
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          -CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 122
                              117 ICTC-RPGWYCALSKOEGCRLCAPLR--KCRPGFGVARPGTETSDVVCKPCAPGTFSNTT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                           Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V., "Cloning and expression of CDNas for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                 TNR2_MOUSE STANDARD; PRT; 474 AA.
P25119; P97893;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
                                                                 |:| | : : || | | STDICRPHQICN----VVAIPGNASRDAVCTSTSP 205
                                                     123 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 158
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-91246168; PubMed-1645445;
                                                                                                                                                                                                                                                                              MEDLINE=91187885; PubMed=1849278;
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EMBL; M59378; AAA40463.1; -.
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                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacob C.O., Liu J.;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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INR2_MOUSE
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MEDLINE-98266353; PubMed-9605317; Karpsusas M., Hsu Y.-M., Slingh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.; Then sole of polar interactions in the molecular recognition of CD40L "The role of polar interactions in the molecular secognition of CD40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 22, Last sequence update)
(Rel. 39, Last annotation update)
OR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
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the ligand binding domain of the human B cell receptor CD40.";
Proteins 27:59-70(1997).
                                                                                                                                                                                              BY SIMILARITY.
N'INKED (GLCHAC. ..) (POTENTIAL).
N'INKED (GLCHAC. ..) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-8935668; Pubmed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
"A B-1ymphocyte activation molecule related to the nerve growth
factor receptor and induced by cytokines in carcinomas.";
EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP
                                  TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 119; DB 1; Length 474;
Pred. No. 0.0015;
3; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               LINKED (GLCNAC. . .) (P. 462EAE398C4D6563 CRC64;
Transmembrane; Glycoprotein; Repeat; Signal.
                                                     EXTRACELLULAR (POTENTIAL) POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
                                                                                       CYTOPLASMIC (POTENTIAL)
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TNFR-CYS 3.
TNFR-CYS 4.
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Bajorath J., Aruffo A.;
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01-MAY-1992 (Rel. 22, Last seq
30-MAX-2000 (Rel. 39, Last anno
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31.0%;
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                                                                                                                                                                                                                                                                                                                               145
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P25942;
 Receptor;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            989 CSGNIDPMDPDACDPHTGQCLRCLHNTEGPHCGYCKP------GFHGQAARQSCHRCTC 1041
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01-NOV-1997 (Rel. 35, Last sequence update)
12-VUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
TNFRSF5 OR CD40.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                      LINKED (GLCNAC. . .) (POTENTIAL).
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Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                    Indels 115;
                                                                                                                                                                                                                                                                                                DB 1; Length 1799;
                              N-LINKED (GLCNAC...) (
        INTERCHAIN (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                Query Match 13.0%; Score 127.5; DB 1
Best Local Similarity 24.7%; Pred. No. 0.00074;
Matches 61; Conservative 8; Mismatches 63
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InterPro; IPR001368;
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Q28203;
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CD40_BOVIN
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LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                          LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                           LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
LAMININ DOMAIN IV.
R X LAMININ EGF-LIKE REPEATS (DOMAII).
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LAMININ EGF-LIKE 7.
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LAMININ EGF-LIKE 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                          88 TCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                           CGKGEFLSTWNREKYC---HEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQ-HCTSHTCE 117
                                                                                                                                                                                                                                                                                                                                                  34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNRC_HUMAN STANDARD; PRT; 435 AA.
P36941.
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LYMPHOTOXINI-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
LYBRATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR
LIBBR OR TNFCR OR TNFRSF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1 - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
Ehreifels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
"A lymphotoxin-beta-specific receptor.";
                                                                                                                                                                                                        (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                    . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       13;
00020; TNFR_C6; 4.
ES00652; TNFR_NGFR_1; 1.
PS50050; TNFR_NGFR_2; 1.
; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                          Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Mar "Construction and evaluation of a hncDNA library of human transcribed sequences derived from a somatic cell hybrid. Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                746903F30F95F387 CRC64;
                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                          12.5%; Score 122.5; DB 1; 28.7%; Pred. No. 0.00049;
                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                    (GLCNAC.
                                                                         CD40L RECEPTOR
                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                  4 X TNFR-CYS.
TNFR-CYS 1.
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TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (G
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                                                                                                                                                                                                                                                  29983 MW;
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                                                                         >269
193
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>269
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tes 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTNKTDVVC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
    Pfam; PF00020;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Liver
                                             Receptor;
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CARBOHYD
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SEQUENCE
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
THERSFIB OR THER2 OR THEBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CPP----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CRDYPGEE----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 121; DB 1; Length 435; Pred. No. 0.00094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                     LYMPHOTOXIN-BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                  624626E6022F656F CRC64;
                                                                                                                                                               Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                               POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 ONTSSPSARCOPHTRCENOGLVEAAPGTAQSDTTC---KNPLEPL
                                                                                                                                                                                                                                                                                               BY SIMILARITY.
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                             TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
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TNFR-CYS 1.
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                                                                                                            InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00055; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE~90260639; PubMed~2160731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 CGPGRLLLGTGTDARCCRVHTTRC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                           EMBL; L04270; AAA36757.1; -
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Matches 43; Conserv
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82
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                                                                                                   MIM; 600979;
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                                                                                                                                                                                                                                                               EMBL: X16563; CAA34561.1; -.

R HSSP: P02468; ILKLO.

R InterPro; IPR000561; -.

R InterPro; IPR0012086; -.

R InterPro; IPR0012086; -.

R Pfam: PF00055; Laminin_REF; 13.

R PRINTS; PR00011; EGFLAMINI.

R PROSTTE; PS01248; LAMININ_TYPE_EGF; 12.

R PROSTTE; PS01248; LAMININ_TYPE_EGF; 12.

W Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                    DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE. DOMAIN: DOMAINS VI AND IV ARE GLOBULAR. SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI). SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 12.5 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5
LAMININ DOMAIN IV.
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REF-LIKE 7.
REF-LIKE 8.
REF-LIKE 9.
REF-LIKE 10.
REF-LIKE 11.
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LAMININ EGF-LIKE
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LAMININ EGF-LIKE
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      CLEFT OF THE NEUROMUSCULAR JUNCTION.
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      Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
Ananini-like addesive protein concentrated in the synaptic cleft
of the neuromuscular junction.";
Instruction: Instr
                                                                                                                                                                                                                                                                                                                                       8
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
                                                                                                                                                                                                                                                                                                      Length 289;
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                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                   Query Match 13.8%; Score 135.5; DB J
Best Local Similarity 26.1%; Pred. No. 3.8e-05;
Matches 49; Conservative 10; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1801 AA
                                                                                                                                                                                 TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GI
Pfam; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; TSIGNAL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
                                              MEDLINE=96278760; PubMed=8662701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U43541; AAC53535.1; -.
EMBL, U42624; AAC53535.1; JOINED.
EMBL, X75928; CAAS5532.1; -.
HSSP, P02468; IKLD.
MGD; MGI:99916; Lamb2.
InterPro; IPR000561; -.
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Pfam; PF00055; laminin_Nterm; 1.
                                                                                                             SEQUENCE OF 348-428 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002049; -
                               SEQUENCE FROM N.A.
                                       STRAIN=129/J
                                                                                                                     TISSUE-Lung;
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                                                                                                                                                                  FUNCTION
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                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   13.7%; Score 134.5; DB 1; Length 1801; 26.9%; Pred. No. 0.00018; tive 6; Mismatches 60; Indels 105;
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INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
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                             SIMILARITY. SIMILARITY.
                                             SIMILARITY. SIMILARITY.
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C. I. SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISCULFIDE BONDS INTO A CROSS-SHARED MOLECULE. COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

C. COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

C. S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

C. S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

C. TISSUE SPECIFICITY: BURROWUSCLLULAR; FOUND IN THE BASEMENT

MEMBRANES (MAJOR COMPONENT).

C. TISSUE SPECIFICITY: BURROWUSCLLULAR; FOUND IN THE BASEMENT

MEMBRANES (MAJOR COMPONENT).

C. TISSUE SPECIFICITY: BURROWUSCLLAR; FOUND IN THE BASEMENT

MITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

MITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

C. TOMAIN: DOMAINS VI AMD IV ARE GLOBULAR.

C. TOMAIN: DOMAINS I LAMININ N-TERRINAL DOMAIN VI)

C. SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions along as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.-G., Ortonne J.P., Meneguzzi G.;
                                                                       mouse laminin beta2 chain end of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Basement membrane; Extracellular matrix; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94319092; PubMed-8043959;
Aberdam D., Galliano M.F., Mattel M.-G., Ortonne J.P., Meneguzzi
"S-laminin gene (Lams) maps to Fl band of mouse chromosome 9.";
Mamm. Genome 5:393-394(1994).
Durkin M.E., Gautem M., Loechel S., Sanes J.R., Merlie J.P., Albrechtsen R., Wewer U.M.; Structural organization of the human and mouse laminin betaigenes, and alternative splicing at the 5' end of the human transcript.
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function.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                             Detween the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 CPPNSFSSAGG--ORTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
                                                                                                                                                                          -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                  "Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
-1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 255;
                                                                            Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                  DATABASE: NAME-PROW; NOTE-CD guide CDw137 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm"
                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 3.
N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
F3A563FE5EF00460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%; Score 160.5; DB 1
30.9%; Pred. No. 2.4e-07;
tive 12; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GNKTHNAVCVPG-----SPPA---EP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFR-CYS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFR-CYS
                                                                                                                                  ACTIVE DURING T CELL ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                           TISSUE-Blood;
MEDLINE-95347766; PubMed~7622190;
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001368; -. Pfam; PF00020; TNFR_c6; 2. PROSITE; PS00652; TNFR_NGFR_1; 1. PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                                                                                EMBL; U03397; AAA53133.1; -. EMBL; L12964; AAA62478.2; -. HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27899
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Best Local Similarity 30.99
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138
149
255 AA;
                                                  SEQUENCE FROM N.A.
[3]
REVISION TO 107.
                                                                                                                                                                                                                                                                                                                                 602250;
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P20334;
                     Schwarz H.
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-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-- TISSUE SPECIFICITY: EXPRESSED ON THE SUBFACE OF ACTIVATED T-CELLS.
-- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
-- SIMILARITY: CONTAINS A LA-NGFR/THRR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHÂRACTERIZATION, AND SEQUENCE OF 25-29.
MEDLINE-93139510; Pubmed-7678621;
Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVE DURING T CELL ACTIVATION.
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 150:771-781(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
MEDLINE-94179805; PubMed-8133039;
Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
"Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWER-CYS 2.

TWER-CYS 3.

TWER-CYS 4.

THENED GLCNAC. . .) (POTENTIAL).

N-LINKED GLCNAC. . .) (POTENTIAL).

93A10D03C60813C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kwon B.S.; "Inducible T cell antigen 4-1BB. Analysis of expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-1BB LIGAND RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB).
TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00020; TNFR_C6; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                  Kwon B.S., Weissman S.M.;
"cDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 X TNFR-CYS.
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-89184547; Pubmed-2784565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 152:2256-2262(1994).
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MGD; MGI:1101059; Tnfrsf9.
InterPro; IPR001368; -.
                                                                                                                                                         (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B32393; B32393
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128
138
256 AA;
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                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen 4-1BB
                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mallett S., Fossum S., Barclay A.N.; "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor."; EMBO J. 9:1063-1068(1990).
                                                                                                                                                              102 -EKDCRPGQELTKQG-----CKTCSLGFFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                                               RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                                                                                           Kattus norvegisus (ratj.
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                     Gaps
                                                                       34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
C06465136B16EB21 CRC64;
                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
Length 256;
                                     52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                          01-ARR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC 0X40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
15.6%; Score 153; DB 1; 31.5%; Pred. No. 1.1e-06;
                                   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 X TNFR-CYS.
TNFR-CYS 1.
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InterPro; IPR001368; -.
Edm; PF00020; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90214614; PubMed-2157591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFRSF4 OR TXGP1L OR OX40.
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
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210
235
235
271
164
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102
123
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PIR; S12783; S12783.
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236
25
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143
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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154 KDVVCGP 160
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                                     40;
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P15725;
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Query Match
Best Local
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DOMAIN
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                                     Matches
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TO AAA
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8
                                                                                                                                                                                                                                                                                                                                                                                             01-CCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                         CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.";
                                                                                                                                                72 CMCVQPEFHCG----DPC--CTTCRHH---------PCPPGQGVQSQGKFSF 108
                                         Gaps
                                                                            26 ORPTGGPGCGPGRLLLG-TGTDARCCRVHTT----RCCRD-YPGEECCSEWD----- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Immunol. 149:3921-3926(1992).

-i-FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

-i-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROPEIN.

-i-SUMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                6 QQPT-----AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92105763; PubMed=1370315;
Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic structure and chromosomal mapping of the murine CD40
15.4%; Score 151; DB 1; Length 271; 28.5%; Pred. No. 1.7e-06; Live 12; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/C; TISSUE=Liver;
BDDLINE=93094586; PubMed=1281194;
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                         289 AA
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M83312; AABO8705.1; -.
EMBL; M94126; AAA37404.1; -.
EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                              (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                         47; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:88336; Tnfrsf5.
InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A46476; A46476.
HSSP; P25942; 1CDF.
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFRSF5 OR CD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Torres R.M.;
                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992
                                                                                                                                                                                                                                                                                                                                            CD40_MOUSE
P27512;
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CD40_MOUSE
                                           Matches
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MGD; MGI:104512; Tnfrsf4.
InterPro; IPR001368; -.
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2139
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416
1713
2871
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20
212
CHAIN
DOMAIN
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; Search time 43.78 Seconds (without alignments) 128.321 Million cell updates/sec
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                                                                                   .....GNKTHNAVCVPGSPPAEPLG 164
                                                                                                                                                                                                                                                                                                                                                          homo
                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                      P25119
P25942
P24062
P55268
Q61555
Q61001
Q600751
P35556
P35556
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P15800
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P20333
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Q64716
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P08069
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P98157
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                                                                                                                                                                                                                                                                                                                                                                                                             005895
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                  93435 segs, 34255486 residues
                                            4, 2001, 16:15:26
                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                               0X40_MOUSE
0X40_HUMAN
41BB_HUMAN
41BB_MOUSE
0X40_RAT
CD40_MOUSE
LMB2_RAT
                                                                                                                                                                                                                                                                                                                                      TNR2_MOUSE
CD40_HUMAN
IG1R_RAT
LMB2_HUMAN
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TNR2_HUMAN
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NTC1_MOUSE
LMA5_MOUSE
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FBN2_HUMAN
TSP2_HUMAN
FBL1_CHICK
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AGI3_WHEAT
IG1R_HUMAN
NTC3_MOUSE
LRP1_CHICK
NTC1_RAT
IRR_RAT
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LMA3_MOUSE
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                   CD40_BOVIN
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                                - protein search, using sw model
                                                                     US-09-512-363-2_COPY_1_164
979
                                                                                  1 MAQHGAMGAFRALCGLALLC....
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                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                                                                Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                   Length
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1370
1798
2907
2531
2531
3635
1373
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956
1367
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2318
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151
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122.5
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119
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Maximum DB :
                                OM protein
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                                            Run on:
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                                                                                                                                    homo sapien
bos taurus
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mus musculu
triticum ae
                                                                                        hordeum vul
                                                                                                             gallus gall
                                                                 drosoph11a
                                              rattus
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Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERFIO; LFKUOLISBS; -.
Pfam; PF00020; TNFR_CS; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                            P10040
P15312
P18519
P18519
P10968
P22105
P50284
                  Q07954
P35444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-55255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                           RESULT 1

OX40_MOUSE
TO OX40_MOUSE STANDARD; PRT; 272 AA.

AC P4741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 40, Last annotation update)
DE OX40_RECEPTOR PRECURSOR (OX40 ANTIGEN).

GN TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                    LRP1_HUMAN
COMP_RAT
CRB_DROME
                                                                                      AGI_HORVU
NGFR_CHICK
LMA3_HUMAN
FBN1_BOVIN
                                                                                                                                                                            AGII_WHEAT
TENX_HUMAN
TNRC_MOUSE
                                                                                                                                                                                                                                                  EGFR MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/C;
MEDLINE=94044750; PubMed=8228223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Immunol. 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z21674; CAA79772.1; -. EMBL; X85214; CAA59476.1; -. HSSP; P25942; ICDF.
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Gene 134:295-298(1993)
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REPEAT
REPEAT
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MEDLINE-95219871; PubMed-7704935;
Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.; "Identification of OX40 ligand and preliminary characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                                                                                                                                                                                                                                   86 -----CPPGOGVOSOGKESFGFOCID 114
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                    39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85
                                                                                                                                                                                                                                                                                                                                                          14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC-----HPCET 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.;
"The human Ox40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its activities on 0X40 receptor.";
Circ. Shock 44:30-34(1994).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFK_TARPE TYPE CYGTEINE-
-!- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                            . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40_HUMAN STANDARD; PRT; 277 AA.
P13489; O13663;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
O1-OCT-2000 (Rel. 40, Last annotation update)
OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY TURESE4 OR TXGP1L.
                                                                                                                                                                                                                                    Length 272;
                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
  CYTOPLASMIC (POTENTIAL).
                                                            TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE)
TNFR-CYS 4.
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CASGIFSGGHEGHCKPWIDCIQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                ; Score 162; DB 1;
; Pred. No. 1.9e-07;
11; Mismatches 51;
                   4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94170844; Pubmed-7510240;
                                                                                                                                                                     30153 MW;
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                                                                                                                                                                                                                                Query Match 16.5'
Best Local Similarity 28.3'
Matches 45; Conservative
  272
165
103
103
124
144
237
26
26
62
104
125
144
15
272 AA;
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CARBOHYD
CONFLICT
SEQUENCE
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REPEAT
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OX40_HUMAN

ID PAX40,H
AC PAX40,H
AC PAX40,D
DT 01-NOV.DT 01-NOV.D
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                       DOMAIN
                                               REPEAT
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55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.; "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GAMGAFRALCGLALLCALSLG-----QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwarz H., Tuckwell J., Lotz M.;
"A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GARRIGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                    InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS0625; TNFR_NGFR_1; 3.
PROSITE; PS06050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 162, DB 1; Length 277;
Pred. No. 1.9e-07;
Mismatches 92; Indels
                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (P. 49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (F
                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                     OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.9e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 AA
                                                                                                                                                                                                                                                                                  4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (T-CELL ANTIGEN ILA) (CD137 ANTIGEN) INFRSF9 OR ILA.
S76792; AAB33944.1; ALT_INIT. P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Immunol. 24:2219-2227(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94374434; PubMed=8088337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94085794; PubMed=8262389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Conservative
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                                                                                                                                                                                  28
277
214
233
277
277
169
65
107
1126
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29
215
236
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108
1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                         MIM; 600315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE-Blood
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Wed Sep 5 09:07:25 2001

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Ouery Match 15.2%;
Best Local Similarity 24.9%;
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ARCCRVHTTRC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-435 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 39; Conserv
                                                                                                              C; Genetics:
A; Gene: GDB: LAMB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Trygg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: tumor mecrosis factor receptor type 2; NGF receptor repeat home (C; Keywords: duplication; glycoprotein; receptor; transmembrane protein (F; 122/Domain: signal sequence #status predicted <SIG> F; 122/Domain: signal sequence #status predicted <SIG> F; 13-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT> F; 10-10/Domain: NGF receptor repeat homology <NG1> F; 110-162/Domain: NGF receptor repeat homology <NG3> F; 164-201/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAlternate names: g-laminin
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Sacession: S53869
R;Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariol
Matrix Biol. 14, 489-497, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 TRCCRDYPGEECCSEWD---CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 117; DB 1; Length 461; 30.4%; Pred. No. 0.0089; tive 11; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laminin beta-2 chain precursor (version 2) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: the list of introns is incomplete
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35; Conserve
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F; 280-461/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 26/3
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal t. A;Reference number: S53869
A;Accession: S53869
A;Accession: S53869
A;Accession: S53869
A;Accelle type: mRNA
A;Residues: 1-1798 <IIV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position: 12p13.3-12p13.1
Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
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C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: 154182
R; Baens, M.; Chaffenet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a hncDNA library of human 12p trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 CNTHIGACLGCRDHIGGEHCER----CI-AGFH-GDPRLPYGGOCRPCPCPEGPGSORHF 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 ATSCHODEYSOOIVCHCRAGYTGLRCEACAPGHFGDPSRPGGRCOLCECSGNIDPMDPDA 999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 3p21.3-3p21.2
C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C; Keywords: basement membrane; extracellular matrix; glycoprotein; F; 1-32/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:73-1798/Product: laminin beta-2 chain #status predicted CMAT>
F:33-1798/Product: laminin beta-2 chain #status predicted CMAT>
F:283-344/Domain: laminin-type EGF-like homology <LE01>
F:347-407/Domain: laminin-type EGF-like homology <LE02>
F:410-467/Domain: laminin-type EGF-like homology <LE03>
F:522-552/Domain: laminin-type EGF-like homology <LE04>
F:522-544/Domain: laminin-type EGF-like homology <LE06>
F:31-874/Domain: laminin-type EGF-like homology <LE06>
F:31-874/Domain: laminin-type EGF-like homology <LE06>
F:37-934/Domain: laminin-type EGF-like homology <LE09>
F:927-983/Domain: laminin-type EGF-like homology <LE09>
F:986-1035/Domain: laminin-type EGF-like homology
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Pred. No. 0.058;
8; Mismatches 47; Indels 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1038-1092/Domain: laminin-type EGF-like homology <LE11>F;1095-1140/Domain: laminin-type EGF-like homology <LE12>F;1143-1187/Domain: laminin-type EGF-like homology <LE13>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: GDB:1230195; OMIM:600979
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:132363; OMIM:150325
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70 AKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRC-QP 128

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R;Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D. Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989
A;Title: Developmental regulation of the rat insulin-like growth factor I receptor ge A;Reference number: A33837; MUID:90017496
A;Accession: A33837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 913-984, 'PV', 987-1017 < KUR>
A; Cross-references: GB:D12679; NID:q220918; PIDN:BAA20983.1; PID:g4433359
C; Superfamily: insulin receptor: protein kinase homology
C; Superfamily: insulin receptor: protein kinase-related transforming protein; transme
F; 1-30/Domain: signal sequence #status predicted <SIG>
F; 31-741/Product: insulin-like growth factor I alpha chain #status predicted <IGB>
F; 971-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>
F; 971-974/Region: GPXX motif
                                                                                                                                                                                                                                                                                                                                       R;Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.
Biochem. Biophys. Res. Commun. 187, 934-939, 1992
A;Title: A new member of the insulin receptor family, insulin receptor-related recept A;Reference number: PC1130; MUID:92412145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 PP-----GTYRFEGWRCVDRDFCANIPNAESSDSDGFVIHDGEC--MQECPS-GFIR- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TTRC---CRDYPGEECCSEWDCMCVQPEFHCGDPC-----CTTCRHH-----PC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 PPGQGVQSQGKFSF-GFQCID---CAS-----GTFSGG---HEGHCKPWTDCTQFGFLTV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110; DB 2; L
Pred. No. 0.071;
15; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;998-1275/Domain: protein kinase homology <KIN>F;1006-1014/Region: protein kinase ATP-binding motif
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Job time: 1110 sec
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28.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.5%
Matches 39; Conservative
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                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-364 <WER>
A;Cross-references: GB:M27293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
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N;Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I beta
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Mar-1990 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: JC2461; A33837; PC1131
R;Pedrini, M.T; Giorgino, F; Smith, R.J.
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994
A;Title: CDNA cloning of the rat IGF I receptor: Structural analysis of rat and human IG
                                                                                                                                                                                                                                                                                                                                           RESULT 14

A-6071

B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Stamenkovic, A: Clark, E.A.; Seed, B.
A;Ritle: A B-lymphocyte activation molecule related to the nerve growth factor receptor A;Reference number: S04460; MUID:89356608
A;Reference number: S04460; MUID:89356608
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A.Map position: 20q13.2
A.Map position: 20q13.2
A.Map position: 20q13.2
C.Superfamily: CD27 antigen; NGF receptor repeat homology
C.Superfamily: CD27 antigen; NGF receptor repeat homology
C.Superfamily: CD27 antigen; NGF receptor repeat homology
C.Superfamily: CD27 antigen; Phosphoprotein; Surface antigen; transmembrane protein
F;11-20/Domain: signal sequence #status predicted <SIG>F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-27/Domain: extracellular #status predicted <EXM>
F;194-215/Domain: intracellular #status predicted <CYT>
F;183,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                   33 EFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF--SGGHEGHCKPW 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
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                                                                                                                                                           87 TDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPL 118
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                                                                                                                                                                                                                                   189 TRCENQGLVEAAPGTAQSDTTC---KNPLEPL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 AFEKCHPWTSCETKDLVVQQAGTNKTDVVCGP 188
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Matches 29; Conservative
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A; Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A60771
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13;

Gaps

48;

Length 1371; Indels 4

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As Status: preliminary; not compared with conceptual translation
As Molecule type: nucleic acid
As Molecule type: nucleic form acide for acide form acide form acide form acide for acid
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C;Species: Mus musculus (house mouse)
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A;Reference number: A38634; MUID:91187885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: I48854
R; Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A; Reference number: I48854; MUID:95178848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 GVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVCAPE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 RCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 RVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTTC-RHHPCPPGQGVQSQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RCCRVHTTRCCRDYPGEECCSEWD---CMCVQPEF----HCGDPCCTTC-RHHPCPPGQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 KFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPGNKTHNAVC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.7%; Score 123; DB 2; Length 305; 30.6%; Pred. No. 0.0021; tive 7; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 120.5; DB 2; Length 30.3%; Pred. No. 0.0045; Live 11; Mismatches 57; Indels
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A;Molecule type: mRNA
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Best Local Similarity
Matches 37; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I48854
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Best Local Similar
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B38634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of pokeweed (Phyto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Phytolaca americana (Virginian pokeweed)
C:Species: Phytolaca americana (Virginian pokeweed)
C:Species: Phytolaca americana (Virginian pokeweed)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
C:Accession: 05559
R:Yamaquchi, K.; Yurino, N.; Kino, M.; Ishiquro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokewee A;Reference number: JC5559; MUID:97290889
A;Accession: JC5559; MUID:97290889
A;Molecule type: protein
A;Residues: 1-295 < YAM>
A;Experimental source: root
C:Comment: This protein is a lectin specific for N-acetylgucosamine-containing s C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homo C;Keywords: glycoprotein
F;96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                48 -----PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 100
                                                                                                                                                                                                                                                                                                                                                             96 PTEDTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPA 155
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                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RCCRDYPG-----EECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGF 65
                                                                                                                                                                                  ----- 47
                                                                                                                                                                                                                                             36 KCCRECOPGHGMVSRCDHTRDIVCHPCEPGFYNEAVNYDICKOCTOCNHRSGSELKONCT
                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.2%; Score 127; DB 2; Length 295; 34.1%; Pred. No. 0.00097;
                                             Length 271;
                                                                                                            Indels
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                                                                                                                                                                              RCCRD-YPGEECCSEWD-----CMCVQPEFHCG----DPC--CTTCRHH-
                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                         20.2%; Score 149; DB 2; 28.9%; Pred. No. 1.4e-05;
                                                                                                            10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 Q-C---IDCASGTFSGGHEGHC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 34.1% nes 28; Conservative
                                                                         Best Local Similarity 28.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lectin-B - Virginian pokeweed
                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 NKTHNAVC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::||
SNSLDTVC 163
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F;786-831/Domain: laminin-type EGF-like homology <LE06> F;788-1196/Domain: III <DOM3> F;834-877/Domain: laminin-type EGF-like homology <LE07> F;880-927/Domain: laminin-type EGF-like homology <LE08> F;930-986/Domain: laminin-type EGF-like homology <LE08> E;930-986/Domain: laminin-type EGF-like homology <LE09>
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Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                       F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                           F;1413-1445/Domain: alpha <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 16.0°
Best Local Similarity 26.0°
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1446-1801/Domain: I <DOM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
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                                                                                             A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laminin beta-2 chain precursor - rat

N;Alternate names: laminin chain B3; S-laminin
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neurch A;Reference number: S03539; MUID:89159410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: interact with cells and with other basement membrane proteins to promote C; Superfamily: laminin beta-1 chain; laminin-type EGF-11ke homology C; Reywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular F; 1-35, Domain: signal sequence #status predicted <SIG>F; 36-1801/Product: laminin beta-2 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;Kissonerghis, W.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995 A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrossis factor receptor type 2; NGF receptor repeat homology
C;Reywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 EIRACTKQQNRVCACEAGRYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGGGVQSQG 59
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F;473-522/Domain: laminin-type EGF-like homology // LE04>
F;525-555/Domain: laminin-type EGF-like homology // LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical // LE05>
F;556-784/Domain: IV // LE04>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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Pred. No. 0.0062;
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F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%;
31.0%;
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A; Accession: S54816
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A; Residues: 1-1801 <HUN>
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Best Local Similarity
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A; Residues: 1-474 <GOO>
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C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 10-Sep-1999 #text_change 08-Dec-2000
C; Date: 10-Sep-1999 #text_change 08-Dec-2000
C; Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R; Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
A; Title: A receptor for tumor necrosis factor defines an unusual family of cellular a A; Reference number: A35356; MUID:90260639
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A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir
Proc. Natl. Acad. Sci. U.S.A. 87, 8311-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                    F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
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A;Title: Two human TNF receptors have similar extracellular, but distinct intracellul A;Reference number: A48416; MUID:91370690
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A;Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758
R;Dembic, 2.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            941 HFATSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDP 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: pretiminally protein
A;Wolccule type: mRNA; protein
A;Residues: 23.461 cDEN;
A;Residues: 23.461 cDEN;
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Cross-references: GB:S63368; NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor necrosis factor receptor 2 precursor [validated] - human N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001 GACDPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTCNLLGTDP 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 118; DB 1; Length 1801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
F;989-1038/Domain: laminin-type EGF-like homology <LE10>F;1041-1095/Domain: laminin-type EGF-like homology <LE11>F;1098-1143/Domain: laminin-type EGF-like homology <LE12>F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------FGFQCIDCASGTF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.019;
```

1

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein

4, 2001, 16:12:12 September Run on:

; Search time 80.15 Seconds (without alignments) 113.098 Million cell updates/sec

US-09-512-363-2\_COPY\_46\_164 Perfect score:

1 DARCCRVHTTRCCRDYPGEE.....GNKTHNAVCVPGSPPAEPLG 119 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

length: 0 length: 2000000000 sed B 8 Minimum 1 Maximum 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	lymphocyte activat	gene ox40 protein	Ox40 homolog - hum	l antigen	OX40 antiqen precu	lectin-B - Virgini	m	gene murine tumour	tumor necrosis fac	laminin beta-2 cha	tumor necrosis fac	laminin beta-2 cha	tumor necrosis fac	B-cell activation	insulin-like growt	insulin-like growt	MEGF6 protein - ra	laminin beta-2 cha	insulin-like growt	ical r	laminin alpha 5 ch	nerve growth facto	thrombospondin 2 p	latent transformin	gene shuttle craft	notch 3 protein	thrombospondin 3 -	hypothetical prote	
SUMMARIES	ΙD	I38426	148700	137552	B32393	S12783	JC5559	A46476	148854	B38634	MMRTS	A35356	S53869	154182	A60771	A33837	A48805	T13954	A55677	IGHUR1	T18975	T10053	JN0006	TSHUP2	A55494	T13938	S45306	$\vdash$	45	T32497
	98	7	~	~	~	~	~	~	7	~	Н	<del>,  </del>	ď	7	~	ď	C	N	7	1	~	7	1	Н	C3	~	7	-	~	7
	Length	255	272	277	256	271	295	302	459	474	1801	461	1798	435	277	1371	329	1574	1797	1367	152	3635	416	1172	1820	1106	2318	926	1106	2150
æ	Query		21.4	20.4	20.3		17.2	16.7	16.4	16.1		S	15.2	S.	15.1	4.	4	٠.		•	2	12.6	2	S	12.5	12.4	•	•	12.3	12.3
	Score	159.5	158	150	149.5	149	127	12	120.5	119	118	117		111.5	111	110	109	108	103	66	94	60	92	92		91.5	91.5		90.5	0
	Result No.	п	7	e	4	'n	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

insulin receptor-r	flbrillin-2 precur	hypothetical prote	thrombospondin 3 p	laminin beta-1 cha	notch3 protein - h	flbrillin-2 precur	Notch homolog prot	crumbs protein - f	Notch-1 protein -	hypothetical prote	disintegrin-like m	hypothetical prote	thrombospondin 2 p	notch4 - mouse
B47417 B36502	A57278	T24272	A57121	MMHUB1	S78549	A54105	T30201	A35672	A46019	T21011	G02390	T26972	A42587	T09059
2.2	7	7	~	_	~	~	~	7	~	~	~	~	~	7
540	2907	164	926	1786	2321	2918	2352	2139	2531	. 259	814	1111	1172	1964
12.2	12.2	12.1	12.1	12.1	12.1	12.1	12.0	11.9	11.9	11.9	11.9	11.9	11.9	11.9
06	90	88	88	68	68	83	88.5	88	88	87.5	87.5	87.5	87.5	87.5
30	32	33	34	35	36	37	38	36	.40	41	42	43	44	45

## ALIGNMENTS

Listabb
Listabbb
Richersonic I38426; JT0752
Richlersonic M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.
Richlersonic M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.
Rythderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.
Rythderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.
A;Accession: 138426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Attle: Richeroces: EMBL:U03397; NID:9571320; PIDN:AAA53133.1; PID:9571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human A;Reference number: JT0752; MUD:94085794
A;Accession: JT0752
A;Molecule type: mRNA
A;Residues: 1-106, RR, 108-255 sSCH>
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne C;Comment: This receptor: receptor: transmembrane factors predicted <AMM>C;Comment: This receptor repeat homology
C;Keywords: 91ycoprotein; phosphoprotein; receptor; transmembrane fastatus predicted <AMM>F;117/Domain: signal sequence fastatus predicted <AMM>F;118-1349/Binding site: carbohydrate (Ann) (covalent) (by caseln kinase II) #status predicter
F;234,235/Binding site: phosphate (Thr) (covalent) (by protein kinase II) #status predicter
F;244,285/Binding site: phosphate (Thr) (covalent) (by protein kinase II) #status predicter

8 Gaps 36; 21.6%; Score 159.5; DB 2; Length 255; 31.9%; Pred. No. 1.8e-06; iive 12; Mismatches 43; Indels 39 Best Local Similarity 31.9 Matches 44; Conservative Query Match

3 RCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ 53 δ

60 RTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGAGCSMC-EQDCKQGQ 110 g

54 GVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG-- 111 ò

112 -----SPPA---EP 117 g δ

RESULT

:||| || DLSPGASSVTPPAPAREP 181

164

q

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PGQ-----GVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNK 102
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33.6%;
                                                                                                                                                                                                                                                                                            T-cell antigen 4-1BB precursor
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Matches 37; Conservative
                                                                                                       103 THNAVCVPGSPPA 115
                                                                                                                                        ::|:|
161 SSDAICEDRDPPA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: 148879
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21
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137552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: 137552
R;Latza, U; Durkpp, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment characterice number: 137552; MUID:94170844
                   gene ox40 protein - mouse

N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Bublimann, J.E.; Van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: I48700; MUID:94044750
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40 A;Reference number: 148334; MUID:95255413
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: BMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
A;Erseland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:9732818; PIDN:CAA59476.1; PID:9732819
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C.Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 RCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 OCTOCNHRSGSELKONCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVPCPPGHFSPGNNQA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RCCRD-YPG----EECCSEWDCMC--VQPEFH----CGDPC--CTTC-----RHHPCP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 158; DB 2; Length 272; Pred. No. 2.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.4%; Score 150; DB 2;
30.8%; Pred. No. 1.2e-05;
tive 11; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: 137552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 CKPWTDCTQFGFLTVFPGNKTHNAVC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 CKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translated from GB/EMBL/DDBJ
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27.4%;
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Best Local Similarity 30.85
Matches 41; Conservative
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Best Local Similarity
Matches 40; Conserv
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A;Molecule type: mRNA
A;Residues: 1-256 <KWO>
A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
A;Cross-references: CB:J74, Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            positive T lymphoc
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9
                                                                                                                                                                                                                                                                                                                                                                            C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: B32393; I48879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40 antigen precursor - rat
NiAlternate names: nerve growth factor receptor homolog
CiSpecies: Rattus norvegious (Norway rat)
CiSpecies: Rattus norvegious (Norway rat)
CiSpecies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
CiAccession: S12783; S08036
EMBO J. 9, 1063-1068, 1990
101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASN 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-271 cMAL2.
A; Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen of activated CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 -----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 SFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKTHNAVCVP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introducts: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Reywords: transmembrane protein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-256/Product: 4-1BB protein #status predicted <MAT>
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F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: Ox40 antigen #status predicted <AMT>
F:211-235/Pomain: transmembrane #status predicted <TWM>
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; Pred. No. 1.2e-05;
15; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: CDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547
A;Accession: B32393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: 148879; MUID: 94179805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SQGKFS------75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9555CF5B24850CB7 CRC64;
BY SIMILARITY.
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Best Local Similarity 23.9
Matches 42; Conservative
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Search completed: September 4, 2001, 16:15:24 Job time: 1136 sec

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                                                                      SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
                                                                                                                                                      SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
  A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS
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Pfam; PF00157; Furin-like; 1.
Pfam; PF001097; Recep_L_domain; 2.
Pfam; PF00109; Recep_L_domain; 2.
Pfam; PF00109; TYRKINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00119; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
TRANSFERSE_DOM; 1.
TRANSFERSE_COM; 1.
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                                                                                                                                                                                            SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
SIGNAL 1 30 POTENTIAL.
                    TYROSINE-PROTEIN KINASE ACTIVITY.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                        PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L29232; AAA41392.1; -. EMBL; M27293; AAA41384.1; -. PIR; A33837; A33837 HSSP; P06213; 11RK.
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Interpro; IPR000719; ...
Interpro; IPR001245; ...
Interpro; IPR00177; ...
Interpro; IPR00171; ...
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                                                                13;
                                                                                                                                                               208 INRCORMCPSVCGRRACTE-NNECCHPE--CLGSCHTPDDNTTCVACRHYYYKGVCVPAC 264
                                                                 Gaps
                                                                                          9 TTRC---CRDYPGEECCSEWDCMCVQPEFHCGDPC-----CTTCRHH-----PC 49
                                                                                                                                              50 PPGQGVQSQGKFSF-GFQCID---CAS----GTFSGG---HEGHCKPWTDCTQFGFLTV 97
                                                                                                                                                                                                                                                                                            CD40_BOVIN STANDARD; PRT; 269 AA.
020203;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38 Last annotation update)
15-UUL-1999 (Rel. 38 Last annotation update)
TNFRSFS OR CD40.
BOS taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
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TWER-CYS 3.
TWER-CYS 3.
TWER-CYS 6.
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TWERF CYS 7.
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TWERF CYS 7.
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MEDLINE=97281225; Pubmed=9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and blological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in
                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19
                                       Length 1370;
                       Score 110; DB 1; Length 15. Pred. No. 0.0082;
1370 AA; 155395 MW; A5946897A41CB145 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD40L RECEPTOR.
                                                                15; Mismatches
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TNFR-CYS 1.
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                                     14.9%;
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                                                                                                                                                                                                   98 FPGNKTHNAVCVPGSPP 114
                                                                                                                                                                                                                           314 ---NSTQSMYCIPCEGP 327
                                                                39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7269
7269
7215
7215
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187
103
1187
1183
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9913;
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SEQUENCE
                                       Query Match
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an email to license@isb-sib.ch).
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IPR001886; -.
IPR002049; -.
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781
1190
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11409
1442
1798
1319
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292
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                                                                                                                     MIM; 150325;
                                                                                                                                      InterPro;
                                                                                                                                                      InterPro;
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 **REQUENCE FROM N.A.*

**X MEDLINE-95316263; Pubmed-7795887;

**X MEDLINE-95316263; Pubmed-7795887;

**A Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,

**A Asiala H., Trygqvason K.;

**A Sainola H., Trygqvason K.;

**Trygvason K.;

**Trygvason K.;

**Trygvason K.;

**A Sainola H., Trygvason R.;

**Trygvason K.;

**A Sainola H., Trygvason R.;

**A Iivanainen A. Sainola H. Sainola H. Sainola H. Sainola Gene.;

**A Sainola H., Trygvason R.;

**A Iivanainen A. Sainola H. Sainola H
                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- TISSUE SPECIFICITY: FOODD IN THE BASEMENT MEMBRANES (MAJOR COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC CLEFT OF THE NEURONGSCULAR JOUCTION.

---- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

---- DOMAIN: DOMAINS UT AND IV ARE GLOBULAR.

---- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAINS.

---- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                    78 HEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQ-HCTSHTCESCTPHSLCLPGFGVKQIAT 136
                                                                                                    Gaps
                                                                                                                                   8 HTTRCCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCTTCRHHP-CPPGQGVQSQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
MEDLINE=95213013; PubMed=7698745;
Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G., Champliaud M.F., Burgeson R.E., Albrechtsen R.;
"Human beta 2 chain of laminin (formerly S chain): cDNA cloning, chromosomal localization, and expression in carcinomas.";
Genomics 24:243-252(1994).
                                                                                                    10;
                                                                                                                                                                                                     61 FSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVC 108
                                                                                                                                                                                                                                    137 GLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKGLVEQHVGTNKTDVVC 186
                                                                   Length 269;
                                                                                                  60; Indels
269
29983 MW; 746903F30F95F387 CRC64;
                                                                 Score 109; DB 1;
Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                 P55268, Q16321,
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).
                                                                                                                                                                                                                                                                                                                       PRT; 1798 AA
                                                                                                  8; Mismatches
                                                                 14.8%;
29.1%;
                                                                                                  32; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
269
269 AA;
                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 32 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMININ DOMAIN IV.
8 X LAMININ EGF-LIKE REPEATS (DOMAIN
III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LÁMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLLED COLL (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 8.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 13.
DOMAIN II.
                                                                                                                                                                                                                                                                                PRINTS; PRO0011; EGFLAMININ.
PROSTIE; PS00122; EGF_1; 10.
PROSTIE; PS01106; EGF_2; 2.
PROSTIE; PS01248; LAMININ_TYPE_EGF; 12.
EMBL: 268155; CAA92279.1; -.
EMBL: 268156; CAA92279.1; JOINED.
EMBL: X79683; CAA56130.1; -.
EMBL: 877512; AAB34682.2; -.
HSSP; P02468; IKLO.
                                                                                                                                                                                                                                Pfam; PF00053; laminin_EGF; 13. Pfam; PF00055; laminin_Nterm; 1.
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TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 29;
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DOMAIN
TRANSMEM
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P24062;
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REPEAT
REPEAT
REPEAT
                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 13|
| 20 STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
| 21 STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
| 22 Singh J., Garber E., van Vijnen H., Karpsusas M., Hsu Y.-M.,
| 23 Asingh J., Garber E., van Vijnen H., Karpsusas M., Hsu Y.-M.,
| 24 Asingh J., Garber E., van Vijnen H., Karpsusas M., Hsu Y.-M.,
| 25 Asingh J., Saber Interactions in the molecular recognition of CD40L
| 27 Asingh J. 1124-1135(1998).
| 28 Asingh J. 1124-1135(1998).
| 29 Asingh J. 1124-1135(1998).
| 30 Asingh J. 1124-1135(1998).
| 31 Asingh J. 1124-1135(1998).
| 41 Asingh J. 1124-1135(1998).
| 52 Asingh J. 1124-1135(1998).
| 53 Asingh J. 1124-1135(1998).
| 54 Asingh J. 1124-1135(1998).
| 55 Asingh J. 1124-1135(1998).
| 56 Asingh J. 1124-1135(1998).
| 57 Asingh J. 1124-1135(1998).
| 58 Asingh J. 1124-1135(1998).
| 58 Asingh J. 1124-1135(1998).
| 59 Asingh J. 1124-1135(1998).
| 50 Asingh J. 1124-1
                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
TUFRSF5 OR CD40.
                                          model of
               33 EFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF--SGGHEGHCKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-89356608; Pubmed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";
EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS0662; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELING OF 24-144.
MEDLINE=97189482. PubMed=9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional mathe ligand binding domain of the human B cell receptor CD40.
Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                        277 AA
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                                                                                                    87 TDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPL 118
                                                                                                                                             189 TRCENQGLVEAAPGTAQSDTTC---KNPLEPL 217
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                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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SIGNAL
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                                                                                                                                                                                                                                                        CD40_HUMAN
P25942;
                                                                                                                                                                                                              RESULT 12
CD40_HUMAN
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Biochem. Biophys. Res. Commun. 187:934-939(1992).
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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Du J., Delafontaine P.; Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                 SEWDCMCVQPE-FHCGDPCCTTC-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Developmental regulation of the rat insulin-like growth factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                                                                                                                                                                     ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-1992 (Rel. 21, Created)
01-WOY-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 46, Last annotation update)
INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 913-1017 FROM N.A.
MEDLINE-92412145; PubMed-1530648;
Kurzenl H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
Kurzenl H., The insuli, receptor family, insulin
receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY;
MEDLINE-90017496; PubMed-2477843;
Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T.
                                                                                                                                                                                                                                                                                                                       Length 277;
                                                                                                                                                                                                                                                                                                                                                     53; Indels
EXTRACELLULAR (POTENTIAL).
                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor gene:";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
                                                                                                                                                                                                                                                                                                                     Score 111; DB 1;
Pred. No. 0.0019;
; Mismatches 53;
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                                         4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AFEKCHPWTSCETKDLVVQQAGTNKTDVVCGP 188
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31.5%;
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                                                                                                                                                                                                                                                          EMBL outstation
                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstati
the Buropean Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                             -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ARCCRVHTTRC-----EWDCMCVQP 32
          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                               MEDLINE=94225209; PubMed=8171323; Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hesslon C., Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                     Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                   LYMPHOTOXIN-BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTODLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%; Score 111.5; DB 1; 25.7%; Pred. No. 0.0025; Live 12; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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Pfam; PF00020; TWRR_G5; 4.
PROSITE; PS00052; TWRR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 3.
                                                                             MEDLINE=93252381; PubMed=8486360;
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 TNFCR OR TNFRSF3.
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                                                           SEQUENCE FROM N.A.
                                        NCBI_TaxID=9606
                                                                    rissue=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
1-OCT-2001 (Rel. 40, Last annotation update)
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   999 DACDPHTGQCLRCLHNTEGPHCGYCKP-----GFHGQAARQSCHRCTCNLLGTDP 1048
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INTERCHAIN (PROBABLE).
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N-LINKED (GLCNAC. .
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Pred. No. 0.0054;
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"Aberrant differentiation of neuromuscular junctions in mice lacking
s-laminin/laminin beta 2.";
Nature 374:258-262(1995).
-I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-I- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
                                                                                                                                                                                                                                                                                                                  941 HFATSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCOLCECSGNIDPTDP 1000
                                                                                                                                                                                                                                            889 CDAHTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPEGPG--SQR 940
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                 60 KFS------75
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                                                                                                                                                                                                             5 CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96278760; PubMed-8662701;

Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,

Albrechtsen R., Wewer U.M.;

"Structural organization of the human and mouse laminin beta2 chain genes, and alternative splicing at the 5' end of the human

Transcript.":
                                                                                                                                                                                                                                                                                                                                                                                    1001 GACDPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTCNLLGTDP 1050
                                                                                                                                                                                                                                                                                                                                                    ---SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                            82;
                                                                                                                                          Score 118; DB 1; Length 1801;
Pred. No. 0.0019;
5; Mismatches 44; Indels 83
N-LINKED (GLCNAC. .) (POTEN
M; 97AEF32F8F31FA75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMB2_MOUSE STANDARD; PRT; 1799 AA. 061292; 062182; 01-NOY-1997 (Rel. 35, Created) 01-NOY-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) LAMININ BETA-2 CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 271:13407-13416(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/J;
MEDLINE=95191650; PubMed=7885444;
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                   1252
1311
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1, 196473 N
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26.0%;
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nes 46; Conservative
                                                                                           AA;
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   1088
1252
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Best Local S
Matches 46
                   CARBOHYD
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   CARBOHYD
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                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

-1 SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRARES (MAJOR COMPONT).

-1 TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.

-1 DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COLLED COIL STRUCTURE.

-1 DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

-1 SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

-1 SIMILARITY: CONTAINS I LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; Lrkuuzuw; -.
Pfam; PF00053; Laminin_EGF; 13.
Pram; PF00055; Laminin_LRerm; 1.
PRINTS; PR00011; EGFLAMININ.
PROSTITE; PS01028; EGFL_1; 10.
PROSTITE; PS01186; EGFL_2; 10.
PROSTITE; PS01288; LAMININ_TYPE_EGF; 12.
Glycoprotein; Basement membrane; Extracellular matrix; Colled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAMININ BETA-2 CHAIN,
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LÁMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 6 (INCOMPLETE).
LAMININ DOMAIN 1V.

EMMININ DOMAIN 1V.
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COIL (POTENTIAL).
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LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 11.
LAMININ EGF-L
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EMBL; U42624; AAC53535.1; JOINED.
EMBL; X75928; CAA53532.1; --
HSSP; P02468; IKLO.
MGD; MGI:99916; Lamb2.
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  -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
-1- FUNCHILE SSSILES LENDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
-1- STHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, 6 ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR WATRIX COMPONENTS,
-1- SUBBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
-1- SIGNEELLULAR LOCATION: EXTRACELLULAR
COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CLEFT OF THE NEUROWISCULAR JUNCTION.
-1- DOMAIN: THE ALCHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COLLED COLL STRUCTURE.
-1- DOMAIN: THE ALCHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ VI AND IV ARE GLOBULAR.
-1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAINS.
-1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
MEDLINE-89159410; PubMed=2922051;
Bunter D.D., Shah V., Merlie J.P., Sanes J.R.;
"A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";
Nature 338:229-234(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix; Coiled coil;
                       60 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP 113
                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
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LAMININ N-TERMINAL (DOMAIN VI)
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                                                                                                                                                                                PRT; 1801 AA
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Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
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HSSP; P02468; IKLO.
InterPro; IPR001561; ..
InterPro; IPR001886; ..
InterPro; IPR001896; ..
                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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HERE WERE REPRESENTED DESCRIPTION OF THE PROPERTY OF THE PROPE

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P20333;
01-FEB-1991 (Rel. 17, Created)
01-FCB-1991 (Rel. 19, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
101-OCT-2000 (Rel. 40, Last annotation update)
100R NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
TNFRSFIB OR TNFR2 OR TNFR2
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90260639; PubMed=2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of
                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96299745; PubMed=8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
                                                                                                                                                                                   . .) (POTENTIAL).
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MEDLING=91045991; PubMed=2172983;
Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Kohno T., Brewer M.T., Hompson R.C., Vannice J.L.;
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
A second tumor necrosis factor receptor gene product can shed
"A second tumor necrosis factor inhibitor.";
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MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
                 CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                            TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. . ) (P.
C791CB6D2FEA574E CRC64;
                                                                       CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 1.
TNFR-CYS 2.
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Nature 398:533-538(1999).

Nature 398:533-538(1999).

- I- FUNCTION: RECEPPOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

- I- FUNCTION: TYPE I EMBHRANE PROFIEIN.

- I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THRENONIRE RESIDUES.

- I- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGANO-BINDING PORTION OF THERE DAY MODERATE TO SERVERE RHEUMATOID.

- I- DATABASE: NAME-BROWN NOTE—CD guide CD120b entry:

- MWW—"http://www.ncbi.nlm.nlh.gov/prow/cd/cd120b.htm".

- WWW—"http://www.enbrelinfo.com/".
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SEQUENCE OF 27-31.

MEDIATE-90110215; PubMed-2153136;

MEDIATE-90110215; PubMed-2153136;

Engelmann H., Novick D., Wallach D.;

"Two tumor necrosis factor-binding proteins purified from human utine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";

J. Biol. Chem. 265:1531-1536(1990).

T. co. 136-141; 300-306 AND 346-362.
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Characterization of ligand binding, internalization, and receptor
phosphorylation "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE=93016040; PubMed=1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and partial amino acid sequence analysis of to distinct tumor necrosis factor receptors from HL60 cells."; J Blol. Chem. 265:20131-20138(1990).
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J. Biol. Chem. 267:21172-21178(1992).
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EMBL; U52157; P
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SEQUENCE FROM N.A.
MEDLINE-91246168; Pubmed-1645445;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SEQUENCE FROM N.A.
MEDLINE=91187885; PubMed=1849278;
Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
"Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is species
specific.";
                                                                                                                                                     NECROSIS FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 119; DB 1; Length 461; Pred. No. 0.00055;
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15-UUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75)
TNFRSFIB OR TNFR2 OR TNFR-2.
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                                            InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS0055; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
                                                                                                                                                                 EXTRACELLULAR (POTENTIAL) POTENTIAL.
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603B580ECD67636F CRC64;
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-> M (IN REF. 1 A).
-> T (IN REF. 4).
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TNER-CYS 3.
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P25119; P97893;
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                                          InterPro; IPR001368;
              CA9; 12-APR-99
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWERCYS 1.

TWERCYS 2.

TWERCYS 3.

TWERCYS 4.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: RECEPTOR FOR TNF-ALPHA.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462EAE398C4D6563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 119; DB 1;
Pred. No. 0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60469; AAA39752.1; -.
EMBL; M59378; AAA40463.1; -.
EMBL; U3948B; AAA85021.1; -.
EMBL; X87128; CAA60618.1; -.
PIR; B38644; B38634.
HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50319 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.1%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1314883; Tnfrsflb.
InterPro; IPR001368; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00020; TNFR_C6; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 AA;
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                               ;
9
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphocytes -- a molecule related to nerve growth factor receptor."; EMBO J. 9:1063-106811990).
-!- PUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-!- SIMILARITY: CONTAINS A LA-NGFR/THFR-TYPE CYSTEINE-RICH REGION.
                                                     5 CRVHTTRCCRDYPGEECCSEW -- - DCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKF 61
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90214614; Pubmed-2157591;
Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·LINKED (GLCNAC. . .) (POTENTIAL). C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                             17;
 Length 256;
                                                                                                           62 SFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKTHNAVCVP 110
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (
                                                                                                                                                                                                                         P15.42;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
01-CT-2000 (Rel. 40, Last annotation update)
                               41;
 Score 149.5; DB 1
Pred. No. 6.5e-07;
                                                                                                                                                                                                          271 AA.
                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29895 MW;
20.3%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X17037; CAA34897.1; -.
                                                                                                                                                                                                                                                                       OX40L RECEPTOR PRECURSOR (C
TNFRSF4 OR TXGP1L OR OX40.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00020; TNFR_c6; 3
                               37; Conservative
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
233
227
102
102
164
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PIR; S12783; S12783.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 AA;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P25942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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DOMAIN
DOMAIN
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                                                                                                                                                                                                       OX40_RAT
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REPEAT
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                                                                                                                                     116
                               Matches
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Length 271;

Score 149; DB 1; Pred. No. 7.5e-07;

20.2%; 28.9%;

Query Match Best Local Similarity

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'n
                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).

-i - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

-i - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                         PTEDTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPA 155
                                                                                                    -----PCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPG 100
 Gaps
                                RCCRD-YPGEECCSEWD-----CMCVQPEFHCG----DPC--CTTCRHH------47
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                 KCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCT
30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-92105763; PubMed-1370315; Torres R.M., Clark E.A.; "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."; J. Inmunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00020; TNFR_c6; 4.
PROSTIE; PS0065; TNFR_NGFR_1; 1.
PROSTIE; PS05005; TNFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
51;
                                                                                                                                                                                                                                                                                                 289 AA.
 Mismatches
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MEDLINE-93094586; Pubmed-1281194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED.
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10;
                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M94126; AAA37404.1;
EMBL; M94129; AAA37404.1;
EMBL; M94128; AAA37404.1;
EMBL; M94127; AAA37404.1;
Conservative
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P25942; 1CDF.
MGD; MGI:88336; Infrsf5.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A46476; A46476.
                                                                                                                                                                         NKTHNAVC 108
                                                                                                                                                                                               SNSLDTVC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                     TNFRSF5 OR CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                    01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Torres R.M.;
37;
                                                                                                                                                                                                                                                                                                 CD40_MOUSE
P27512;
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                                                                                                                                                                                                                                                                RESULT 6
CD40_MOUSE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                   Kwon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                          SEQUENCE FROM N.A.
MEDLINE-92219871; PubMed=7704935;
Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
"Identification of OX40 ligand and preliminary characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 RCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 PGQ------GVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGPROGACKPWTNCTLAGKHTLQPASN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RCCRD-YPG----EECCSEWDCMC--VQPEFH----CGDPC--CTTC-----RHHPCP 50
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.; "The human Ox40 homolog: cDNs structure, expression and chromosomal assistgment of the ACT35 antigen."; Eur. J. Immunol. 24:677-683(1994).
                                                                                                         Interpro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS05052; TNFR_NGFR_1; 3.
PROSITE; PS050050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 150; DB 1; Length 277; Pred. No. 6.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS. TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 AA.
                                                                                                                                                                                                                                                                                                                                                                          OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.4%; Score 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                               EMBL; X75962; CAA53576.1; --
EMBL; S76792; AAB33944.1; ALT_INIT
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MΣ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             169
65
107
126
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 THNAVCVPGSPPA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSDAICEDRDPPA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                             MIM; 600315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41BB_MOUSE
P20334;
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELULLAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
-:- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
-:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. Immunol. 150:771-781(1993).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY ACTIVE DURING T CELL ACTIVATION
-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.; Renomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Inducible T cell antigen 4-1BB. Analysis of expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB),
THERSEP OR ILA OR LX63 OR CD137 OR CD157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00020; TNFR_c6; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS00650; TNFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                    Kwon B.S., Weissman S.M.;
"CDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 X TNFR-CYS
TNFR-CYS 1.
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MEDLINE-93139510; PubMed-7678621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C;
MEDLINE=94179805; PubMed=8133039;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-89184547; Pubmed-2784565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen 4-1BB.";
J. Immunol. 152:2256-2262(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J04492; AAA40167.1; -.
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InterPro; IPR001368; -.
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HSSP; P25942; 1CDF.
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86
118
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256 AA;
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OM protein - protein search, using sw model

Run on:

September 4, 2001, 16:15:23; Search time 43.78 Seconds (without alignments) 93:111 Million cell updates/sec

US-09-512-363-2\_COPY\_46\_164
737
1 DARCCRVHTTRCCRDYPGEE......GNKTHNAVCVPGSPPAEPLG 119 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	1 homo sapien 1 homo sapien 9 homo sapien 2 rattus norv 2 mus musculu 3 mus musculu 9 mus musculu 1 homo sapien 1 homo sapien 2 rattus norv 2 mus musculu 0 rattus norv 2 mus musculu 1 homo sapien 1 homo sapien 1 mus musculu 9 gallus gall 9 gallus gall 1 homo sapien 1 mus musculu 9 gallus gall 6 homo sapien 1 homo sapien 6 homo sapien 1 homo sapien 6 homo sapien 6 homo sapien 6 homo sapien 7 homo sapien 8 mus musculu 9 mus musculu	1
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SUMMARIES	41BB HUMAN OX40_MOUSE OX40_HUMAN A1BB_MOUSE OX40_RAT CD40_MOUSE TUR2_HUMAN TNR2_MOUSE TUR2_HUMAN CD40_HUMAN CD40_HUMAN CD40_BOVIN CD40_BOVIN LMB2_RAT CD40_BOVIN LMB2_HUMAN IG1R_RAT IRR_HUMAN STC_DROME TSP3_MOUSE TSP3_HUMAN	
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DB		
% Query Match Length	2227577 227777 227777 227777 22777 22777 22777 22777 2277 207	
% Query Match		
Score	159.55 140.15.86 111.11.11.11.11.11.11.11.11.11.11.11.11	
Result No.	1284200111111111111111111111111111111111	

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2531 867 1172 1964 415 961 1394 1786 1170 1173
111 111.9 111.9 111.8 111.7 111.7
88 87.5 87.5 87.5 87.8 87 87 86 86
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## ALIGNMENTS

ALBB_HUMAN STANDARD; PRT; 255 AA.  AC Q07011; DT 01-FEB-1995 (Rel. 31, Created) DT 01-FEB-1995 (Rel. 31, Last sequence update) DT 01-CT-2000 (Rel. 40, Last annotation update) DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG) DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).		RN 11) RP SEQUENCE FROM N.A.  RC TISSUE-Blood; RX MEDLINE-94374434; PubMed-8088337; RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J. RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.; RA "Molecular and biological characterization of human 4-1BB and its RI ligand."; RI Eur. J. Immunol. 24:2219-2227(1994).	121 SEQUENCE TISSUE=BI MEDLINE=9 Schwarz H A recept the human family "; Gene 134: [3]	RA Schwarz H.;  RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.  RI (4)  RE TISSUE-Blood;  RX MEDLINE-95347766; Pubmed-7622190;  RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,	
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                                                                                                                                                                                                                                                                                                                                                                                                                         60 RTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGAGCSMC-EQDCKQGQ 110
                                                                                                                                                                                                                                                                                                                                                                                                            54 GVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG-- 111
                                                                                                                                                                                                                                                                                                                                                                  3 RCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J., Claassen E., Noelle R.J., Fell H.; "Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene structure and chromosomal localization of the mouse homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                 TNFR-CYS 3.

N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
FRAK63FEBEFO0460 CRC64;
                                                                                                                                                                                                                                                                                                                    21.6%; Score 159.5; DB 1; Length 255; 31.9%; Pred. No. 8.2e-08; tive 12; Mismatches 43; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                     4-1BB LIGAND RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                          PROSITE: PS00652: TNFR_06; 2.
PROSITE: PS00652: TNFR_NGFR_1; 1.
PROSITE: PS00503: TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Repeat: Signal; Transmembrane.
SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
3 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) 0x40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 AA
                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                         149 NW;
27899 MW;
                                                       EMBL; U03397; AAA53133.1; -.
                                                                  EMBL; L12964; AAA62478.2; -., HSSP; P19438; 1EXT.
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213
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86
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                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                         MIM; 602250;
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P47741;
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DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 CVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC-----HPCETGFYNEAVNYDTCK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CTTCRHHP------CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGH 82
                           Eur. J. Immunol. 25:926-930(1995).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARIIX: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECUENCE (RCT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
ACTIVATED GLYCOPROTEIN 1 RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%; Score 158; DB 1; Length 272; ilarity 27.4%; Pred. No. 1.2e-07; Conservative 11; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL) POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKPWTNCTLSGKQTRHPASDSLDAVC 164
rat OX40 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                         PEGM: PF00020; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=94170844; PubMed=7510240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ψ.,
                                                                                                                                                                                                                                                                                                               EMBL; Z21674; CAA79772.1; -. EMBL; X85214; CAA59476.1; -. HSSP; P25942; ICDF.
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                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:104512; Infrsf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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Matches 40; Conserv
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P43489; 013
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TRANSMEM
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SIGNAL
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F;120-162/Domain: NGF receptor repeat homology <NG3>F;164-201/Domain: NGF receptor repeat homology <NG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: GDB:TNFR2
A,Cross-references: GDB:125914; OMIM:191191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: Cloning, sequencing and partial A:Reference number: 138094; MUID:95121934 A:Accession: 138094
   A; Reference number: A35356; MUID: 90260639
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A; Residues: 27-31 <ENG>
R; Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-195,'R',197-461 <KOH>
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                                                                                                              A; Molecule type: mRNA
A; Residues: 1-461 <SMI>
                                   A; Accession: A35356
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A48416
                                                                                                                                                                                                                                                                                                                                                                                         Subsection beta-2 chain precursor (version 2) - human Nathernate names: s-landin to Nathernate names: Nathernation Signed Native Diol. 14, 489-497, 1994

Native Diol. 14, 489-497, 1994

Antick Diol. 14, 1994

Antick Diol. 14, 1994

Antick Diol. 14, 1994

Antick Diol. 14, 1994

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N;Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
C;Species 10-Sep-1999 (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A33356; A36475; A46416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              940 ATSCHODEYSQOIVCHCRAGYTGLRCEACAPGHFGDPSRPGGRCQLCECSGNIDPMDPDA 999
                                                                      --CCCRPKCCCTCCRTCCTRCCTCCR-- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQ--- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                    105 Pcccecec ----- ecececes 122
                                                                      61 GCGGG----GGGCGCCCCR---PRCC---
                                                                                                                                                 61 PCPPGQGVQSQGKFSFGFQCIDCASG 86
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A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 23.461 CDEM>
A; Residues: 23.461 CDEM>
A; Residues: 23.461 CDEM>
A; Cross-references: GB:S63388; NID:9235648; PIDN:AAB19824.1; PID:9235649
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A; Titler: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A; Reference number: A36007; MUID:90349572
A,Cross-references: GB.M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A;Reference number: A36475; MUID:91045991
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A; Residues: 23-40; 56-56; 136-141; 300-306 <LOE>
A; Residues: 23-40; 56-56; 18-141; 300-306 <LOE>
J. Biol. Chem. 265, 1531-1536, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A; Reference number: A35010; MUID:90110215
A; Accession: B35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellul A;Reference number: A48416; MUID:91370690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 116-140, ', 142-195,'R', 197-362,'T', 364-461 <HEL>
A; Residues: 116-140,' ', 142-195,' R', 197-362,'T', 364-461 <HEL>
A; Cross-references: GB: M35857; NID: 9339751; PIDN: AAA63262.1; PID: 9339752
A; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Blol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Reference number: A23666; MUID: 91056048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Note: the list of introns is incomplete C; Superfamily: tumor necrosts factor receptor type 2; NGF receptor repeat homology C; Reywords: duplication; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
```

.; 8

39; Gaps

40;

; Score 105.5; DE; Pred. No. 0.25; 11; Mismatches

14.0%; 26.8%;

DB 2; Length 2907; Indels

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2 CGPGRLLLGTGTDARCC------RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG 50
                                                                                                                                                                                                                                                                                                                   DPCCTTCRHHPCPPGQGVQSQGKFSFGF------QC-ID---CASG---TFSGGHE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 4, 2001, 16:12:13
Job time: 1110 sec
     F;2488-2523/Domain: EGF homology <EGF>
                                                                                    Query Match
Best Local Similarity 26.8%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :1
786 CNC 788
                                                                                                                                                                                                                                                                                                                                                                                                                           94 GHC 96
                                                                                                                                                                                                                                                                                                                   51
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457278
fibrillin-2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jan-2000
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jan-2000
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jan-2000
R;Zhang, H; Hu, W; Ramirez, F.
J; Cell Biol. 129, 1165-1176, 1995
A;Title: Developmental expression of fibrillin genes suggests heterogeneity of extracell A;Reference number: A57278; MUID:95263670
A;Status: preliminary
                                                                                                                                                                                                     8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:266499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T01B7.8
A;Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T01B7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24272
                                                                                                                                                                                                                                                                                                             57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116
                                                                                                                                                                                                                                                                                                                                                                                                          74 GCGGG----GGGCGCCCCR---PRCC-----CCCRRCCTCCRT--CCCTRCCTCCR-- 115
                                                                                                                                                                                                                                                                                                                                                                       40 -CMCVQPEFHC-----GDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSG-- 90
                                                                                                                                                                                                                                                            2 CGPG---RLLLGTGTDARC------39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-2907 <2HA>
A; Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
C; Superfamily: unassigned EGF-related proteins; EGF homology
F; 1239-1274/Domain: EGF homology <EGFI>
F;262-279/Domain: transmembrane #status predicted <TMN>F;280-461/Domain: intracellular #status predicted <INT>F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                     38;
                                                                                                                                           14.7%; Score 111; DB 1; Length 461; 25.8%; Pred. No. 0.027; Live 14; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 2; Length 164;
Pred. No. 0.029;
1; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1995
A;Reference number: 219867
A;Accession: T24272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| | : :|||
174 SSTDICRPHQICN----VVAIPGNASMDAVC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCCCGCGC -----GCGCCGCGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PCPPGQGVQSQGKFSFGFQCIDCASG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.2%;
Best Local Similarity 34.9%;
Matches 30; Conservative
                                                                                                                                                                        Best Local Similarity 25.8
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-164 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2
A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: T01B7.8
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                                                                                                                                              Query Match
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the murine CD40 gene

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A; Accession: A46515
A; Status: preliminary: not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-287, 'LV' <GRI>
A; Residues: 1-287, 'LV' <GRI>
A; Residues: 1-287, 'LV' <GRI>
A; Experimental source: BABM312; NID:q1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A; Experimental source: BALBJC, liver
A; Note: sequence extracted from NCBI backbone (NCBIP:120357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A) Description: interact with cells and with other basement membrane proteins to promo C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C; Keywords: basement membrane, calcium binding; cell binding; coiled coil; extracellu F; 1-35/Domain: signal sequence #status predicted <SIG> F; 36-1801/Product: laminin beta-2 chain #status predicted <MAT>
        R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
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R; Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A; Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the A; Reference number: S03539; MUID:89159410
A; Accession: S03539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CDSGEFSAQWNREIRC---HQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Comment: For an alternative splice form, see PIR: A46515. C; Comment: For an alternative splice form, see PIR: A46476. C; Superfamily: CD27 antigen: NGF receptor repeat homology C; Keywords: alternative splicing; transmembrane protein F; 105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:1041-1095/Domain: laminin-type EGF-like homology <LE11>F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;989-1038/Domain: laminin-type EGF-like homology <LE10>
                                                            J. Immunol. 149, 3921-3926, 1992
A,Title: Genomic structure and chromosomal mapping of
*Reference number: A46515, MUID:93094586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 127.5; DB Pred. No. 0.00089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laminin beta-2 chain precursor - rat
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28.9%;
            R;Grimaldi, J.C.; Torres, R.; Ko;
J. Immunol. 149, 3921-3926, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Conservative
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F;286-555/Domain: V <DOM5>
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A; Residues: 1-1801 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 TSQTNVIC 186
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A46476
B cell-associated surface molecule CD40, long splice form - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C; Accession: A46476; A46515
R; Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A; Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A; Recence number: A46476; MUID:92105763
A; Accession: A46476
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-305 < TOR>
A; Residues: 1-305 < TOR>
A; Residues: 1-305 < TOR>
A; Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A; Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Phytolacca americana (Virginian pokeweed)
Cispecies: Phytolacca americana (Virginian pokeweed)
Cispecies: Phytolacca americana (Virginian pokeweed)
Cispecies: Division 105559
Cispecession: JC5559
Mills: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytogeneon number: JC5559; MUID:97290889
A;Reference number: JC5559; MUID:97290889
A;Reference number: JC5559; MUID:97290889
A;Residues: J-295 < YAM>
A;Residues: J-295 < YAM>
A;Residues: Toote from the roots of pokeweed (Phytogeneous in the roots of pokeweed (Phytogeneous in the roots of pokeweed (Phytogeneous in the roots)
A;Residues: J-295 < YAM>
A;Resi
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A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53376.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 CRP----GNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 TCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCT
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96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
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31.7%; Pred. No. 0.00011;
tive 17; Mismatches 31;
                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                 19.3%; Score 145.5; DB 2
31.0%; Pred. No. 2.7e-05;
tive 10; Mismatches 66
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.0%
Matches 39; Conservative
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Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSDAIC 166
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#status atypical <LE05>

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Gaps

11;

72; Indels

Length 305;

DB 2;

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57 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%;
34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 25.2%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.9
Best Local Similarity 34.9
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; McMurray, A. submitted to the EMBL Data A; Reference number: 219054 A; Accession: T18975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-152 <WIL>
                                                                                                                                                      179 TNKTDVVC 186
                                                                                                     114 NKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: C06A1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T18975
                                                                                                                                                                                                                                                                                                                                                          C; Accession: I54182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: m
A;Residues: 1-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: LTBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
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R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Blochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Superdas: B-cell, givosprotein; broadcted <SIG5
F;1-20/Domain: signal sequence #status predicted <SIG5
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: intracellular #status predicted <CYT>
F;216-277/Domain: intracellular #status predicted <CYT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
S;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: SO4460; A60771
C;Accession: SO4460; A60771
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor A;Reference number: SO4460; MUID:89356608
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
F;1197-1412/Domain: II <DOM2>
F;1197-1412/Megion: heptad repeats
F;1197-1445/Domain: alpha <ALE>
F;1446-1801/Megion: heptad repeats
F;1446-1801/Momain: I <DOM1>
F;1446-1801/Momain: I <DOM1>
F;1445-1801/Megion: heptad repeats
F;145-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                 6
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889 CDAHTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SQR 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 18 CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQG
                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                   Length 1801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1001 GACDPHTGQCLRCLHHTEGPHCGHCKP-----GFHGQAARQSCHRCTC 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----FGFOCIDCASGTF-----
                                                                                                                                                                                                                                                                              Score 117.5; DB 1;
Pred. No. 0.019;
3; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;ExperImental source: Burkitt lymphoma cell line Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 15.2%; Score 114.5; DB 2; Local Similarity 27.3%; Pred. No. 0.0099; les 35; Conservative 10; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                15.6%;
25.9%;
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.99
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S04460
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Best Local S
Matches 35
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R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq A;Reference number: 154182; MUID:93252381
A;Reference number: 154182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..6
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                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C06A1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CPP-----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --CRDYPGEE---C 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: L04270; NID: 9339761; PIDN: AAA36757.1; PID: 9339762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                       tumor necrosis factor receptor 2-related protein - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 112.5; DB 2;
Pred. No. 0.019;
2; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 112; DB 2;
Pred. No. 0.011;
); Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 ONTSSPSARCOPHTRCENOGLVEAAPGTAQSDTTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
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4, 2001, 16:12:13; Search time 80.15 Seconds (without alignments) 115.949 Million cell updates/sec
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753
1 GCGPGRLLGTGTDARCCRV.....TQFGFLTVFPGNKTHNAVCV 122
 4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                        219241 seqs, 76174552 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: Minimum

DB seq length: 0 DB seq length: 200000000 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Σ.	TA8700	138/36	512783	B32363	137552	JC5559	A46476	MMRTS	A60771	I54182	T18975	S53869	A35356	T24272	A57278	I48854	T13954	A54105	B38634	A55677	T15651	A33837	A48805	A55494	B47417	A55347	JN000E	B36502	T05936
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Length	27.2		170	256	277	295	305	1801	277	435	152	1798	461	164	2907	459	1574	2918	474	1797	188	1371	329	1820	540	1713	416	1268	212
& Query Match	21 5	200	•			18.4		15.6	S.	14.9	14.9	14.8	14.7			13.9	13.7				13.6			12.9	12.8			12.6	12.4
Score	162	150.5	149.5	149	145.5	138.5	127.5	117.5	114.5	112.5	112	111.5	111	107	105.5	104.5	103.5	103.5	103	103	102.5	102	98	97	96.5	96.5	96	95	66
Result No.	-		a m	4	· w	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	53

intrinsic factor-B	laminin alpha 5 ch	apolipoprotein E r	thrombospondin 3 -	latent transformin	insulin-like growt	fibrillin I - bovi	fibrillin 1 precur	tenascin-X precurs	agglutinin isolect	gene shuttle craft	agglutinin isolect	hypothetical prote	hypothetical prote	notch4 - mouse	lectin precursor -
T08618	T10053	JE0237	A46016	A57293	IGHUR1	A55567	A47221	A40701	AEWT2	T13938	A28401	T32497	T44598	T09059	LNRZ
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3623	3635	966	926	1251	1367	2871	3002	3566	213	1106	186	2150	1106	1964	227
12.4	12.4	12.3	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.1	12.0	12.0	12.0
93	93	92.5	92	92	92	92	92	85	91.5	91.5	91	91	90.5	90.5	06
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

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N'Alternate names: OX10 antigen
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequenc_2_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48344; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J
J Immunol. 151, 5561-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A;Reference number: 148700; MUID:94044750
                                                                                                                                                                                                                                                                                                              A) Accession: 148700
A) Status: translated from GB/EMBL/DDbJ
A) Status: translated from GB/EMBL/DDbJ
A) Molecule type: mRNA
A) Residues: 1-272 < REGS
A) Cross-references: EMBL:221674; NID:9312827; PIDN:CAA79772.1; PID:9312828
B) B) A) Cross-references: EMBL:221674; NID:9312827; DIDN:CAA79772.1; PID:9312828
A) Cross-references: EMBL:221674; NID:9312827; DIDN:CAA79772.1; PID:9312828
A) Fittle: Gene structure and chromosomal localization of the mouse homologue of rat OX
A) Reference number: 148334; MUID:95255413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Accession: I48334
A)Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A);Residues: 1-14, G', 16-272 <RE2>
A);Residues: 1-14, G', 16-272 <RE2>
A);Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 -----CTTCRHHP-----CTTCRHB 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC------HPCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.5%; Score 162; DB 2; Length 272; 28.3%; Pred. No. 1.2e-06; ive 11; Mismatches 51; Indels
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138426
lymphocyte activation-induced receptor ILA precursor - human
C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: 0x40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | | : : :||| | CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 28.39
Matches 45; Conservative
gene ox40 protein - mouse
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A; Molecule type: mRNA
A; Residues: 1-256 <KMO-
A; Cross-references: GB:J004492; NID:g201121; PIDN:AAA40167.1; PID:g201122
A; Cross-references: CB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
B; Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A; Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B
A; Reference number: 148879; MUID:94179805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: 137552
R:Latza, U.: Durkop, H.: Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo
Eur.-J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: CDNA structure, expression and chromosomal assignmen
A;Reference number: 137552; MUID:94170844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell antigen 4-1BB precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000 C; Accession: B32393; 148879 R; Kwon, B.S.; Weissman, S.M. Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989 A; Title: CDNA sequence of two inducible T-cell genes. A; Reference number: A32393; MUID:89184547
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A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 116
                                                                                                                                                                                                                                                                                         72 NYDTCKOCTOCNHRSGSELKONCTPTEDTVCOCRPGTQPRQDSSHKLGVDCVPCPPGHFS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 CPPSTFSSIGGOPNCNICRV----CAGYFRFKKFCSSTHNAECECIE-GFHCLGPQCTRC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                    12 LLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAV 71
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                                                                                                                                                                                                   ----PCPPGQGVQSQGKFSFGFQCIDCASGTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>
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19.8%; Score 149; DB 2;
Best Local Similarity 31.2%; Pred. No. 1.3e-05;
Matches 39; Conservative 17; Mismatches 51.
              7 LLLG--TGTDARCCRVHTT----RCCRD-YPGEECCSEWD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 PGSNQACKPWTNCTLSGRQIRHPASNSLDTVC 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arities: A receptor induced by lymphocyte activation (ILA): a new member of the human new Reference number: JT0752; MUID:94085794

A.Reference number: JT0752; MUID:94085794

A.Reference number: JT0752; MUID:94085794

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Residues: 1-106, 'R', 108-255 <SCH>
C.Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro comment: This protein belongs to a member of cell-surface bound or extracellular matrix cicomment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro comment: This protein hopoprotein; receptor; transmembrane protein

C.Comment: Signal sequence #status predicted <SCHOP F.1-17/Domain: signal sequence #status predicted <SCHOP F.1-17/Domain: transmembrane #status predicted <CHANT>
F.187-213/Domain: transmembrane #status predicted <CHANT>
F.187-213/Domain: signal sequence (Asn) (covalent) #status predicted F.23/Filnding site: carbohydrate (Asn) (covalent) #status predicted F.23/Filnding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
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A;Reference number: $12783; MUD:90214614
A;Reference number: $12783; MUD:90214614
A;Residues: 1271 cMAL>
A;Residues: 1-71 
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000 C;Accession: I38426; JT0752 R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, I Eur. J. Immunol. 24, 2219-2227, 1994 A;Tile: Molecular and biological characterization of human 4-IBB and its ligand. A;Reference number: I38426; MUID:94374434 A;Accession: I38426 A;Accession: I38426 A;Status: preliminary; translated from GB/EMBL/DDBJ
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$12783
N/AO antigen precursor - rat
N/Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: $12783 $508036
EMBO J. 9, 1063-1068, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;cross references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 CPPNSFSSAGG--ORTCDI-----CRQCKGVFRIRKECSSISNAECDC---TPGFHCLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
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Best Local Similarity 28.99
Matches 44; Conservative
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A; Residues: 1-255 <RES>
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                                                                                                                                         Print; Process; TB; 9.
PRINTS; PRO0010; EGFBLOOD.
PROSTTE; PS00010; ASX HYDROXYL; 43.
PROSTTE; PS00022; EGF_1; 2.
PROSTTE; PS01186; EGF_2; 37.
PROSTTE; PS01187; EGF_CA; 43.
Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
                                                                                                                                                                                                                                                AORTA AND THE EYES.
-1- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING EGF-LIKE DOMAINS.
                                      EQUENCE OF 752-1505 FROM N.A.
MEDLINE=91304567; PubMed=1852206;
Lee B., Godfrey M., Vitale E., Hori H., Mattel M.-G., Sarfarazl M.,
Tsipouras P., Ramirez F., Hollister D.;
Linkage of Marfan syndrome and a phenotypically related disorder to
two different fibrillin genes.";
Nature 352:330-334(1991).
"Structure and expression of fibrillin-2, a novel microfibrillar component preferentially located in elastic matrices.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Signal; Multigene family; Disease mutation; Polymorphism. SIGNAL
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                                                                                                                        VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964 MEDLINE-96083599; PubMed=7493032;
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EGF-LIKE 2, N
EGF-LIKE 3, N
EGF-LIKE 4, C
EGF-LIKE 5, C
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EMBL; X62009; -; NOT_ANNOTATED_CDS.
PIR; S17063; S17063.
PIR; S31101; S31101.
MISSP; P35555; 1EMO.
MIM; 121050; --
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InterPro; IPR000158; ...
InterPro; IPR001438; ...
InterPro; IPR001881; ...
InterPro; IPR002312; ...
Pfam; PF00008; EGF; 46.
Pfam; PF00683; TB; 9.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-94165150; PubMed-8120105;
Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguineti C.,
Bonadio J., Mecham R.P., Ramirez F.;
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(Rel. 33, Last sequence update)
(Rel. 35, Last annotation update)
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Glycoprotein; EGF-like  2.  NON-CALCIUM BINDING. NON-CALCIUM BINDING. NON-CALCIUM BINDING. CALCIUM-BINDING.
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PF00008; EGF; PF00008; EGF; PF00008; EGF; PF00008; EGF; PF000008; EGF; PF000010; EGF; EGF; EGF; EGF; EGF; EGF; EGF; EGF
Interpro; Pfam; PFOC Pfam; PFOC Pfam; PFOC PRINTS; PFRINTS; PFROSITE; PROSITE; PROSININ DOMAIN DO

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                                                                                                                                                                                                                                                                                                                                                   LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (INCOMPLETE).
LAMININ BOMAIN IV.
8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
                                                                                                                                                                                                                                                                                               LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).
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Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
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LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 8.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 13.
DOMAIN IN II.
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Pfam: PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF: 12.
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EMBL, 268156; CAA92279.1; JOINED.
EMBL, X79689; CAA56130.1; -.
EMBL, S77512; AAB34682.2; -.
HSSP, P02468; IKLO.
MIM, 150325; -.
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Interpro; IPR001886; -.
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   8
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DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: CONTAINS 1 LAMININ N-FERNINAL DOMAIN (DOMAIN VI).
SIMILARITY: CONTAINS 1.5. LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1.5. LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sariola H., Tryggvason K.;
"The human laminin beta 2 chain (S-laminin): structure, expression in fetal tissues and chromosomal assignment of the LAMB2 gene.";
Matrix Biol. 14.489-497(1995).
-i- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
                                                                                                                                Gaps
                                                                                                                    20
                                                                                                                                                                51 DPCCTTCRHHPCPPGQGVQSQGKFSFGF------QC-ID---CASG---TFSGGHE 93
                                                                                                                    CGPGRLLLGTGTDARCC------RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
MEDLINE-95213013; PubMed-7698745;
MEDLINE-95213013; PubMed-7698745;
Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
Champliaud M.F., Burgeson R.E., Albrechtsen R.;
"Human beta 2 chain of laminin (formerly 5 chain): cDNA cloning,
chromosomal localization, and expression in carcinomas.";
Genomics 24:243-252(1994).
                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-95316263; PubMed-7795887;
Itvanainen A., Vuolteenaho R., Salnio K., Eddy R., Shows T.B.,
Itvanainen A., Vuolteenaho R.,
                                                                       Length 2907;
                                                                                             Indels
                                                                       DB 1;
                                                                                             40;
                                                                                                                                                                                                                                                                                         LIMBALL HUMAN STANDARD; PRT; 1798 AA. P55268; Q16321; 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last sequence update) LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).
                                                                       Score 105.5; DB Pred. No. 0.029;
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                             11; Mismatches
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BY
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26.8%;
                                                                                             Conservative
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1701
1710
1725
1817
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                                                                                 Best Local Similarity
 1670
1689
1696
1712
1805
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Coiled coil;

Loechel S., Sanes J.R., Merlie J.P.,

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                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                          CPP-----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           --CRDYPGEE---C 34
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                      ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                             LYMPHOTOXIN-BETA RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                LINKED (GLCNAC. . .) (P. 624626E6022F656F CRC64;
                                                                                                                            Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL.
                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 112.5; DB 25.2%; Pred. No. 0.0017,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE STANDARD; PRT; 1799 AA. 061292; 062182; 01-807-1997 (Rel. 35, Created) 1-10V-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 ONTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                       4 X TNFR-CYS.
                                                                                                                                                                                             TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                   POTENTIAL.
                                                                                             Pfam; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96278760; PubMed-8662701;
                                                                                                                                                                                                                                                                                                                                                                                                                          2 CGPGRLLLGTGTDARCCRVHTTRC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMININ BETA-2 CHAIN PRECURSOR LAMB2 OR S-LAM OR LAMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                         .,
Σ.
                                                          EMBL; L04270; AAA36757.1; -.
                                                                                                                                                                                                                                                                                                                                                        46709
                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 25.2
Matches 39; Conservative
                                                                                       InterPro; IPR001368; -
                                                                                                                                                                   248
435
211
211
1124
1168
211
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72
72
80
80
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                                                                   P25942; 1CDF.
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                                                                            MIM; 600979
                                                                                                                                                        DOMAIN
TRANSMEM
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REPEAT
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REPEAT
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C. --- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMAA), WHICH ARE BOUND TO EACH OTHER BY DISCULTIDE BONDS INTO A CROSS-SHAPED MOLECULE. COMPRISING ONE LONG THREE SHORT ARMS WITH GLOBULES AT EACH END.

THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

C. --- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

C. --- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS I OF FORM A COILED COIL STRUCTURE.

WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

C. --- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

C. --- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, 6 ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR NERVE TERMINALS.
                                                                                                                                                                                                                                                                                                                                     Aberdam D., Galliano M.F., Mattel M.-G., Ortonne J.P., Meneguzzi G.; "S-laminin gene (Lams) maps to Fl band of mouse chromosome 9."; Mamm. Genome 5:393-394(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/J;
MEDLINE-95191650; PubMed-7885444;
Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
"Abberrant differentlation of neuromuscular junctions in mice lacking
                                                                mouse laminin beta2 chain end of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMININ EGF-LIKE
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entities requires a license agreement (See h
or send an email to license@isb-sib.ch).
Durkin M.E., Gautam M., Loechel S., Sanes Albrechtsen R., Wewer U.M.; "Structural organization of the human and
                                                                                                       genes, and alternative splicing at the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                           Biol. Chem. 271:13407-13416(1996).
                                                                                                                                                                                                                                                                            TISSUE=Lung;
MEDLINE=94319092; PubMed=8043959;
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BMBL, U4524; AAC53535.1; JOINED.
EMBL, X75928; CAA53532.1; --
HSSP; P02468; 1KLO.
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Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                            SEQUENCE OF 348-428 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s-laminin/laminin beta 2.";
Nature 374:258-262(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:99916; Lamb2.
InterPro; IPR000561; -.
InterPro; IPR001886; -.
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36
284
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                                                                                                                                               transcript."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQG 72
                                                                                                                                                                                                                                                                                                                                                                                                                              genes suggests heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
Francke U.;
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
MW; 1F28967A67A67AEDE33 CRC64;
                                                                            81;
                                                       DB 1; Length 1799;
                                                                                                                                                                                                   999 DACDPHTGOCLRCLHNTEGPHCGYCKP-----GFHGQAARQSCHRCTC 1041
                                                                                                                                                                                      -----SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                            Indels
                                                                            42;
                                                      14.9%; Score 112.5; DB 3 25.3%; Pred. No. 0.0047; tive 4; Mismatches 43
                                                                                                                                                                                                                                                                FBN2_MOUSE STANDARD; PRT; 2907 AA. Q61555; Q63957; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) FIBRILLIN 2 PRECURSOR.
                                                                                                                                             ----FGFQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95263670; PubMed=7744963; Zhang H., Hu W., Ramirez F.; Developmental expression of fibrillin of extracellular microfibrils."; J. Cell Biol. 129:1165-1176(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 210-317 FROM N.A. MEDLINE=94140368; Pubmed=8307578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L39790; AAA74908.1; -. EMBL; S69359; AAC60685.1; -.
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IPR001881;
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Matches 43; Conserv
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119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAG 178

114 NKTHNAVC

C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 113

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                                                                                                              model of
"A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas."; EMBO J. 8:1403-1410(1989).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal; 3D-structure.
                                       3D-STRUCTURE MODELING OF 24-144.
MEDLINE-97189482; PubMed-9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional mothe ligand binding domain of the human B cell receptor CD40."
Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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MIM; 109535; -.
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01-FEB-1991 (Rel. 17, Created)
01-AG-1991 (Rel. 19, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBBII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
THERSFIB OR INFR2 OR INFBR.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90260639; PubMed-2160731;
MEDLINE-90260639; PubMed-2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 27-31.
MEDLINE=90110215; PubMed=2153136;
MEDLINE=90110215; PubMed=2153136;
Engelmann H., Novick D., Wallach D.;
Two tumon necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1999).
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Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
Brockhaus M.;
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MEDLINE=90349572; PubMed=2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
Ringold G.M., Complementary DNA cloning of a receptor for tumor necrosis factor
and demonstration of a shed form of the receptor.";
Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.";
                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=9104591; PubMed=2172983; Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Kohno T., Brewer M.T., Thompson R.C., Vannice J.L.; As second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Physical mapping and genomic structure of the human TNFR2 Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BELLINE-96299745; PubMed-8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jense Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
                                                                                                  461 AA.
                                                                                                  STANDARD;
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179 TNKTDVVC 186
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P20333;
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CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQXGTSETDTICTCEEGWHCTSEACES 118

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CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 56

15.2%; Score 114.5; DB 1; Length 277; 27.3%; Pred. No. 0.00078; Live 10; Mismatches 72; Indels 11.

Conservative

Query Match Best Local Similarity Matches 35; Conserv us-09-512-363-2\_copy\_33\_154.rsp

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NATURE 3983-538 (1999).

NATURE STATE STA
                                           Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS A LA-NGFR/TNFF-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
WWW-FITEP://www.ncbl.nlm.nlh.gov/prow/cd/cd120b.htm".
DATABASE: NAME-Enberj; NOTE-Clinical information on Enbrel;
WWW-*http://www.enbrelinfo.com/".
                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX BEDLINE-9221490; PubMed-10206649; Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; Structural basis for self-association and receptor recognition on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR 2.
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Phosphorylation; Pharmaceutical; 3D-structure.
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AACS0622.1; JOINED.
AAA36755.1; -
CHARACTERIZATION.
MEDLINE~93016040; PubMed-1328224;
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PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 4.
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A36007; A36007.
A36475; A36475.
B35010; B35010.
A23666; A23666.
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US2156; 2
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MS5994;
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U52163;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
Ehrenfels B. Alpmphotoxin-beta-specific receptor.";
Science 264:707-710(1994).
-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 -CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGPG---RLLLGTGTGTARC------39
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01-CCT-2000 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
LYBEATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
LIBR OR INFCR OR INFRSF3.
                                      BY SIMILARITY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93252381; PubMed-8486360; Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.; Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
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--- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
--- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%; Score 113; DB 1; Length 461; 25.8%; Pred. No. 0.0016; tive 14; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
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Best Local Simin
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P36941;
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P15800;
   PROSITE;
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                       PROSITE;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CDSGEFSAQWINREIRC---HQHRHCEPNQGLRVKKEGTAAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                     CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 56
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunology 90:294-300(1997).
-- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
--- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROPEIN.
--- SIMILARITY: CONTAINS A LA-NGFR/TWFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
N-LINKED (GLCNAC. . .) (POTENTIAL).
C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-97281252; PubMed-9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
                                                                                                                                                                                                                                                                                                                                                                                  11;
Pfam; PF00020; INFR_C, ..., PROSITE; PS00652; TNFR_NGFR_1; 1. PROSITE; PS00650; TNFR_NGFR_2; 4.

Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                            DB 1; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologue: role in B-lymphocyte growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                            CD40L RECEPTOR, EXTRACELLULAR (POTENTIAL)
                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                          Score 127.5; DB 1;
Pred. No. 5.4e-05;
8; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA
                                                                                                                                                                       4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                            16.9%;
28.9%;
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                                                                                                                                                                                                                                                                                     32111
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Best Local Similarity 28.9
Matches 37; Conservative
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194
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289 AA;
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ID CD40_BOVIN
AC Q28203;
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SEQUENCE
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Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;

"A lamini-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";

"A lamini-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.";

"I ature 338.229-234(1989).

"I STHOUGHT TO MEDIATE THE ATTACHENTY, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUBS DURING BERRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

"SUBBURIT: LAMININ IS A COMPLEX GLYCORROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BNDS INTO A CROSS-SHARED MOLECULE

COMPRESING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ), LAMININ-4

(S-BEROSIN), AND LAMININ-7 (KS-LAMININ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC CLEFT OF THE NEUROMOSCULAR JUNCTION.

DOMAIN: THE ALPHA-HELIZAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 TCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWIDCTQFGFLTVFP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 CGKGEFLSTWNREKYC---HEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQ-HCTSHTCE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CGPGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 55
                                                                                                                                                                                                                                                                             TWER-CYS 2.

TWER-CYS 3.

TWER-CYS 3.

TWER-CYS 6.

WHINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                     Glycoprotein; Transmembrane; Repeat; Signal. 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 122.5; DB 1; Length 269;
Pred. No. 0.00015;
9; Mismatches 70; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        746903F30F95F387 CRC64;
                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                CD40L RECEPTOR
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TNFR-CYS 1.
                                                                                                                                                                        POTENTIAL
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MEDLINE-89159410; PubMed-2922051;
TNFR_NGFR_1; 1.
TNFR_NGFR_2; 1.
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16.3%;
Best Local Similarity 28.7%;
Matches 37; Conservative
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215
215
>269
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103
144
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269 AA;
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                                                     B-cell;
PS00652;
                             PS50050;
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CD40_HUMAN
P25942;
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long, as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                HISP, POSJ468, IKLO.
InterPro; IPR000561; -
InterPro; IPR0012049; -
Pfam; PF00053; laminin_BGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; BGFLAMININ.
PROSITE; PS01022; BGF_1; 10.
PROSITE; PS01248; LAMININ_TYPE_BGF; 12.
PROSITE; PS01248; LAMININ_TYPE_BGF; 13.
                                                                                                                                                                                                                                                                                LAMININ BETA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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-i- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
-i- SIMILARITY: CONTAINS 12.1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-i- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                      LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 5.
LAMININ DOMAIN IV.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
BY SIMILARITY.
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LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 8.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
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PIR; S03539; MMRTS.
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-2000 (Rel. 39, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
(TUMOR NECROSIS FACTOR RECEPTOR 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Homin1dae; Homo.
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Pred. No. 0.0017;
3; Mismatches 42;
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Local Similarity 25.9%;
les 44; Conservative
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MEDLINE-89184547; PubMed-2784565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 NYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                     lymphocytes -- a molecule related to nerve growth factor receptor."; EMBO J. 9:1063-1068(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PCPPGQGVQSQGKFSFGFQCIDCASGTFS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD-----CMCVQPEFHCG-- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLGLSLGVTVKLNCVKDTYPSGHKCCRECOPGHGMVSRCDHTRDTVCHPCEPGFYNEAV 71
Mallett S., Fossum S., Barclay A.N.; Characterization of the MRC OX40 antigen of activated CD4 positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi; Muridae; Murinae; Mus.
                                                              -i- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                  PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                        LINKED (GLCNAC. . .) (POTENTIAL) C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB).
THERSE9 OR ILA OR LY63 OR CD137 OR CD157.
                                                                                                                                                                                                                                                                                                        OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      TNER-CYS 2.
TNER-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (1
                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                          -i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.9%; Score 149.5; DB 1
28.9%; Pred. No. 5.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
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INFR-CYS 1.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                   29895 MW;
                                                                                                                                                                                  EMBL; X17037; CAA34897.1; -. PIR; S08036; S08036. PIR; S12783; S12783.
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InterPro, IPR001368, -.
Pfam; PF00020, TNFR_C6; 3.
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271 AA;
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P20334;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
-!- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVE DURING T CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     function.";
J. Immunol. 150:771-781(1993).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGPGRL-LLGTGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC
                                                                                                                                                                                 Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.; "Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                               CHARACTERIZATION, AND SEQUENCE OF 25-29.
MEDLINE-93139510; PubMed-7678621;
Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
4 X TNER-CYS.
1 TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CXS 3.
TNFR-CXS 3.
TNFR-CXS 3.
TNFR-CXS 3.
TNFR-CYS 6.
TNFR-CYS 6.
TNFR-CYS 6.
TNFR-CYS 6.
TNFR-CYS 7.
TNFR-CYS 7.
TNFR-CYS 6.
TNFR-CYS 6.
TNFR-CYS 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4-1BB LIGAND RECEPTOR
                        cDNA sequences of two inducible T-cell genes."; roc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00652; TNFR NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                      STRAIN=BALB/C;
MEDLINE=94179805; PubMed=8133039;
                                                                                                                                                                                                                                                                 Immunol. 152:2256-2262(1994).
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EMBL; U02567; AAA93113.1; -.
PIR; B32393; B32393.
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Best Local Similarity 31.27
Matches 39; Conservative
Kwon B.S., Welssman S.M.;
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                                                                                                       SEQUENCE FROM N.A.
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MEDLINE-95219871; PubMed=7704935;

Baum P. R., Gayle R. B. III, Ranadell F., Srinivasan S., Sorensen R.A., Batson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;

"Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";

"Is extivities on OX40 receptor.";

-I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-I- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROYEEN.

-I- SIMILARITY: CONTAINS A LA-NGFK-TNFR-TYPE CYSTEINE-RICH REGION.

-I- DATABASE: NAME-PROW; NOTE-CD quide CD134 entry;

WWWH-"http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILINE-94170844; PubMed=7510240;
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
Hummel M., Fonatsch C., Stein H.;
"The human OX40 homolog: CDNA structure, expression and chromosomal
assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
TNFR-CYS (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
ACTIVATED GIXCORROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                              277 AA.
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TNFR-CYS 1.
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EMBL; S76792; AAB33944.1; ALT_INIT.
HSSP; P25942; 1CDF.
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P43489; Q13663;
Q1-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
01-OCT-2000 (Rel. 40, Last anno
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TNFR_c6; 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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277 AA;
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                                                           154 KDVVC 158
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117 HNAVC 121
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0040_HUMAN
10 00440_HUMAN
10 00440_HUMAN
10 01-NOV
10 01-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SUBCELLULAR: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                   56 TCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNK 115
                                                                                                                                                                                              46 CRP----GNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCT 100
                                                                           Gaps
                                                                                                                                      2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCT 55
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Torres R.M., Clark E.A.; "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."; J. Immunol. 148:620-626(1992).
         DB 1; · Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-93094586; PubMed=1281194;
Grimmldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                        : 99
                                       : Pred. No. 1.2e~06;
10; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AA
         19.3%; Score 145.5; 31.0%; Pred. No. 1.20
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MEDLINE-92105763; Pubmed-1370315;
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EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
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                                                                        Conservative
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InterPro; IPR001368; -.
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HSSP; P25942; ICDF.
Query Match
Best Local Similarity
Matches 39; Conserv
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ID OX40_MOUSE
AC P47741;
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SIGNAL
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Copyright (c) 1993 - 2000 Compugen Ltd.
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IRR_RAT
LMA3_HUMAN
NGFR_CHICK
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OX40_HUMAN
CD40_MOUSE
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CD40_HUMAN
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FBN2_MOUSE
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TNRC_MOUSE	SORL_RABIT	NTC4_MOUSE	AGI_ORYSA	LMB1_HUMAN	MCS_HUMAN	ITBX_DROME	FBL2_MOUSE	CRB_DROME	KRUA_HUMAN	AGI1_WHEAT	NEL1_HUMAN		ALIGNMENTS
7	7	-	ч	-	Н	7	-	-	Н	~	Н		
415	2213	1964	227	1786	116	846	1221	2139	169	212	810		
12.1	12.1	12.0	12.0	11.9	11.8	11.8	11.8	11.8	11.7	11.7	11.7		
91	16	90.5	90	89.5	89	89	88.5	88.5	88	88	88		
34	32	36	37	38	39	40	41	42	43	44	45		

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                                                                                                                                                                                                                                                                                                                                                 STAIN-BALB/C;
MEDLINE-94044750; PubMed-8228223;
Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse 0x40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gene structure and chromosomal localization of the mouse homologue
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of rat OX40 protein.";
Eur. J. Immunol. 25:926-930(1995).
-I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
BEDLINE-99255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z21674; CAA79772.1; -. EMBL; X85214; CAA59476.1; -. HSSP; P25942; 1CDF.
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InterPro; IPR001368; -.
                                                                                                                                                                             TNFRSF4 OR TXGP1 OR OX40.
STANDARD;
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NCBI_TaxID=10116;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94374434; PubMed-8088337;
Alderson M.K., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
"Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                        14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC------HPCET 65
                                                                                                                                                                                                                                                                                                                                                              54 -----CTTCRHHP-----CTPCRHB 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schwarz H., Tuckwell J., Lotz M.; "A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor
                                                                                                                                                                                                                                                                                     LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
-i- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                 . .) (POTENTIAL)
                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
TOELL ANTIGEN ILA) (CD137 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
Kwon B.S.;
                                                                                                                                                                                                             Length 272
                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwarz H.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                               A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
TNFR-CYS 1.
                                                  TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE)
TNFR-CYS 4.
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                        83 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 121
                                                                                                                                                                                                       b; Score 162; DB 1;
b; Pred. No. 3.9e-08;
11; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Immunol. 24:2219-2227(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Blood;
MEDLINE=94085794; PubMed=8262389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95347766; PubMed=7622190;
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MM
                                                                                                                                                                                                           21.5%;
28.3%;
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Best Local Similarity 28.3%
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272
165
61
103
124.
165
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237
26
26
62
104
125
144
272 AA;
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Q07011;
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                                                                                                                 CARBOHYD
                                                                                                                                                    SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (kat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 CPPNSFSSAGG--ORTCDI-----CROCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                    SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. DATABASE: NAME-PROW; NOTE-CD guide CDw137 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
ACTIVE DURING T CELL ACTIVATION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
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TNFR-CYS 1.

TNFR-CYS 3.

N-LINKED (GLCNAC. . ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.3%; Score 152.5; DB 1; Length 255; Best Local Similarity 31.8%; Pred. No. 2.7e-07; Matches 41; Conservative 11; Mismatches 50; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-1BB LIGAND RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (P
F3A563FE5EF00460 CRC64;
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01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
10-CT-2000 (Rel. 40, Last annotation (MRC 0x40),
10-CT-2000 (Rel. 0x40),
10-CT-2000 (Rel.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00652; TWFR_NGFR_1; 1. PROSITE; PS50050; TWFR_NGFR_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U03397; AAA53133.1; -. EMBL; L12964; AAA62478.2; -. HSSP; P19438; 1EXT. MIM; 602250; -.
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Query Match
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high-sulfur keratin - human
high-sulfur keratin - human
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: 837650
R;Zhumabaeva, B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A;Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A;Reference number: 837649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00710.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone C27A2
A;Title: Amino acid sequences of eight phospholipases A-2 from the venom of Australian A;Reference number: A34860; MUID:90260881
                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15651
R;Nhan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-177 <ZHU>
A; Cross-references: EMBL:X63337; NID:g311879; PIDN:CAA44937.1; PID:g311880
C; Superfamily: keratin high-sulfur matrix protein IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.9%; Score 61; DB 2; Length 188; llarity 38.9%; Pred. No. 7.3; Conservative j; Mismatches 13; Indels
                                                                                                                                                                                                                                                             Length 118;
                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2.
A;Reference number: Z18382
A;Accession: T15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCS 36
                                                                                                                                                                                                                                                      Score 61; DB;
Pred. No. 5.2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                 2 CGPGRLLLGTGTDA --- RCCRVHTTRCCRDYPGEECC-
                                    A.Accession: C34860
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-118 <TAK>
C.Superfamily: phospholipase A2
C.Keywords: carboxylic ester hydrolase
F.48,92/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                      Query Match 23,9%;
Best Local Similarity 34.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
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Best Local Similarity
Matches 14; Conser
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Matches 12; Conser
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A; Residues: 1-188 <NHA>
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A; Introns: 19/3; 91/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A; Note: the reaction is strongly enhanced when the phospholipid is condensed into a m C; Superfamily: phospholipase A2
C; Superfamily: phospholipase A2
C; Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; m F; 4,67/Binding site: micellar substrate (Gin, Tyr) #status predicted F; 11-71,27-118,29-45,44-99; 51-92,60-85,78-90/Disulfide bonds: #status predicted F; 28,30,32,49/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted F; 93/Active site: His #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Tryptophan 110, a residue involved in the toxic activity but not in the enzy A; Reference number: $06655; MuID:90060109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Molecule type: protein A; Residues: 1-17, X', 19-24; 96-112 < MOL>
A; Residues: 1-17, X', 19-24; 96-112 < MOL>
A; Note: chemical modification shows that Trp-110 is required for toxin activity, but R; Yang, C.C.; Chang, L.S.
Biochem. J. 280, 739-744, 1991
A; Title: Dissociation of lethal toxicity and enzymic activity of notexin from Notechi A; Reference number: S19286; MUID:92109676
A; Accession: S19286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The role of phospholipase activity in the action of a presynaptic neurotoxin A;Reference number: A91426; MUID:76092395
A;Contents: annotation; active site
A;Note: both enzyme and and toxin activity are lost upon chemical modification of His C;Comment: Notexin inhibits acetylcholine release at the neuromuscular junction (pres fect). These toxin activities are distinct from phospholipase A enzyme activity. C;Function:
                                                                                                                                                                                                                                                                                                                             C;Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 14-Feb-1997
C;Accession: A00749; S06655; S19286
R;Halpert, J.; Eaker, D.
J. Biol. Chem. 250, 6990-6997, 1975
A;Title: Amino acid sequence of a presynaptic neurotoxin from the venom of Notechis A;Reference number: A92185; MUID:76005594
A;Accession: A00749
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A;Residues: 3-17;64-79 <RMN>
A;Residues: chemical modification studies of four tyrosine residues
R;Halpert, J: Eaker, D: Karlsson, E.
FEBS Lett. 61, 72-76, 1976
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                                                                                                                                                                                                                                                           phospholipase A2 (EC 3.1.1.4) notexin - common tiger snake N;Alternate names: phosphatidylcholine 2-acylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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13 TDARCCRVH--TTRCCR-DYPGEECCSEWDC 40
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Pred. No.
                                                                 139 TPPSCCQLHHAEASCCRPSYCGQSCCRPVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-119 <4ML>
R; Mollier, P.; Chwetzoff, S.; Bouet,
Eur. J. Blochem. 185, 263-270, 1989
A; Title: Tryptophan 110, a residue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.5%;
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Matches 14; Conserv
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Matches

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C;Accession: JC6547
R;Mitsui, S.; Obuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.
Rentsui, S.; Obuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.
A;Title: Structure and hair follicle-specific expression of genes encoding the rat hi
A;Reference number: JC6547; MUID:98201605
A;Accession: JC6547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actracellular matrix protein 1 precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Dec-1995 C; Accession: A57474 R; Bhalerao, J; Tylzanowski, P; Filie, J.D.; Kozak, C.A.; Merregaert, J. J. Biol. Chem. 270, 16385-16394, 1995 A; Title: Molecular cloning, characterization, and genetic mapping of the cDNA coding A; Reference number: A57474; MUID:95332352
                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phospholipase A2 (EC 3.1.1.4), Pa 5 - mulga snake
C;Species: Pseudechis australis (mulga snake)
C;Species: O-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Jul-1997
C;Accession: C34660
R;Takasaki, C.; Yutani, F.; Kajiyashiki, T.
Toxicon 28, 329-339, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: DDBJ:AB003753; NID:93046870; PIDN:BAA25573.1; PID:9
C;Comment: This protein is a cysteine-rich, keratin associated protein.
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              29 CGPG----GHGTPVDELDRCCKIHDD--CYGEAGKKGCFPKLTLYSWKC 71
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A;Residues: 1-559 <BHA>
A;Cross-references: GB:L33416
A;Experimental source: stromal osteogenic cell line MN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: b2E
C;Superfamily: keratin high-sulfur matrix protein IIIA
C;Keywords: hair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61.5; DB
Pred. No. 6.4;
4; Mismatches
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Pred. No. 14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 TPPTCCQLHHAQASCCRPSYCGQSCCRPACC 170
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Best Local Similarity 37.8%;
Matches 14; Conservative
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Best Local Similarity 38.7
Matches 12; Conservative
                                                                                                                                                                                                                                                 JC6547
high sulfur protein B2E -
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C;Species: Phytolacca americana (Virginian pokeweed)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Mar-2000
C;Accession: 05559
R;Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phyto A;Reference number: 05559; MUID:97290889
A;Molecule type: protein
A;Residues: 1-295 <TAN>
A;Residues: 1-295 <TAN
A;Residues: 1-295 <TAN
A;Residues: 1-295 <TAN
A;Residues: 1-295
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C;Species: Pseudechis porphyriacus (red-bellied black snake)
C;Date: 05-0ct-1989 #sequence_revision 05-0ct-1989 #text_change 24-Jul-1997
C;Accession: B32416
R;Schmidt, J.J; Middlebrook, J.L.
R;Schm
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-152 <WILD-
A;Cossidues: 1-152 <WILD-
A;Cross-references: EMBL:249886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:C06Al.6
A;Experimental source: clone C06Al
C;Genetics:
C;Genetics:
A;Genetics:
A;Map postition: 2
A;Introns: 22/3
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 24.7%; Score 63; DB 2; Length 295; Best Local Similarity 33.3%; Pred. No. 6.1; Matches 14; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC-----SEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCSEW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%; Score 62; DB 2; 32.7%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63; DB
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCGGG----GGGCGCCCCRPRCCCCCR----PKCC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.78;
40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lectin-B - Virginian pokeweed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Gaps

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Gaps

Query Match Best Local S Matches 16

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R;Takasaki, C.; Yutani, F.; Kajiyashiki, T.
Toxicon 28, 329-339, 1990
A;Title: Amino acid sequences of eight phospholipases A-2 from the venom of Australia
A;Reference number: A34860; MUID:90260881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:266499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T01B7.8 A;Experimental source: clone T01B7
                                                                                                                                                                                                                      hypothetical protein T01B7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18975
R;McMurray, A.
R;Beference number: 219054
A;Reference number: 219054
A;Accession: T18975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c:Species: Pseudechis australis (mulga snake)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 164;
                          Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 CGPG----GRGTPVDELDRCCKIHDD--CYIEAGRDGCYPKLTWYSWQC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CGPGRLLLGTGTDA----SEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
2 CGPG----RLLLG-TGTDARCCR---VHTTRCCRDYPGEECC--SEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C06A1.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: T24272
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DINA
A;Residues: 1-164 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 GCGGG----GGCCCCRPRCCCCCR----RCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phospholipase A2 (EC 3.1.1.4), Pa 15 - mulga snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63.5; DB Pred. No. 3.5; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCS 36
                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, October 1995 A; Reference number: 219867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.7%; Score 63; DB 3 Best Local Similarity 32.7%; Pred. No. 3.2; Matches 16; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: carboxylic ester hydrolase F; 48, 92/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Moleoule type: profesin
A;Residues: 1-118
C;Superfamily: phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP:T01B7.8
A; Map position: 2
A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: H34860
                                                                                                                                                                                                                                                                                                                       C; Accession: T24272
R;Sims, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: H34860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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ô
                                                                                                                                                                                                                                                                                                                                       RESULT 3
G86232
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
C;Date: 068232
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T5-oct-1999 #sequence_revision 15-oct-1999 #text_change 18-Feb-2000
C;Accession: T25061
R;Cottage, A.
Submitted to the EMBL Data Library, November 1995
A;Recence number: 219975
A;Recence number: 219975
A;Recession: T25061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-788 < MLL>
A;Cross references: EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T21B6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-416 <STO>
A;Cross-references: GB:AE005172; NID:g2160175; PIDN:AAB60738.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 788;
                                                        Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                        12; Indels
                                                                                                                                                                                                                      29 CGPG----GRGTPVDELDRCCKIHDD--CYIEAGKDGCYPKLTWYSWDC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: papain
F;140,283,303/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                        DB 1;
0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 2;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64.5; DB
Pred. No. 8.3;
4; Mismatches
                                                     Score 69; DB 1
; Pred. No. 0.7;
4; Mismatches
                                                                                                                                                                                    2 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 CCCARELFGLCFSWKCCEIESAVCCKD--GRHCC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECC 35
                                                        27.18;
34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.9%;
Best Local Similarity 35.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%;
ilarity 39.6%;
Conservative
                                 Query Match
Best Local Similarity 34.78
"atches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:T21B6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Gaps

Gaps

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4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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protein - protein search, using sw model

4, 2001, 16:12:13; Search time 80.15 Seconds (without alignments) 38.966 Million cell updates/sec September Run on:

US-09-512-363-2\_COPY\_33\_73 255 1 GCGPGRLLLGTGTDARCCRV.....TTRCCRDYPGEECCSEWDCM score: Perfect

Sequence:

Scoring table:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

length: 2000000000 Minimum DB seq length: 0 Maximum DB seq length: 20

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CHANABLEC

SUMMARIES	DB ID	3 2 E34860 phospholipase A2 (	1 PSSNK3 phospholipase	2 G86232 hypothetical	2 T25061 hypothetical	2 T24272 hypothetical	2 H34860 phospholipase	2 T18975 hypotheti	2 JC5559 lectin-B - Vi	2 B32416 phospholi	2 JC6547	2 A57474	2 C34860	2 T15651	2 S37650 high-sulfur k	1 PSNOAT	1 PSNOAS	2 JC6548	1 LNRZ	2 A32416	1 psoxB	1 PSSNK1	2 F34860	1 KRSHHC	2 147111	2 I47108 high-sulfur	1 KRSHHB	2 I47106	
	Length	118	118	416	788	164	118	152	295	117	188	559	118	188	177	119	119	122	227	117	118	118	118	152	152	152	156	172	
ď	Query Match	27.5	•					24.7	24.7	24.3	24.1	•								23.1				23.1			23.1		
	Score	70	69	99	64.5	3	63	63	63	62	61.5	$\leftarrow$	61	61	60.5	9	9	59.5	φ.	59	59	29	59	59	29	29	59	59	
	Result No.	П	7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	

high-sulfur kerati	tenascin-X - bovin	phospholipase A2 (	high-sulfur wool m	high-sulfur wool m	high-sulfur wool m	keratin high-sulfu	high-sulfur wool m	hypothetical prote	phospholipase A2 (	otogelin - mouse	tenascin-X precurs	phospholipase A2 (	fibrillin-2 precur	structural polypro	structural polypro
S37649	T42629	PSOXG	147109	147112	147107	KRSHHA	147105	S43070	A27099	T42214	A40701	B34860	A57278	GNWVR4	GNWV77
~	~	Н	7	7	7	7	7	7	~	7	П	7	~	Н	~
175	4135	133	152	152	162	172	182	331	145	2910	3566	118	2907	1063	1063
22.9	22.9	22.7	22.7	22.7	22.7	22.7	22.7	22.7	22.5	22.5	22.5	22.4	22.4	22.2	22.2
		æ	89	28	28	28	28	28	7.5	7.5	7.5	22	23	56.5	6.5
58.5	58.5	S							വ	S	in			Ñ	ທີ

## ALIGNMENTS

E3486

990 #text\_change 24-Jul-1997

R;Takasaki, C.; Yutani, F.; Kajiyashiki, T.
Toxicon 28, 329-339, 1990
A;Title: Amino acid sequences of eight phospholipases A-2 from the venom of Australia A;Reference number: A34860; MUID:90260881
A;Reference number: E34860

A; Status: preliminary A; Molecule type: protein A; Residues: 1-118 <TAK>

C;Superfamily: phospholipase A2 C;Keywords: carboxylic ester hydrolase F;48,92/Active site: His, Asp #status predicted

Gaps 16; Length 118; 11; Indels DB 2; Score 70; DB 2 Pred. No. 0.55; 4; Mismatches 27.5%; 36.7%; Ouery Match
Best Local Similarity 36.7
Matches 18; Conservative

4;

2 CGPGRLLLGTGTGTDA----RCCRVHTTRCCRDYPGEECC-----SEWDC 40 ŏ qq

phospholipase A2 (EC 3.1.1.4) Pa 13 - mulga snake N;Alternate names: phosphatidylcholine 2-acylhydrolase

of an Australian C;Species: Pseudechis australis (mulga snake)
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 28-Feb-1997
C;Accession: A00748
R;Nishida, S;; Terashima, M; Tamiya, N.
Toxicon 23, 87-104, 1985
A;Title: Amino acid sequences of phospholipases A-2 from the venom of an Austricence number: A94319; MUID:85193286

A; Accession: A00748 A; Molecule type: protein A; Residues: 1-118 <NIS>

A; Residues: 1-118 <NIS> C; Comment: There are many protein components with phospholipase A2 activity in the mu C; Function:

A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A; Note: the reaction is strongly enhanced when the phospholipid is condensed into a m C; Superfamily: phospholipase A2 C; Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; p F; 4, 5/Fbinding site: micellar substrate (Gln, Tyr) #status predicted F; 28, 30, 32, 49, 49+98, 51-91, 60-84, 78+98/pisulfide bonds: #status predicted F; 28, 30, 32, 49/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted F; 48, 92/Active site: His, Asp #status predicted

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between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb.sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 CRPDCRVEGTSLPPCCVVSCTSPSCCQLYYAQASCCRPSYCGQSCCRPACC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CGPGRLLLGTG-----TDARCCRVHTTR--CCR-DYPGEECCSEWDC 40
                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.1%; Score 59; DB 1; Length 181; Best Local Similarity 29.4%; Pred. No. 2.3; Matches 15; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                      D3E4874E21757B12 CRC64;
                                                                                                                                                                                                           6 X 10 AA TANDEM REPEATS.
                                                                                                        EMBL; X01610; CAA25759.1; --
PIR; S07911; KRSHHD.
InterPro; IPR002494; --
Pfam; PF01500; Keratin_B2; 1.
Keratin; Repeat.
INIT_MET 26 85 6.
REPEAT 26 35 1.
REPEAT 36 45 2.
                                                                                                                                                                                                                                                                                                                      18679 MW;
                                                                                                                                                                                                                                                                                                                       181 AA;
                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Search completed: September 4, 2001, 16:15:25 Job time: 1137 sec

SHEEP

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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                   MEDILIRE-83299218; PubMed=6193483;
Powell B.C., Sleigh M.J., Ward K.A., Rogers G.E.;
Powell B.C., Sleigh M.J., Ward K.A., Rogers G.E.;
"Mammalian keratin gene families: organisation of genes coding for the B2 high-sulphur proteins of sheep wool.";
Nucleic Acids Res. 11:5327-5346(1983).
-!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 KDA, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                 KERATINS (40-56 KDA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 CRPDCRVEGTSLPPCCVVSCTSPSCCQLYYAQASCCRPSYCGQSCCRPACC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59; DB 1; Length 156;
Pred. No. 2.1;
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EE549ADCF1F1FB39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CGPGRLLLGTG------TDARCCRVHTTR--CCR-DYPGEECCSEWDC
              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                       MEDLINE=72206034; PubMed=4555954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16040 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002494; -.
Pfam; PF01500; Keratin_B2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.1%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.49
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KERATINS (40-56 KDA).
                                                                                                                                                        Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keratin; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02838; KRSHHB.
                                                                                                 Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KR2D_SHEEP
P08131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
SEQUENCE
                                                                                                                                                                                                                  SEQUENCE
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REPEAT
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KR2D_SHEEP
QΩ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE New Biol. 234:148-1481971)
-!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
MATRIX OF OFTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
6-20 KDA, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
KERATINS (40-56 KDA).
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                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Powell B.C., Sleigh M.J., Ward K.A., Rogers G.E.; "Mammalian keratin gene families: organisation of genes coding for the B2 high-sulphur proteins of sheep wool."; Nucleic Acids Res. 11:5327-5346(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THE SOURCE OF THIS KERATIN IS LINCOLN WOOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 CRPDCRVEGTSLPPCCVVSCTSPSCCQLYYAQASCCRPSYCGQSCCRPACC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elleman T.C.; "Amino-acid sequence of a high-sulphur protein from wool.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                  ---SEWDC 40
                                      29 CGWG----GSGTPVDELDRCCQVHDN--CYEQAGKKGCFPKLTLYSWKC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.1%; Score 59; DB 1; Ler
29.4%; Pred. No. 2;
ive 6; Mismatches 18;
                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2C.
Ovis aries (Sheep).
                2 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC
                                                                                                                                                        151 AA
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                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=83299218; PubMed=6193483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=72077141; PubMed=5289313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
15475 MW;
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Pfam; PF01500; Keratín_B2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keratin; Acetylation; Repeat.
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                                                                                                                                                          STANDARD;
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Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S07349
                                                                                                                                                        KR2C_SHEEP
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MOD_RES
REPEAT
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RESULT 14 KR2B\_SHEEP

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REPEAT REPEAT

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Gaps

12;

18; Indels

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PA2A_PSEAU
P20255;
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   FTFFFF
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **Amino-acid sequence of the beta 1 isosubunit of taipoxin, an extremely potent presynaptic neurotoxin from the Australian snake taipan (Oxyuranus s. scutellatus).";

**Eur. J. Biochem. 128:11-75(1982)."

-I- FUNCTION: TAIPOXIN IS THE MOST POTENT ANIMAL TOXIN KNOWN.

THE BETA CHAIN IS NEITHER TOXIC NOR ENZYMATICALLY ACTIVE BY ITSELF. IT DOES NOT BIND CALCIUM.

-I- SUBUNIT: CONTAINS THREE NONCOVALENTLY BOUND CHAINS (ALPHA, BETA, AND GAMMA), BACH RELATED TO PHOSPHOLIPASE A2.

-I- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2.

PIR: A00755; PSOXB.
PHOSPHOCHOLINE + A FATTY ACID ANION.
--- MISCELLANEOUS: LD(50) IS 0.24 MG/KG BY INTRAVENOUS INJECTION.
--- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH
PHOSPHOLIPASE AZ ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1988 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
Oxyuranus scutellatus scutellatus (Australian taipan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Elapidoaeuria; Squamata; Scleroglossa; Serpentes; Colubroidea;
NCBI_TaxID-8667;
                                                                                                                                          Multigene family; Venom.
                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                              23.1%; Score 59; DB 1; Length 118; 32.7%; Pred, No. 1.7;
                                                                                                                                                                                                                                                                                                                                         2 CGPGRLLLGTGTGTDA----RCCRVHTTRCCRDYPGEECC----SEWDC 40
                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                  BY SIMILARITY.
                                                  -i- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PIR; A00747; PSSNK1.
HSSP; P00608; 1AE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presynaptic neurotoxin; Multigene family; Venom. DISULFID 11 71 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                118 AA
                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                           Calci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom;
MEDLINE=83079319; PubMed=6756920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001211; -. Pfam; PF00068; phoslip; 1. PRINTS; PR00389; PHPHLIPASEA2.
                                                                                            Pfam; PF00068; phoslip; 1.
PRINTS: PR0389; PHPHLIPASEA2.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_SPF; 1.
Hydrolase; Lipid degradation; (
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                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                      InterPro; IPR001211; -.
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92
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                                           THEM ARE MYOTOXIC
                                                                                                                                                                                                                                                                                                         Local Similarity
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P00615;
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SEQUENCE
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PA22_OXYSC
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Gaps
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15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 ISOZYME PA-12A (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostoml;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophlinae; Pseudechis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                              32;
                                                                                                                                                                                                              2 CGPGRLLLGTGTGTDA----RCCRVHTTRCCRDYPGEECCSE------WDC
                                                                                                                                                                                                                                 29 CGKG----GSGTPVDDLDRCCQVH------DECYAEAEKHGCYPSLTTYTWEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene family; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 1; Length 118;
                                                                                                                                                Length 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
BY SIMILARITY.
3; 94392A8EA5A28273 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY PIR; F34860; F34860.
HSSP; P00608; 1AE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
SIMILARITY.
75C705C7B35E5161 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudechis australis (Mulga snake) (King brown snake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                               DB 1;
1.7;
                                                                                                                                             Score 59; DB 1
Pred. No. 1.7;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                             118 AA
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                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Venom;
MEDLINE-90260881; PubMed-2343466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCEPPOS DROUGHL; -.
INCEPPOS DROUGH; -.
Pfam: PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Lipid degradation;
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                                                                                                 MM.
                                                                                                                                               23.18; 28:18;
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32.78;
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12969
                                                                                               13236
                                                                                                                                               Query Match 23.1
Best Local Similarity 28.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                             STANDARD;
   117
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Matches 16; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity
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                                                               TISSUE=Venom
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P04056;
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SEQUENCE
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PA21_PSEAU
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 (EC 3.1.1.4) (PSEUDEXIN A CHAIN) (PHOSPHATIDYLCHOLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 CGLGRDYCGTGCQSGACCSSQRCGSQGGGATCSNNQCCSQYGYCGFGSEYCGSGCQNGPC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
FUNCTION: N-ACETYL-D-GLUCOSAMINE BINDING LECTIN. SIMILARITY: CONTAINS FOUR COPIES OF A CHITIN-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL). 691EB39F6690BAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                      CHITIN-BINDING 2.
CHITIN-BINDING 3.
CHITIN-BINDING 3.
CHITIN-BINDING 4.
PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 227
                                                                                                                                            HSSP; P10968; 1WGC.
InterPro; IPR001002; -.
Pfam; PF00187; chitin_linding; 4.
PRINTS; PR00451; CHITINBINDNG.
PROSITE; PS00056; CHITINBINDNG; 4.
Lectin; Duplication; Chitin-binding; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59.5; DB 1; I
Pred. No. 2.4;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudechis porphyriacus (Red-bellied black snake)
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                                                                                                                                                                                                                                                        CHITIN-BINDING 1.
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                                                                                                                                                                                                                                          KDA
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8
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P20258;
01-FEB-1991 (Rel. 17, Created)
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Best Local Similarity 20.2
Matches 17; Conservative
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122
122
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PIR; A23616; A23616.
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Schmidt J.J., Middlebrook J.L.;
"Purification, sequencing and characterization of pseudexin phospholipases A2 from Pseudechis porphyriacus (Australian red-bellied black snake).",
Toxicon 27:805-818(1989).
-!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
-!- CATALYTIC ACTIVITY: PHOSPHOGLYCERIDES.
-!- CATALYTIC ACTIVITY: PHOSPHOGLYCERIDES.
-!- CATALYTIC ACTIVITY: PHOSPHOGLYCERIDES.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosuuria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophilnae; Pseudechis.
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01-NOV-1986 (Rel. 03, Last Sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 ISO2YME PA-11 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PIR; A32416; A32416.
HSSP; POGGO8; LAE7.
INTERPORT INTERPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Acanthophiinae; Pseudechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 1; Length 117; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC-----SEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 CGWG----GSGTPVDELDRCCQTHDN--CYDQAGKKGCFPKLTLYSWKC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43804BC379277D9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
                                                                                                                                                                                                 MEDLINE-89388835; PubMed=2675391;
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MM
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92
71
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302
373
463
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535
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Best Local Similarity
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P20252;
                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                       VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                           CHAIN
DOMAIN
REPEAT
                                                                                                            Repeat.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1-CATALTIC ACTIVITY: PROSPRATIONING.
-1-CATALTIC ACTIVITY: PROSPRATIONING.
-1-SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-1-SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-1-SIMILARITY: BIS2416.
-1-SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-1-SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-1-SIMILARITY: BOOGOS: 1AE7.
-1-SIMILARITY: BOOGOS: 1AE7.
-1-SIMILARITY: BOOGOS: 1AE7.
-1-SIMILARITY: PROBLED: 1AE7.
-1-SIMILARITY: BOOGOS: 1AE7.
-1-SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
phospholipases A2 from Pseudechis porphyriacus (Australian red'bellided black snake).";
Toxicon 27:805-818(1989).
-i- FUNCTION: PA2 CATALEZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EXTRACELULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 20-37; 71-83 AND 109-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62; DB 1; Length 117;
Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGPGRLLLGTGTGTDA----RCCRVHTTRCCRDYPGEECC-----SEWDC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                566A4F45E23E268B CRC64;
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32.78;
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Les 16; Conserv
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Q61508;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophlinae; Pseudechis,
                                                                                                                                                                                                 Signal; Alternative splicing; Extracellular matrix; Glycoprotein;
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN SHORT ISOFORM).
BBF37FAB7D67E2E8 CRC64;
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15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 ISOZYME PA-5 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
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Pred. No. 2.9;
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01-JUL-1989 (Rel. 11, Created)
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1AE7; 15-MAY-97.
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S08258; PSNOAS.
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AC P11219;
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MEDLINE-92233936; PubMed=1568473;
Westerlund B., Nordlund P., Uhlim U., Eaker D., Eklund H.;
Westerlund B., Nordlund P., Uhlim U., Eaker D., Eklund H.;
The three-dimensional structure of notexin, a presynaptic neurotoxic phospholipase A2 at 2.0-A resolution.";
FEBS Lett. 301.159-164(1992).
-!- FUNCTION: PA2 CAPALIZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
                                                                                                                                                                                                                      Gaps
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toxic activity but not in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-TENDEN.,
MEDLINE-TENDEN,
Halpert J., Eaker D.;
"Amino acid sequence of a presynaptic neurotoxin from the venom of Notechis scutatus scutatus (Australian tiger snake).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chwetzoff S., Mollier P., Bouet F., Rowan E.G., Harvey A.L., Menez On the purification of notexin. Isolation of a single amino acid variant from the venom of Notechis scutatus scutatus."; FEBS Lett. 261:226-230(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Elapidae, Acanthophiinae, Notechis.
                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PHOSPHOLIPASE A2 (EC 3.1.1.4) (NOTEXIN) (PHOSPHATIDYLCHOLINE 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Notechis scutatus scutatus (Mainland tiger snake) (Common tiger
                                                                                                                                                                                                                      16;
                                                                                                                                                                              Length 118;
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Mollier P., Chwetzoff S., Bouet F., Harvey
"Tryptophan 110, a residue involved in the
the enzymatic activity of notexin.";
Eur. J. Blochem. 185:263-270(1989).
                                                                                                                                                                                                                    4; Mismatches
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FEBS Lett. 61:72-76(1976).
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FUNCTION: INHIBITS NEUROMUSCULAR TRANSMISSION BY BLOCKING CETYLCHOLINE REBLEASE FROM THE NERVE TERMINI. ACT PRESYNAPTICALLY CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYLPOSPHOCHOLINE + A FATTY ACID ANION.
                                                                                                                                                                                                                                                          TOXIC
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Chapot M.-P., Peumans W.J., Strosberg A.D.;
"Extensive homologies between lectins from non-leguminous plants.";
FEBS Lett. 195:231-234(1986).
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae;
                                                                                                                                                                   SUBUNIT: MONOMER.
DISEASE: NOTEXIN INHIBITS THE RELEASE OF ACETYLCHOLINE AT THE
                                                                                                                                                                                                                                                     NEUROMUSCULAR JUNCTION (PRESYNAPTIC EFFECT) AND IS DIRECTLY TO TO SKELETAL MUSCLE UPON LOCAL APPLICATION IN VIVO (DYSTROPHIC
                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANEOUS: LD(50) IS 0.025 MG/KG BY INTRAVENOUS INJECTION -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
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Wilkins T.A., Raikhel N.V.;
Expression of rice lectin is governed by two temporally and spatially regulated mRNAs in developing embryos.";
Plant Cell 1:541-549(1989).
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Pred. No. 1.3;
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MEDLINE=92404719; Pubmed=2535550;
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Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                       NCBI_TaxID-8670;
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DISULFID
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   SOUR REPT TO THE PROPERTY OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE—Venom;

X MEDLINE—85193286; PubMed=3887651;

A Nishida S., Terashina M., Taniya N.;

A Nishida S., Terashina M., Taniya N.;

A ustralian acid sequences of phospholipases A2 from the venom of an arralian acid sequences of phospholipases A2 from the venom of an arralian acid sequences of phospholipases A2 from the venom of an arralian acid sequences of phospholipases A2 from the venom of an arralian acid sequences CI TO TO TO TO TO TO THE TO TO TO TO THE TO TO TO THE TO TO TO THE TO TO THE TO TO THE TO THE TO TO THE TO TO THE TO T
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                                                                                                                                                                                                                                                                                                        01-NOV-1986 (Rel. 03, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 ISOZYME PA-13 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 ISO2YME PA-15 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
                                                                                                                                                                                                                                                                                                                                                             Fernicolass).

Eukaryota; Metazoa; Chulga snake) (King brown snake).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Caleroglossa; Serpentes; Colubroidea; Elapidae; Acanthophiinae; Pseudechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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2 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC-----SEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECCFDFDB8D91AC8F CRC64;
                                                                                                                                                                                                       118 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA
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                                                                                                                                                                                                                                                                        (Rel. 03, Created)
(Rel. 03, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00118; PA2_HIS; 1. PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
Matches 17; Conserv
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01-NOV-1986 (
15-DEC-1998 (
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P20257;
                                                                                                                                                                                                       PA2D_PSEAU
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D PASD_PSEAU
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DT 15-DEC
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PAZE_PSEAU
ID PAZE_P
AC P20257
DT 01-FEB
DT 15-DEC
DE PHOSPH
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 (EC 3.1.1.4) (PSEUDEXIN B CHAIN) (PHOSPHATIDYLCHOLINE
                                                                                                                       Gaps
Pseudechis australis (Mulga snake) (King brown snake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophilnae; Pseudechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium; Multigene family; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudechis porphyriacus (Red-bellied black snake).
Eukaryota, Metazoa; Chordate; Craniata; Vertebrate; Euteleost
Lepidosauria; Squamata; Sclerogiossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Pseudechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 CGPG----GRGTPVDELDRCCKIHDD--CYIEAGKDGCYPKLTWYSWQC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC----SEWDC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                            THEM ARE MYOTOXIC.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PIR; H34860; H34860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAOFDFC13D91AC9A CRC64;
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SIMILARITY.
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SIMILARITY
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MEDLINE=89388835; Pubmed=2675391;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001211; -.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPLITASEA2.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13200 MW;
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bothrops as notechis sc bacillus br mus musculu rattus norv

P24605 P08873 P34905

dictyosteli mus musculu homo sapien pseudechis trimeresuru vaccinia vi

061292 P15800 P54643 Q60675 Q07954 P20256 P70090

variola vir

P33841

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TATALOLE YOUR STATE OF THE PHOSPHOLIPSE AS A FROM the venom of Takasaki C., Yutani F., Kajiyashiki T.;

Takasaki C., Yutani F., Kajiyashiki T.;

Takasaki C., Yutani F., Kajiyashiki T.;

RT Takasaki C., Yutani F., Kajiyashiki T.;

RT Takasaki C., Yutani F., Kajiyashiki T.;

Taustralian king brown snake, Pseudechis australis.";

Taustralian king brown snake, Pseudechis australis.";

TATALYIC ACTIVITY: PHOSPHOLIUME + H(2)O = 1-ACYLGLYCERYL-CCC - CATALYIC ACTIVITY: PHOSPHOGLYCERIDES.

C. - CATALYIC ACTIVITY: PHOSPHOLINE + H(2)O = 1-ACYLGLYCERYL-CCC - PHOSPHOLINE + A FATTY ACID ANION.

C. - MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH PHOSPHOLIPASE A ACTIVITY IN THE WULGA SNAKE VENOM AND SOME OF THEM ARE MYOTOXIC.

C. - SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A FAMILY.

C. - SIMILARITY: PROOBS : PHPHLIPASEA 2.

DR FASP; PO00608; PAPA:

R PROSTITE; PS00119; PAZ-HIS; 1.

R PROSTITE; PS00119; PAZ-HIS; 1.

R PROSTITE; PS00119; PAZ-ASP: 1.

M Hydrolase; Lipid degradation; Calcium; Multigene family; Venom. STATE AND STATE
                                                                                                                                                                                                                                                                                                        ul-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 ISOZYME PA-10A (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
                                                                                                                                                                                                                                                                                                                                                                     Pseudechis australis (Mulga snake) (King brown snake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eppidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Pseudechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.5%; Score 70; DB 1; Length 118; 36.7%; Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGPGRLLLGTGTDA----RCCRVHTTRCCRDYPGEECC----SEWDC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                884D1D3A6E2B5FCB CRC64;
                                                                                                                                                                                                                                                                          118 AA
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                                                                                                                                                                                                      ALIGNMENTS
                                         LMB2_MOUSE
LMB2_RAT
SP87_DICDI
LMA2_MOUSE
PA22_BOTAS
PA20_NOTSC
MTB1_BACBR
                                                                                                                              PA25_TRIGA
VA16_VACCV
VA16_VARV
                                                                                                                  PA2C_PSEAU
PA25_TRIGA
                                                                                                   LRP1_HUMAN
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01-FEB-1991 (Rel. 17, Last seq
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Matches 18; Conserv
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P20254;
ACT_SITE
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sus scrofa
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Compugen Ltd
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                                                                                                                                                                                                                                                             93435 segs, 34255486 residues
                                                                                                   4, 2001, 16:15:24
             GenCore version Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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KR2D_SHEEP
AGI_HORVU
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PA23_OXYSC
KR2A_SHEEP
NIC1_HUMAN
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PAZI_PSEAU
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KR2C_SHEEP
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PA26_BUNFA
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PA22_NOTSC
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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559
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Query Match 1

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Searched:

Perfect score:

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Sequence:

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                                                                                     A; Accession:
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5/1; 1724/1; 1771/1; 1819/1; 1874/1; 1888/3; 1948/1; 2021/3; 2086/1; 2266/3; 236 C; Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von C; Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat F; 22.7Domain: signal sequence #status predicted <SIG> F; 23-763/Product: von Willebrand antigen II #status predicted <MAI> F; 34-386/Domain: type D repeat 1 <DDI> F; 34-386/Domain: type D repeat 2 <DDI> F; 387-745/Domain: cell attachment (R-G-D) motif F; 764-2813/Product: von Willebrand factor #status predicted <MA2> CDDD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F;857,1211,1515,1574,2223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (Asn)
F;1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
F;1248,1255,1256,1468,1477,1467,1679,2298/Binding site: carbohydrate (Thr) (covalent) #s
F;1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the principal metal-binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metallothionein 1 - mud crab
C;Species: Scylla serrata (mud crab)
C;Species: Scylla serrata (mud crab)
C;Accession: A03283
R;Lerch, K.; Ammer, D.; Olafson, R.W.
J. Blol. Cham. 257, 2420-2426, 1982
A;Title: Crab metallothionein. Primary structures of metallothioneins 1 and A;Reference number: A92363; MUID:82142340
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S65778
chithnase class IV precursor - rape (fragment)
c.Species: Brasslca napus (rape)
C.Species: Brasslca napus (rape)
C.Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C.Accession: S65778
R;Hanfrey, C.; Fife, M.; Buchanan-Wollaston, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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repeat homology <VWA2>
repeat homology <VWA3>
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cell attachment (R-G-D) motif
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A;Molecule type: protein
A;Residues: 1-58 <LER>
A;Residues: 1-58 <LER>
C;Superfamily: metallothionein
C;Superfamily: metallothionein
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                                                                                                                                                                                                                                             F;788-833, 2216-2261/Region: duplication
F;826-853, 2400-2515, 2544-2662/Region: duplication
F;842-1130,1934-2203/Region: duplication
                                                                                                                                                                                                                                                                                                                                          F:1275-1443/Domain: Von Willebrand factor type A F:1496-1654/Domain: von Willebrand factor type A F:1689-1854/Domain: von Willebrand factor type A
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Pred. No. 60
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      type D repeat 4 <DD4>
type B repeat 1 <VB1>
type B repeat 2 <VB2>
type B repeat 3 <VB3>
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30.8%;
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Best Local Similarity
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Best Local Similarity
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A Residues: 1-266 - HANN-A Residues: 1-1266 - HANN-A Residues: 1-266 - HANN-A Residues: 1-266 - HANN-A Residues 1-17 and the corresponding nucleotide sequence are native the sequence of residues 1-17 and the corresponding nucleotide sequence are native the sequence of residues the sequence of residues 1-17 and the corresponding nucleotide sequence are native repeted plant that this the sequence are native residues and residual residues are native residual native residual pomology of the sequence are native residual resi
Plant Mol. Biol. 30, 597-609, 1996
A;Title: Leaf senescence in Brassica napus: expression of genes encoding pathogenesis
A;Reference number: S65777; MUID:96189271
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A;Residues: 1-527 <FLI>
A;Cross-references: GB:M77637; NID:g211737; PIDN:AAA48759.1; PID:g211738
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Mol. Cell. Biol. 12, 883-893, 1992
A;Title: An alternatively processed mRNA from the avian c-erbB
A;Reference number: A42032; MUID:92123214
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                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown A;Molecule·type: mRNA
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Llarity 47.8%; Pred. No. 12;
Conservative 2; Mismatches
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C;Date: 31-Dec-1993 #sequence_revi
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ilarity 33.3%;
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Best Local Similarity
Matches 11; Conserv
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A;Cross-references: EMBL:K03028; NID:g340308; PIDN:AAA61293.1; PID:g340309
R;Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.;
Nucleic Acids Res. 13, 4699-4717, 1985
A;Title: Construction of CDNA coding for human von Willebrand factor using antibody p
A;Reference number: S07363; WUID:85269603
                                                                                                                               A; Molecule type: protein
A; Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TIT>
A; Note: 789-Thr was also found
R; Chopek, W.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
Biochemistry 25, 3146-3155, 1986
A; Title: Human von Willebrand factor: a multivalent protein composed of identical sub
A; Reference number: A23464; MUID:86269892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clo
A;Reference number: A44178; MUID:85244588
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A;Accession: A60913
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A;Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 2731-2813 <VE3>
A; Cross-references: EMBL:X02672; NID:937939; PIDN:CAA26503.1; PID:937940
B; Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Cell 41, 49-56, 1985
A; Title: Molecular cloning of CDNA for human von Willebrand factor: authentication A; Reference number: S28678; MUID:85201687
A;Title: Cloning and characterization of two cDNAs coding for human von Willebrand A;Reference number: A94060; WUID:86016708 A;Accession: A94060
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R;Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, Biochemistry 25, 3171-3184, 1986
A;Title: Amino acid sequences of human von Willebrand factor.
A;Reference number: A90505; MUID:86269895
A;Recession: A90505
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A; Residues: 764-773;2803-2813 <CHO>
R; Residues: 764-773;2803-2813 <CHO>
R; Dent, J.A.: Berkowitz, S.D.: Ware, J.: Kasper, C.K.: Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A; Title: Identification of a cleavage site directing the immunochemical detection A; Reference number: A36013; MUID:90349604
A; Accession: A36013
                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 781-788, A',790-1424 <SHE>
A;Note: 852-Gln, 857-Asp, and 1381-Thr were also found
A;Note: 852-Gln, B:7-Asp, and 1381-Thr were also found
R;Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, Science 228, 1401-1406, 1985
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A;Cross-references: GDB:119125; OMIM:193400
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A; Residues: 2731-2813 <LYN>
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A; Residues: 1606-1617 <DEN>
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A; Residues: 2621-2813 <GIN>
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A; Residues: 576-590 <FAY>
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       Concession, A34400, 602777, A71199, S2676, A5393, 1004, Chance 22-Jun-1999
Concession, A34400, 602777, A71199, S2676, A5393, 1004, A5366; S25618; S25618, A94
Fibraciano, D.J.; A1400, 602777, A71199, S2676, A5393, A5366, A5366; S25618; S25618, A94
Fibraciano, D.J.; A1400, 602777, A71199, S2676, A5396, A5366, A5366; S25618; S2618, S2648, A94
Fibraciano, D.J.; A1400, A44800, A1419, A1419, A1410, A1410
Willebrand factor precursor - human
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840 CTTPRADCGHPCMAPCHISSPCP 862
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R; Song, Z.; Krishna,
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C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; A33 F;Ulrich, A.; Coussens, L.; Hayfilck, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.; Y rg, P.H.

Nature 309, 418-425, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of A;Reference number: A00641; MUID:84219729
A;Accession: A00641
A;Molecule type: mRNA
A;Residues: 1-1210 cULL.
A;Note: the authors translated the codon AAG for residue 540 as Asn
B;Cross-references: EMBL:X00588; NID:931113; PIDN:CAA25240.1; PID:9757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
B;Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human epidermal grc
A;Reference number: A25772; MUID:85270438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R;Haley, J.D.; Waterfield, M.D.
Y Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature transcript terminat
A;Reference number: A38672; WUID:91107677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195,'M', 197,'A', 199-222,'S', 224-304,'RA', 307-321
'798-799,'TD', 802-811,'K', 813-942 <XUNY
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF recept
R; LIn, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.
Science 224, 843-848, 1984
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R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification
A;Reference number: S30024; MUID:88217333
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R:Silman, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W.
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A:Reference number: A23062: WUID:85046483
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A;Experimental source: carcinoma cell line A431-7
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A; Molecule type: protein
A; Residues: 25-30, 'S', 32-51; 454-467 <WEB>
R; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
B. Blol. Chem. 260, 5205-5208, 1985
A; Title: Identification of residues in the nucleoti.
A; Reference number: A60143; MUID: 95182650
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A:Reference number: A43615; MUID:84196372
A;Accession: A43615
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A; Residues: 1028-1210 <SIM>
R; Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A; Reference number: A05281; MUID:84172183
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A,Molecule type: protein
A;Residues: 740-744,'X',746-747 <RUS>
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A; Residues: 713-964 <LIN>
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A; Residues: 1-29 <ISH>
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A; Residues: 1-29 <HA2>
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A; Residues: 1-29 <HAL>
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A) Contents: annotation; receptor activity
A; Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R; Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C
Cell 59, 33-43, 1989
A; Title: Functional independence of the epidermal growth factor receptor from a domai
A; Reference number: A3331; WID:990003233
A; Contents: annotation; internalization signal
C; Comment: Binding of EGF to the receptor leads to internalization of the EGF-recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; signal sequence #status predicted <SIG> F; 12-10/Promain: signal sequence #status predicted <MIN> F; 25-1210/Promain: extracellular #status predicted <EXT> F; 75-545/Domain: EGF receptor extracellular domain repeat <EE1> F; 75-300/Domain: EGF receptor extracellular domain repeat <EE2> F; 76-600/Domain: EGF receptor extracellular domain repeat <EE2> F; 76-600/Domain EGF receptor extracellular domain repeat <EE2> 
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F:128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status pre
F:745/Active site: Lys #status experimental
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: APP-stimulated interaction between epidermal growth factor receptor and supe
A;Reference number: A38023; MUID:84191554
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A;Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with no and functions as a transcriptional repressor.
A;Reference number: 138869; MUID:9505370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ĥ
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C.Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
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C;Superfamily: RING finger homology
F;338-398/Domain: RING finger homology <RRN>
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A;Map position: 7p12.3-7p12.1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication: alvonantein.
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28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:710-975/Domain: protein kinase homology <KIN>F:718-726/Region: protein kinase ATP-binding motif F:999-1046/Region: coated-pit mediated internalization signal
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A;Molecule type: mRNA
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Pred. No.
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C,Accession: B59037
R;Bergmann, D.J.; Arciero, D.M.; Hooper, A.B.
J. Bacteriol. 176, 3148-3133, 1994
A;Title: Organization of the hac gene cluster of Nitrosomonas europaea: genes for two A;Reference number: A59037; MUID:94252980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A36325
R;Petch, L.A.: Harris, J.; Raymond, V.W.; Blasband, A.; Lee, D.C.; Earp, H.S.
Mol. Cell. Biol. 10, 2973-2982, 1990
A;Title: A truncated, secreted form of the epidermal growth factor receptor is encode A;Reference number: A36325; MUID:90258888
                                                                                            cytochrome c, tetraheme, precursor - Nitrosomonas europaea
C;Species: Nitrosomonas europaea
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermal growth factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             perfermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Homo sapiens (man) C;Species: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-233 <BER>
A;Cross-references: GB:U08288; NID:g476339; PIDN:AAA19968.1; PID:g476341
A;Note: submitted to GenBank, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: chromoprotein; heme; iron; metalloprotein
F;1-28/Domain: signal sequence *status predicted <SIG>
F;29-233/Product: cytochrome c, tetraheme *status predicted <MAT>
F;39,42/Binding site: heme (Cys) (covalent) #status predicted
F;43/Binding site: heme (Cys) (axial ligand) #status predicted
F;71/Binding site: heme (Cys) (covalent) #status predicted
F;71/Binding site: heme (Cys) (covalent) #status predicted
F;131/Binding site: heme iron (His) (axial ligand) #status predicted
F;135/Binding site: heme iron (His) (axial ligand) #status predicted
F;159,162/Binding site: heme iron (His) (axial ligand) #status predicted
F;163/Binding site: heme iron (His) (axial ligand) #status predicted
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growth factor receptor
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5; Mismatches
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C;Superfamily: epidermal growth factor
C;Keywords: alternative splicing; ATP;
                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
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Matches 12; Conservative
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Matches 9; Conserv
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                      gastric mucin MUC5AC - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Secuession: S56015; S53361
R; Klomp, L. W.J.; Van Rens, L.; Strous, G.J.
Biochem. J. 308, 831-838, 1995
A; Title: Cloning and analysis of human gastric mucin CDNA reveals two types of conserved A; Reference number: S56015; MUID:97104281
A; Status: prelliminary
A; Molecule type: mRNA
A; Residues: 1-850 < KLO>
A; Cross-references: EMBL: X81649; NID:9547516; PIDN:CAA57309.1; PID:9547517
R; Guyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galiegue-Biochem. J. 305, 211-219, 1995
A; Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich doma A; Reference number: S53361; MUID:95126907
A; Status: prelliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 648-678, L', 660-733, L', 735-760 < GUY>
A; Cross-references: EMBL: 234280; NID:9563380; PIDN:CAA84034.1; PID:9563381
A; Status: prelliminary
A; Cross-references: EMBL: 234280; NID:9563380; PIDN:CAA84034.1; PID:9563381
A; Cross-references: EMBL: 234280; NID:9563380; PIDN:CAB84034.1; PID:9563381
A; Cross-references: EMBL: 234280; NID:9563380; PIDN:CAB84034.1; PID:9563381
A; Cross-references: EMBL: 234280; NID:9563380; PIDN:CAB84034.1; PID:9563381
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JECUSS

GASTIC mucin MUC5AC precursor - human

C;Species: Homo sapiens (man)

C;Date: 22-May-1998 #text_change 07-May-1999

C;Accession: JE0095

C;Accession: JE0095

B;Van de Bovenkamp, J.H.B.; Hau, C.M.; Strous, G.J.A.M.; Bueller, H.A.; Dekker, J.; Eine

Biochem. Biophys. Res. Commun. 245, 853-859, 1998

A;Title: Molecular cloning of human gastric mucin MUC5AC reveals conserved cysteine-rich

A;Reference number: JE0095; MUID:98249803

A;Molecule type: mRNA

A;Residues: 1-137 acbov>

A;Cross-references: GB:AFV43909

A;Cross-references: GB:AFV43909

A;Experimental source: stomach

F;1-19/Domain: leucine zipper #status predicted <LZP>

F;273-300/Domain: leucine zipper #status predicted <LZP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 850;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                11;
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Pred. No. 27;
6; Mismatches 11;
                                                                                                                                                            HCGDPCC - TTCRHH - - - PCPPGQGVQSQGKF - SFGFQC
Score 60.5; D. Pred. No. 7.1;
                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%; Score 60.5; D
29.8%; Pred. No. 19;
ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0%;
29.8%;
24.0%;
llarity 43.6%;
Conservative
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Matches 17; Conserv
                                Local Similarity
nes 17; Conserv
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Matches 17; Conserv
   Query Match
Best Local
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                                                                Matches
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September 4, 2001, 16:12:14; Search time 80.15 Seconds (without alignments) 38.016 Million cell updates/sec
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252
1 CVQPEFHCGDPCCTTCRHPCPPGGGVQSQGKFSFGFQCI 40
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    219241 segs, 76174552 residues
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

	Description	i ii	T-cell antigen 4-1	급	o	platelet aggregati	gastric mucin MUC5	gastric mucin MUC5	cytochrome c, tetr	epidermal growth f		+	von Willebrand fac	metallothionein 1	chitinase class IV	epidermal growth f		integrase homolog	mucin MUC5B, trach	OX40 antigen precu	lectin-B - Virgini	fibrillin-2 precur	fibrillin-2 precur	B cell-associated	insulin receptor-r	thrombospondin 4 p	insulin receptor-r	insulin-like growt	hypothetical prote	insulin-like growt
SUMMARIES	QI	T13954	B32393	A53183	T41146	JX0265	S56015	JE0095	B59037	A36325	GQHUE	I38869	VWHU	SMKD1S	S65778	A42032	TVCHLV	C35147	JE0352	S12783	JC5559	A57278	A54105	A46476	B47417	Ξ	B36502	A48805	T29562	A33837
	DB	7	~	N	N	~	~	~	7	N	Н	7	_	-	~	~	Н	7	N	~	7	C)	~	7	N	-	~	N	~	7
	Query Match Length	,	256	1210	1077	216	850	1373	233	644	1210	1104	2813	28	266	527	1223	437	1321	271	295.	2907	2918	305	540	961	1268	329	488	1371
dР	Query Match	28	26.6					24.0			23.8			23.4	23.4	23.4		23.2		23.0									22.6	
	Score	72	67	64	62.5	60.5	60.5	60.5	9	9	9	59.5	59.5	59	59	59	59	58.5	58.5	58	58	28	58	57.5	57.5	57.5	57.5	57	57	57
	Result No.	-	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	<b>5</b> 6	27	28	53

notch 3 protein 'B-cell activation	proteoliaisin - se	chymotrypsin/elast	atrolysin A (EC 3.	metallothionein 4	OX40 homolog - hum	differentiated ker	collagen alpha 1(I	collagen alpha 1(I	collagen alpha 1(I	gene shuttle craft	hypothetical prote	collagen alpha 1(I	metallothionein IV	CT105 hypothetical
S45306 A60771	T30274	S07127	S44.607	A53640	137552	A48679	S40495	S42617	S13580	T13938	T44598	CGHU7L	B53640	C86541
7 7	~	~	N	~	7	~	~	~	~	~	~	Н	~	7
2318 277	1297	63	419	62	277	502	921	921	931	1106	1106	1466	62	258
22.6	22.4	22.2	22.2	22.0	22.0	22.0	21.8	21.8	21.8	21.8	21.8	21.8	21.6	21.6
57 56.5	56.5	26	99	55.5	55.5	55.5	55	55	55	52	55	55	54.5	54.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

219241

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

RESULT 1  MEGF protein - rat  C.Species: Rattus norvegicus (Norway rat)  C.Species: Rattus norvegicus (Norway rat)  C.Species: Rattus norvegicus (Norway rat)  C.Accession: T1954  M. Nakajama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  C.Accession: T1954  Ratkayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  Ganomics 51, 27-34, 1998  A.Title: Identification of high-molecular-weight proteins with multiple EGF-like moti  A.Accession: T1954  A.Accession: Bassion: Bassion: Bassion: Bassion: Bassion: Bassion: Bassion: Bassion:	A; Accession: B32393 A; Molecule type: mRNA A; Residues: 1-256 < KWO> A; Coss = references: GB: U04492; NID: 9201121; PIDN: AAA40167.1; PID: 9201122 A; Coss = references: GB: U04492; NID: 9201121; PIDN: AAA40167.1; PID: 9201122 R; Kwon, B.S.; Kozak, C.A.; Klm, K.K.; Pickard, R.T. J. Immunol. 152, 2256-2262, 1994 A; Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B A; Reference number: 148879; MUID: 94179805 A; Accession: I48879 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Mosidues: 1-256 < RES> A; Residues: 1-256 < RES> A; Cross-references: EMBL: U02567; NID: 91117783; PIDN: AAA93113.1; PID: 9409178
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Gaps

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us-09-512-363-2\_copy\_74\_113.rpr

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F.648-670/Domain: transmembrane #stetus predicted <TMM>
F.712-977/Domain: protein kinase homology <KIN>
F.712-977/Domain: protein kinase homology <KIN>
F.720-728/Region: protein kinase APP-binding with F.860,695/Binding site: phosphate (Fir) (covalent) #status experimental
F.697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F.993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F.1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F.1197/Binding site: (or logophate (Tyr) (covalent) #status experimental
C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phospho F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Title: Primary structures of platelet aggregation inhibitors (disintegrins) autopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: AL031907; PIDN: CAA21417.1; GSPDB: GN00068; SPDB: SPCC18.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C; Accession: T41146
R; Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. A; Reference number: 21973
A; Reference number: 21973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: disintegrin
C;Species: Crotalus ruber ruber (red diamond rattlesnake)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 KPEFVKNLVPHSCGDPCGKTRGQDCEHPCPLLCHPGPCPPCTATVEKFCLCGKESIHARC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GKFSFGFQC
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    red diamond rattlesnake (fragment)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1077;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:BXperimental source: venom
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;7-89/Domain: disintegrin homology <DIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 QDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62.5; DB Pred. No. 14; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 972h-; cosmid c18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: RING finger homology
C;Superfamily: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hese enzymes.
A;Reference number: JX0265; MUID:93293798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                            25.4%;
34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet aggregation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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A; Molecule type: protein
A; Residues: 1-216 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1077 <HIL>
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SPDB:SPCC18.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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A;Reference number: A43818; MUID:91232866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A28941
A; Molecule type: protein
A; Residues: 689-694, 'X', 696-704, 'L', 706-707; 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1009, A; Residues: 689-694, 'X', bare, Alexander, W.S.
B; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A; Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA R, A; Molecule type: mRNA R, Molecule type: mRNA R, Molecule type: mg-971, K', 973-1115, D' <EIS>
A;Residues: 969-971, K', 973-1115, D' <EIS>
A;Cross-references: EMBL: 212668
R;Heisermann, G.J.; Gill, G.N.
B;Heisermann, G.J.; Gill, G.N.
A;Heisermann, G.J.; Gill, G.N.
A;Hille: Epidermal growth factor receptor threonine and serine residues phosphorylated A;Reference number: A28941; MUID:88330814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The mouse waved 2 phenotype results from a point mutation in the EGF receptor A; Reference number: A53183; MUID:94170986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulated in mouse
                                                                                                                                                                                                                                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A53183
epidermal growth factor receptor precursor - mouse
(Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
R;Luetteke, N.C.; Phillipps, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jen Genes Dev. 8, 399-413, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X78987; NID:9488830; PIDN:CAA55587.1; PID:9488831
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C;Genetics:
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A;Residues: 1-1210 <LUE>
A;Residues: 1-1210 <LUE>
A;Cross-references: GB:U03425
A;Cross-references: GB:U03425
CORcogene 6, 673-676, 1991
Oncogene 6, 673-676, 1991
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Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor receptor gene is A;Reference number: 149643; MUID:93126380
                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                  Length 256;
                                                                                                                                                                                                                                                                                                                                           Indels
                        Aintrons: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1 (S.Superfamily: CD2/ antigen; NGF receptor repeat homology C; Keywords: transmembrane protein C; Keywords: transmembrane protein F:1-23/Domain: signal sequence #status predicted <SIG>F:24-256/Product: 4-1BB protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                  Score 67; DB 2;
Pred. No. 1.5;
3; Mismatches 1.
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R;Eisinger, D.P.; Serrero, G.
submitted to the EMBL Data Library, June 1992
A;Reference number: S24942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 CIE-GFHCLGPQCTRC-EKDCRPGQELTKQG 115
                                                                                                                                                                                                                                                                                                                                                                                                         1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSQG 31
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A; Residues: 1-971, 'K', 973-1210 <VER>
                                                                                                                                                                                                                                                                      26.6%;
45.2%;
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A;Residues: 12-20,22-132 <RES>
                                                                                                                                                                                                                                                                  Query Match 26.6
Best Local Similarity 45.2
Matches 14; Conservative
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A; Accession: S45325
A; Status: preliminary
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A; Residues: 1-714 <AVI>
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PROSITE; PS01286; FA58C_2; 1.
PROSITE; PS01209; LDLRA_1; 3.
PROSITE; PS0068; LDLRA_2; 3.
PROSITE; PS50092; TSP1; 4.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

IISSUB-Ependymocyte;
MEDLINE-96338614; PubMed-8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,
Lamalle D., Dastuque B., Meiniel A.;
"SCO-spondin: a new member of the thrombospondin family secreted by
the subcommissural organ is a candidate in the modulation of neuronal
                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggregation.",

J. Cell S21. 109.1053-1061(1996).

1 Cell S21. 109.1053-1061(1996).

1 FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.

1 STREELLUAR LOCATION: EXTRACELLUAR.

1 TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.

1 DEVELOPMENTAL STAGE: EMBRYO.

1 SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

1 SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.

1 SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.

1 SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.

2 SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
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EGF-LIKE 1.
EGF-LIKE 2.
TSP TYPE-2.
F5/8 TYPE C.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
TSP TYPE-1 3.
TSP TYPE-1 4.
26 CVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPG 65
                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) SCO-SPONDIN (FRAGMENT).
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Pfam; PF01826; TIL; 1.
Pfam; PF000057; 1d1_recept_a; 3.
Pfam; PF000090; tsp_1; 4.
Pfam; PF000093; vwc; 1.
                                                                                                                                                                              (Rel. 34, Created)
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InterPro; IPR000884; -.
InterPro; IPR001007; -.
InterPro; IPR002172; -.
InterPro; IPR00219; -.
                                                                                                                             STANDARD;
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                                                                                                                                                                         01-0CT-1996
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SSPQ_BOVIN
ID SSPQ_BOVIN
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DT 01-0CT-
DT 01-0CT-
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BY SIMICARITY.
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Pred. No. 13;
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Job time: 1138 sec
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Pfam; PF00093; vwc; 3.
Pfam; PF010094; vwd; 3.
Pfam; PF010094; vwd; 3.
Pfam; PF010094; vwd; 3.
PRINTS; PR00365; ENDOTHELIN.
PROSITE; PS50234; VWFADOWAIN.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS011265; CTCK_1; 1.
Blood coagulation; Platelet; Glycoprotein; Extracellular matrix; Plasma; Endotheilal cell; Repeat; Cell adhesion.
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VON WILLEBRAND FACTOR.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-T-cell;
Mallett S., Fossum S., Barclay A.N.;
Characterization of the MRC OX40 antigen of activated CD4 positive T
lymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063:1068(11990).
-- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-- SUBCELLULAR COTATION: ATIVATED T-CELLS.
-- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                          Gaps
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CYTOPLASHIC (POTENTIAL).
4 N TURR-CYS.
THER-CYS.
THER-CYS 3.
THER-CYS 3 (INCOMPLETE).
THER-CYS 4 (GLONAC. ..) (POTENTIAL).
W. LINKED (GLONAC. ..) (POTENTIAL).
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PIR; S08036; S08036
PIR; S12783; S12783.
HSSP; P25942; LCDF.
InterPro; IPR001368; -
Ffam; PF00020; TNFR_C6; 3.
PROSITE; PS500652; TNFR_NGFR_1; 3.
PROSITE; PS500652; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                       15;
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                                                                                                                                        330 QVYLQCGTPCNLICRSLSYPDEECAEDCLEGCFCPPGLYLDGSGDCVPKAQC 381
  DB 1; Length 2482;
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Pred. No. 5;
3; Mismatches 9; Indels
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                                                       Indels
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC 0X40).
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23.2%; Score 58.5; D
30.8%; Pred. No. 26;
ive 2; Mismatches
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                                                                                                            3 QPEFHCGDPCCTTCR--HHP---
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                                                       Conservative
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nes 12; Conserv
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Plasmid pSE211
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01-OCT-2000
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SEQUENCE
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                                                                                                                                                                                                                                                                                             RESULT 11
INTR_SACER
                                                                                                                                                                                                                                                                                                                                       P22877
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                                                                                                                                                                                                                                                                                                                                                                         Lax I., Johnson A., Howk N., Sap J., Bellot F., Winkler M.,
Ullrich A., Vennstrom B., Schlessinger J., Givol D.;
"Chicken epidermal growth factor (EGF) receptor: cDNa cloning,
expression in mouse cells, and differential binding of EGF and
transforming growth factor alpha.";
Mol. Cell. Biol. 8:1970-1978(1988).

-I. FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIROS GROWTH FACTOR (BY SIMILARITY).

-I. CATALYTIC ACTIVITY: ATP A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                              Galius gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000434; ...
InterPro; IPR000434; ...
InterPro; IPR001245; ...
InterPro; IPR001214; ...
Pfam; PF00130; Recep_L_domain; 2.
Pfam; PF00130; Recep_L_domain; 2.
PROSITE; PS00109; PROTEIN_KINASE_ATP; PARTIAL.
PROSITE; PS00109; PROTEIN_KINASE_ATP; PARTIAL.
PROSITE; PS00109; PROTEIN_KINASE_ATP; TATAL.
PROSITE; PS00109; PROTEIN_KINASE_DOW; PARTIAL.
Transmembrane; Glycoprotein; Duplication; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIDERMAL GROWTH FACTOR RECEPTOR
 DB 1; Length 58;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL PROLIFERATION. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                      1 CVQPEFHCGDPC-CTTCRHHPCPPGQGVQSQGKFSFGFQC 39
                                                                    01-JAN'1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC
                                                                                                                                                     703 AA.
13.4%; Score 59; DB 11arity 37.5%; Pred. No. 1.1; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88261272; PubMed-3260329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M20386; AAA48760.1; -.
                                                                                                                                                     STANDARD;
 Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                    (FRAGMENT).
                                                                                                                                                     CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                        EGFR_CHICK
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                 Score 59; DB 1; Length 703;
Pred. No. 8.3;
5; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                MW; AFF2DE11B735A690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharopolyspora erythraea (Streptomyces erythraeus).
                                                                     (GLCNAC. . .)
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                                                                                      (GLCNAC.
                                                                                                                          (GLCNAC.
                                   (GLCNAC
                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; C3514/, C27
Interpro; IPR002104; -. Pfam; PF00589; Phage_integrase; 1. Plasmid. DNA recombination; DNA integration; Plasmid. TRANSIENT COVAI CTRANSIENT COVAI
                                                                                                                                                                                                                                                                                                                                                                                                                         437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.2%; Score 58.5; Di
32.4%; Pred. No. 6.4;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 CSDPHRCGATYHKTEPCKAACKRHTRACPPPCPP 281
                                                                                                                                                                                                                                                                                                                1 CVQPE-----FHCGDPCCTTCRHH-----PCPP 23
                                                                                                                                                                                                                                                                                           8 CGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 40
N-LINKED
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                                                                                                                                                                                                                   Query Match 23.4%;
Best Local Similarity 33.3%;
Matches 11; Conservative
                                                                                                                                                                77427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTEGRASE (RECOMBINASE).
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359
368
573
573
613
633
703
AA;
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NCBI_TaxID=1836;
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DISULFID
                                                                                                                    SEQUENCE
                                                                                                      CARBOHYD
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Q28833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-LIKE 1.
EGF-LIKE 2. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 5.
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InterPro; IPR001881; -.
PROSITE; PS00102; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 2.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain;
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
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                                                                                             01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
01-077-2000 (Rel. 40, Last annotation update)
THBS4 OR TSP4 OR TSP-4.
                                                                 980 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X89963; CAA62002.1; -. HSSP; P35444; IVDF.
                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
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348
353
371
401
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                                                                 TSP4_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 194:1019-1024(1993).

-!- FUNCITON: INFORTANT IN THE MAINTENNED OF HOMEOSTASIS, IT
PARTICIPATES IN PLATELET-VESSEL WALL INFERACTIONS BY FORMING A
NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
VASCULAR INJURY (BY SIMILARITY).
-!- SUBUNIT: MULTIMERIC (BY SIMILARITY).
-!- FTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 3 VWFC DOMAINS.
-!- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lavergne J.M., Piao Y.C., Ferreira V., Kerbiriou-Nabias D.,
Bahnak B.R., Meyer D.;
"Primary structure of the factor VIII binding domain of human, porcine
and rabbit yon Willebrand factor.";
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                     . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                     Length 980;
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTE N-LINKED (GLCNAC. . .) (POTE N-LINKED (GLCNAC. . .) (POTE MW; 056041EB66206FCF CRC64;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Seaman W.T., Read M.S., Bellinger D.A., Nichols T.C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                6 FHCGDPC-----CT---TCRHHPCPPGQGVQSQGKFSFGFQC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT).
                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                   Score 58.5; DF Pred. No. 12; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 397-553 FROM N.A.
MEDLINE-93356762; PubMed-8352759;
                                                                                                                                                                     Ж.
Ж
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01-OCT-2000 (Rel. 40, Last seq
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                                                                                                                                                                                                                                        23.2%;
31.9%;
                                                                                                                                                                  108213
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HSSP; P04275; 1ATZ.
                                                                                                                                                                                                                                   Query Match 23.29
Best Local Similarity 31.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00007; Cys_knot; Pfam; PF00092; vwa; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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InterPro; IPR001007; -.
    421
436
456
466
480
631
960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                  980 AA;
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    4444
4442
4450
4468
631
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MEDLINE=9747299; PubMed=9331419;
Huizinga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liddington R.;
contain a metal ion-
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                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.
MEDLINE-98221174; PubMed-9553097;
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MEDILIE-89264455; PubMed=2786201;
Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,
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Bienkowska J., Cruz M., Atiemo A., Handin R.,
"The von Willebrand factor A3 domain does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
MEDLINE-91185601; PubMed-2010538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dependent adhesion site motif.";
J. Biol. Chem. 272:25162-25167(1997).
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                                                                                                                                                                                                        Eur. J. Blochem. 158:295-298(1986)
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                           PubMed=3502076;
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                                                                                Biochemistry 26:8099-8109(1987).
                                                                   Willebrand factor
                           MEDLINE-88163465;
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    Sadler J.E.;
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-!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY. PIR; A03283; SHKD1S.
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J. Clin. Invest. 87:1220-1226(1991).
                                                                                                                                                                      15;
                                                                                                                                                                                                                     Length 2813;
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                                                                                           VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399
MEDLINE-91185602; PubMed-1672694;
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Eubrachyura; Portunoidea; Portunidae; Scylla.
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CLUSTER A.
CE8A24C590B027B8 CRC64;
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Metal-binding; Metal-thiolate cluster; Chelation.
                                                                                                                                           DB 1;
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01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                        Score 59.5; DB
Pred. No. 22;
3; Mismatches
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J. Biol. Chem. 257:2420-2426(1982).
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MEDLINE-82142340; PubMed-7061431;
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PRINTS; PR00858; MTCRUSTACEAN.
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Matches 16; Conservative
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P02805;
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"Full-length von Willebrand factor (vWF) cDNA encodes a highly
"repetitive protein considerably larger than the mature vWF subunit.";
EMBO J. 5:1839-1847(1986).
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                                                    Repressor; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                        APPROXIMATE REPEATS, CYS-RICH.
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                                                                                                                                                                                                                                                                                             DB 1; Length 1104;
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EMBO J. 5:3074-3074(1986).
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TISSUE-Umbilical vein endothelial cells;
MEDLINE-87213253; PubMed-3495266;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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Pred. No. 10;
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MEDLINE-90062044; Pubmed-2584182;
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MEDLINE-87004550; Pubmed-3019665;
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                 Pfam; PF01424; R3H; 1.
Pfam; PF01422; zf-NF-X1; 8.
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IPR001374; -.
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Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L., Le Beau M.M., Sorace J.M., Sadler J.E.; "Human von Willebrand factor gene and pseudogene: structural analysis and differentiation by polymerase chain reaction."; Biochemistry 30:253-269(1991).
                                                                                                                                                                                                                                                  SEQUENCE OF 781-1424 FROM N.A.
MEDLINE-6626984; PubMed-3488076;
Shelton-Inloces B.B., Titani K., Sadler J.E.;
-CDMA sequences for human von Willebrand factor reveal five types of repeated domains and five possible protein sequence polymorphisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonthron D., Orkin S.H.; "The human von Willebrand factor gene. Structure of the 5' region."; Eur. J. Biochem. 171:51-57(1988).
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MEDLINE-85269603; PubMed=3875078;
Verwell C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
Verwell C.L., and Wourlik J.A., Pannekoek H.;
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MEDLINE-86269895; PubMed-3524673;
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"Amino acid sequence of human von Willebrand factor.";
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MEDLINE-85201687; Pubmed-3873280;
Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
Ling E.H., Livingston D.M.;
"Molecular cloning of cDNA for human von Willebrand factor:
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                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND
CELL PROLIFERATION.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
"ATP-stimulated interaction between epidermal growth factor receptor and supercoiled DNA."; Nature 309:270-273(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Duplication; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                  Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M., Howk R., Gilvol D., Ullrich A., Schlessinger J.;
"All autophosphorylation sites of epidermal growth factor (EGF) receptor and HER2/neu are located in their carboxyl-terminal tails. Identification of a novel site in EGF receptor.";
J. Biol. Chem. 264:10667-10671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIDERMAL GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                "Receptors for epidermal growth factor and other polypeptide intogens.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
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SIMILARITY).
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PROTEIN KINASE.
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(BY
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InterPro; IPR000494; -.
InterPro; IPR00719; -.
InterPro; IPR001245; -.
InterPro; IPR0012174; -.
Pfam; PF00757; Furin-like; 1.
Pfam; PF0130; Recep_L_domain; 2.
                                                                      MEDLINE-89278137; PubMed-2543678;
                                                                                                                                                                                                   MEDLINE-87297456; PubMed-3039909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A00641; GQHUE.
PIR; A00642; GQHUE2.
PIR; A30642; A33062.
SWISS-2DPAGE; P00533; HUMAN.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95053707; bubmed-7964459; Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.; Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.; Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.; a novel cysteine-rich sequence-specific DNA-binding protein interacts with the conserved X-box motif of the human major histocompatibility complex class II genes via a repeated Cy9-His domain and functions as a transcriptional repressor."; J. Exp. Med. 180:1763-1774 (1994).

--- FUNCTION: REPRESSOR OF HLA-DRA TRANSCRIPTION BINDS TO THE X-BOX MOTIF OF CLASS II MHC GENES. MAY PLAY AN IMPORTANT ROLE IN REGULATING THE DURATION OF AN INFLAMMATORY RESPONSE BY LIMITING THE DERIOD IN WHICH CLASS II MHC MOLECULES ARE INDUCED BY
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- INDUCTION: BY INTERFERON-GAMMA.
-!- SIMILARITY: TO D.MELANOGASTER SHUTTLE CRAFT PROTEIN (STC) AND YEAST YNL023C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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Pred. No. 9.8;
5; Mismatches 19; Indels
                                                                               MAJOR
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                                         PHOSPHORYLATION (AUTO-)
PHOSPHORYLATION (AUTO-)
PHOSPHORYLATION (AUTO-)
N-LINKED (GLCNAC . . . ) (P
N-LINKED (GLCNAC . . ) (P
                PHOSPHORYLATION (BY PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                       257 EATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCV 292
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01-NOV-1997 (Rel. 35, Last annotation update)
TRANSCRIPTIONAL REPRESSOR NF-X1.
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Best Local Simi
Matches 12;
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Q12986;
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InterPro; IPR000967; -.

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MEDLINE-84219729; PubMed-6328312;
MEDLINE-84219729; PubMed-6328312;
Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whittle N., Materfield M.D., Seeburg P.H.;
"Human epidermal growth factor receptor CDNA sequence and aberrant
expression of the amplified gene in A431 epidermoid carcinoma cells.";
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J. Biol. Chem. 266:1746-1753(1991).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 713-924 FROM N.A.
MEDLINE-84196372; PubMed-6326261;
Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
"Expression cloning of human EGF receptor complementary DNA: gene amplification and three related messenger RNA products in A431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-84245835; Pubbled-6330563; Xu Y., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P., Roe B.A., Merlino G.T., Pastan I.; "Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs overproduced in A431 carcinoma cells."; Nature 309:806-810(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation of an evolutionarily conserved epidermal growth factor receptor cDNA from human A431 carcinoma cells.";
Biochem. Biophys. Res. Commun. 124:125-132(1984).
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The human EGF receptor gene: structure of the 110 kb locus and identification of sequences regulating its transcription."; Oncogene Res. 1:375-396(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1028-1210 FROM N.A.
MEDLINE-85046483; PubMed=6093780;
Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
O'Malley B.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-29 FROM N.A.
MEDLINE-88217333; PubMed-3329716;
Haley J., Whittle N., Bennett P., Kinchington D., Ullrich A.,
Waterfield M.;
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1997) to the SWISS-PROT data bank
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MEDLINE-91107677; PubMed-1988448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 224:843-848(1984).
                                                                                                                                                                                                                                                                                                                                         Nature 309:418-425(1984).
                                                                                      Homo sapiens (Human).
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                                                                EGFR OR
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"Organization of the hao gene cluster of Nitrosomonas europaea: genes
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  17; Indels 17; Gaps
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HEME 1 (COVALENT) (POTENTIAL).
HEME 1 (COVALENT) (POTENTIAL).
IRON 1 (HEME AXIAL LIGAND) (POTENTIAL).
HEME 2 (COVALENT) (POTENTIAL).
HEME 2 (COVALENT) (POTENTIAL).
IRON 2 (HEME AXIAL LIGAND) (POTENTIAL).
HEME 3 (COVALENT) (POTENTIAL).
HEME 3 (COVALENT) (POTENTIAL).
HEME 4 (COVALENT) (POTENTIAL).
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                                             1 CVQPEFH--CGDPCCTTCR--HHP------CPPGQGVQSQGKFSFGFQC 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: PERIPLÁSMIC (POTENTIAL).
-i- PIM: BINDS FOUR HEME GROUPS PER MOLECULE (POTENTIAL).
-i- SIMILARITY: TO NAPC PROTEINS AND TO P.STUTZERI NIRT.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
010-NOV-1997 (Rel. 35, LOST annotation update)
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    Mismatches
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Ammonia-oxidizing bacteria; Nitrosomonas.
NCBI_TaxID=915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for two tetraheme c cytochromes.";
J. Bacteriol. 176:3148-3153(1994).
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PROSITE; PS00190; CYTOCHROME_C; 4.
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MEDLINE=94252980; PubMed=8195067;
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134 HE
135 IS
159 HE
162 HE
25486 MW;
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P00533; P06268; Q14225;
21-JUL-1986 (Rel. 01, Created)
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Best Local Similarity 45.0
Matches 9; Conservative
  17; Conservative
                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
33
42
43
                                                                                                                                                                                                                                                                                                                       Nitrosomonas europaea
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                                                                                                                                                                                       CYCX_NITEU
Q50926;
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                                                                                                                                                                                                                                                                                                Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;

**A Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;

**A "The canine von Willebrand factor gene: sequence and expression of

**A region encoding the glycoprotein ID/IX binding domain.";

**Submitted (JAN-1994) to the EMBL/GenBank/DBU databases.

**C :- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTAGIS, IT

**PARTICIPATES IN PLATELET-VESSEL WALL INVERACTIONS BY FORMING A

**C :- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTAGIS,

**INCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF

**VASCULAR INJUNY (BY SIMILARITY).**

**INSECRIAL MULTIMERIC (BY SIMILARITY).**

**INSECRIAL DISULFIDE BONDS (BY SIMILARITY).**

**INSECRIAL DISULFIDE BONDS (BY SIMILARITY).**

**INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).**

**INTERCHAIN SOUTAINS 3 WARC DOMAINS.**

**INTERCHAIN SOUTAINS 4 WAFD DOMAINS.**

**INTERCHAIN SOUTAINS 4 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).**

**INTERCHAIN SOUTAINS HEMOSTIN.**

**INTERCHAIN SOUTAINS HEMOS
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Pfam: PFULU...

Pfam: PFO0093; vwc,

Pfam: PF00094: vwd; 4.

PROSITE; PS001285; CTCK_1: 1.

DR PROSITE; PS01208; vwrc, 3.

TR BLOOD COAGULATOR.

SIGNAL 1 22 BY SIMILARITY.

PROPEP 764 2813 VON WILLEBRAND FACTOR.

179 VWFD 1.

VWFD 1.

VWFD 2.

VWFD 2.
                                                                                                                                                                             Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Schall W.D., "Complete sequence of the structural gene for canine von Willebrand factor and identification of a mutation causing Scottish terrier von Willebrand's disease.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
[1]
SLOY S.J., Shibuya H., Nonneman D.J., Holzhauer J., Mohammed I.H.
Johnson G.S.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                            SEQUENCE FROM N.A.
Montgomery R.R., Fahs S., Montgomery M.W.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                            SEQUENCE OF 1234-1669 FROM N.A.
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EMBL; L16903; AAA30903.1; -.
EMBL; AF099154; AAB04919.1; -
EMBL; U66246; AAB93766.1; -.
HSSP; P04275; 1ATZ.
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InterPro; IPR002919; -.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF01826; TIL; 4.
Pfam; PF00092; vwa; 3.
Pfam; PF00093; vwc; 3.
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• L (IN REF. 2).
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INTERCHAIN DISULFIDE BONDS (BY SIMILARITY). SIMILARITY: CONTAINS AT LEAST 3 VWFD DOMAINS.
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Best Local Similarity 34.0
Matches 16; Conservative
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                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96028118; PubMed-7588715;
Takagi J., Aoyama T., Ueki S., Ohba H., Saito Y., Lorand L.;
Takagi J., Aoyama T., Ueki S., Ohba H., Saito Y., Lorand L.;
Takagi J., Aoyama T., Ueki S., Ohba H., Saito Y., Lorand L.;
Totopolypeptide of bovine von Willebrand factor.";
Eur. J. Biochem. 232:773-777(1995).
-!- FUNCTION: IMPORTANT IN THE MAINTENNNCE OF HOMEOSTASIS, IT
PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                              (POTENTIAL).
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Janel N., Schwachtgen J.L., Bakhshi M.R., Barek L., Meyer D.,
Kerbiriou-Nablas D.;
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N-LINKED (GLCNAC. ...) (POTENN
C -> S (IN REF. 2).
C -> W (IN REF. 5).
L -> F (IN REF. 5).
HP -> DR (IN REF. 6).
WW; 690E20D46DFZD2F5 CRC64;
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01-OCT-2000 (Rel. 40, Last annotation update)
VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT)
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MEDLINE-91192039; PubMed-1707363;
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P80012; Q28011;
01-NOV-1995 (Rel. 32, Created)
01-CCT-2000 (Rel. 40, Last sequol-OCT-2000 (Rel. 40, Last anno
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Matches 13; Conservative
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N-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (IN REF. 3).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Pred. No. 3.2;
1; Mismatches 15; Indels 15
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AMINO-TERMINAL
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human cytom

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P47945 Q01083 P54643 P16827 P20063 P06432 P14585 P07852

rhesus

drosophila homo sapien mus musculu drosophila dictyostell

P40798 P02461

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/C;
MEDLINE=94179805; PubMed=8133039;
KWON B.S., KOZAK C.A., Kim K.K., Pickard R.T.;
"Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION, AND SEQUENCE OF 25-29.
MEDLINE-93139510; PubMed-7678621;
Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard
                                                                                                                                                                                         -13BB_MOUSE STANDARD; PRT; 256 AA. P20334; 01-FEB-1991 (Rel. 17, Last sequence update) 01-FEB-1999 (Rel. 17, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB). THFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
                                                                                                                                                                                                                                                                                                                                    Kwon B.S., Weissman S.M.;
"cDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
                                                                                                                                          ALIGNMENTS
        STC_DROME
CA13_HUMAN
MT4_MOUSE
SPIT_DROME
SP87_DICDI
HEPA_HCMVA
                                                                                        LI12_CAEEL
ICE2_ASCSU
VE4_RHPV1
                                                                      LDLR_RABIT
                                                                               VMSA_WHV8
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-89184547; PubMed-2784565;
                                                                                                                                                                                                                                                                                                                                                                                                                    antigen 4-1BB.";
J. Immunol. 152:2256-2262(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04492; AAA40167.1; -.
EMBL; U02567; AAA93113.1; -.
PIR; B32393; B32393.
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                                                                    4, 2001, 16:15:25; Search time 43.78 Seconds
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         4.5
Compugen Ltd
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         GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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CYCX_NITEU
EGFR_HUMAN
NFX1_HUMAN
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MT1_SCYSE
EGFR_CHICK
INTR_SACER
TSP4_RAT
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NTC3_MOUSE
CD40_HUMAN
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EGFR_MOUSE
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Listing first 45 summaries
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length: 2000000000
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   SEQUENCE FROM N.A.
STRAIN-BALB/C, AND CD-1; TISSUE-Liver, and Decidua;
MEDLINE-93126380; PubMed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
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BEDLINE-39026370; PubMed-1408137;
AVIVI A., Skoreov, Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor 2
                                                                                                                                                                                              4 X TWFR-CYS.
TWFR-CYS 1.
TWFR-CYS 2.
TWFR-CYS 3.
TWFR-CYS 4.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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SEQUENCE FROM N.A.
STRAIN-BE5/C3; TISSUE-Liver;
MEDLINE-94170986; Pubmed-8125255;
Luetreke N.C., Phillips H.K., Qlu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
The mouse waved-2 phenotype results from a point mutation in the leceptor tyrosine kinase.";
Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                               26.6%; Score 67; DB 1; Length 256; 45.2%; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
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Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           4-1BB LIGAND RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             93A10D03C60813C4 CRC64;
              InterPro; IPR001368; -.
Pfam; PF00020; TNFR_c6; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
RECEPTOr; Glycoprotein; Repeat; Signal; Transmembrane.
SIGNAL 1 24
                                                                                                                                                              POTENTIAL. CYTOPLASMIC (POTENTIAL).
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Oncogene 7:1957-1962(1992).
MGD; MGI:1101059; Infrsf9
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Matches 14;
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Q01279;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@illower.
                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                 Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B., "Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.
PROSITE; PSO0101; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
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                                                                                                                                                                                                                            Eisinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000494; -
InterPro; IPR000199; -
InterPro; IPR001245; -
InterPro; IPR02174; -
Pfam; PF001030; Recep_L_domain; 2.
Pfam; PF00069; pkinase; 1.
                                                       MEDLINE-91232866; PubMed-2030916;
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EMBL; U03425; AAA17899.1; -.
EMBL; X59689; CAA42219.1; -.
EMBL; L06664; AAA53029.1; -.
EMBL; Z12608; CAA78249.1; -.
                                                                                                                                                                                      SEQUENCE OF 969-1117 FROM N.A.
[5]
SEQUENCE OF 1-714 FROM N.A.
                                                                                                                                             Oncogene 6:673-676(1991).
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                                        TISSUE-Brain;
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Gaps 6

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C; Accession: JC7105
R; Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A; Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platele A; Reference number: PC7027; MUID:99443731
A; Accession: JC7105
                                                                                                                                                                                                                                                                                                                                               aggretin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 146;
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A; Residues: 1-146 <CHU>
A; Residues: 10-146 <CHU>
C; Superfamental Source: venom gland
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; platelet aggregation; venom
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Pred. No. 7.9;
2; Mismatches 7;
                   2; Mismatches
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Job time: 1112 sec
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N;Alternate names: protein J1145
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Becies: D5-May-1995 #sequence_revision 08-Sep-1995 #text_change 05-Nov-1999
C;Accession: S56828
R;Pohl, T.M.; Aljinovic, G.
Submitted to the Protein Sequence Database, September 1995
A;Reference number: S56928
A;Reference number: S56931; NID:g1008196; PIDN:CAA89347.1; PID:g1008197; GSPDB:GNOC C;Genetics:
A;Reference number: NID:g1008196; PIDN:CAA89347.1; PID:g1008197; GSPDB:GNOC C;Genetics: 108
A;Reference number: NID:g1008196; PIDN:CAA89347.1; PID:g1008197; GSPDB:GNOC C;Reference number: NID:g1008197; GSPDB:GNOC C;Reference number: NID:g1008197; GSPDB:GNOC C;Reference number: NID:g1008197; GSPDB:GNOC C;Reference nu
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R; Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Blochem. 118, 965-973, 1995
A; Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav
A: Reference number: JC4329; MUID: 96318509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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JC4329
Ccagulation factor IX-binding protein A chain - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 06-Dec-1995 #sequence_revision 08-Peb-1996 #text_change 13-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A; Molecule type: mRNA
A; Residues: 1-152 < CHE>
A; Cross-references: GB:AF176420
A; Cross-references: GB:AF176420
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 24-53; 84-66; 87-94; 125-136; 137-152 < CH2>
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; heterodimer; venom
F; 1-23/Pomain: signal sequence #status predicted < SIG>
F; 24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
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A; Residues: 1-129 cATO>
C; Comment: This protein binds calcium.
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: anticoagulant; blood coagulation; calcium binding; venom
F; 2-127/Domain: C-type lectin homology <LCH>
F; 2-13,30-127,102-119/Disulfide bonds: #status predicted
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28.6%; Pred. No. 34;
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Pred. No. 7.1;
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41.9%; Pred. No. 4.6;
Live 2; Mismatches
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Matches 13; Conservative
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Matches 16; Conservative
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Best Local Similarity
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F;166-203/Domain: NGF receptor repeat homology <NG4>
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A; Residues: 1-474 <GOO>
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A;Molecule type: DNA
A;Residues: 1-22 <KIS>
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Asyloceule type: protein
Asyl
                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A;Reference number: A35356; MUID:90260639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991
                                                                                 7
                                                                                 Gaps
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DB 2; Length 459;
                                                                             15; Indels
                                                                                                                                                                                                  151 CAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVC 187
                                                                                                                                                     2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
Score 61; DB 2
Pred. No. 4.6;
5; Mismatches
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24.8%;
36.6%;
                                                                             Conservative
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Query Match
Best Local Similarity
Matches 15; Conserv
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A; Residues: 1-461 <SMI>
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Gene 150, 381-386, 1994
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A; Status: preliminary
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tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequenc_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A; Reference number: A38634; MUID:91187885
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R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor A;Reference number: 554816
             region
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A; Residues: 1-474 < CLES
A; Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828
A; Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828
R; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.;
Mol. Cell. Biol. 11, 3020-3036, 1991
Mol. Cell. Biol. 11, 3020-3036, 1991
A; Title: Molecular cloining and expression of the type 1 and type 2 murine receptors
A; Reference number: A40254; MUID: 91246168
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A;Title: Cloning, sequencing and partial functional characterization of the A;Reference number: I38094; MUID:95121934
A;Accession: I38094
                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
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F;120-162/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <IMN>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 4.6;
4; Mismatches 16; Indels
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C.Superfamily: tumor necrosis factor receptor type 2; NGF
C.Keywords: duplication; glycoprotein; receptor; transmemb
F:1-22/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
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36.6%;
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Best Local Similarity 36.6'
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Query Match

Matches

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A)Cross-references: EMBL:X02396
R;Guarino, L.A.; Ghosh, A.; Dasmahapatra, B.; Dasgupta, R.; Kaesberg, P.
Viriology 139, 199-203, 1984
A;Title: Sequence of the black beetle virus subgenomic RNA and its location in the vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agkisacutacin alpha chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: UC7134; PC7037
E;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic ve
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A; Description: Near identity in the polymerase gene of two serologically distinct nod
A; Reference number: $41397
A;Cross-references: EMBL:X02396; NID:g60679; PIDN:CAA26238.1; PID:g60680
R;Dasmahapatra, B.; Dasgupta, R.; Ghosh, A.; Kaesberg, P.
J. Mol. Biol. 182, 183-189; 1985
A;Title: Structure of the black beetle virus genome and its functional implications. A;Reference number: S28728; MUID:85210903
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C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
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C;Superfamily: black beetle virus B1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 1;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: genomic RNA
A; Residues: 897-998 <GUA>
A; Cross-references: GB:M33065; NID:g210673; P
C. Superfamily: black beetle virus B1 protein
C; Keywords: RNA biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59;
Pred. No.
                                                                                                                                                                                                                                                                             A; Molecule type: genomic RNA
A; Residues: 1-883, 'AALRETPWINRYQC' <DAW>
A; Cross-references: EMBL:X02396
A; Accession: S28729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|||||
| 361 HCRPWTDCPDRALVYTIP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 HCRPWTDCPDRALVYTIP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 HCKPWTDCTQFGFLTVFP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 HCKPWTDCTQFGFLTVFP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: genomic.RNA
A;Residues: 1-998 <DAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: genomic RNA
A; Residues: 897-998 <DA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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R; Dasgupta, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S41397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Mecletuce number: JN0000; MOLD:901005/9
A; Molecule type: mRNA
A; Mecletuce number: JN0000; MOLD:901005/9
A; Mecletuce: JN00006
A; Molecule type: mRNA
A; Residues: 1-416 CaLRA
A; Experimental source: embryonic chick brain
B; Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Bov. Balol. 137, 287-344, 1990
A; Title: Structure and developmental expression of the chicken NGF receptor.
A; Reference number: A60504
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 21-35, Y', 37-172, K', 174-275, S', 277-395, K', 397-416 <HEU>
C; Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
A; Molecule type: mRNA
A; Residues: 21-35, Y', 37-172, K', 174-275, S', 277-395, K', 397-416 <HEU>
C; Comment: This protein is thought to form a high-affinity receptor when it associates w
C; Comment: This protein is thought to form a high-affinity receptor when it associates w
C; Comment: This protein is thought to form a high-affinity receptor when it sequence #status predicted <SIGS
C; Comment: Signal sequence #status predicted <SIGS
F; 1-20/Domain: signal sequence #status predicted <SIGS
F; 1-219/Domain: Signal sequence #status predicted <AMT>F; 1-219/Domain: NGF receptor repeat homology <AMCS>F; 1-134/Domain: NGF receptor repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Decies: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter; E.M.; Reich Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in t A;Reference number: JN0006; MUID:90166579
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QUBBB1

B1 protein - black beetle virus

C;Species: black beetle virus

C;Species:
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 416;
                                                                                            DB 2; Length 474;
                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                16 CAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVC 202
                                                                                                                                                                                                                                                                             2 CASGIFSG -- GHEGHCKPWIDCIQFGFLIVFPGNKIHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;101-139/Domain: NGF receptor repeat homology <NG3>F;141-181/Domain: NGF receptor repeat homology <NG4>
                                                                                        Score 61; DB;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.5; Di
Pred. No. 4.8;
                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
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                                                                                   24.8%;
36.6%;
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35.98;
                                                                                                                                                                                     15; Conservative
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A; Accession: S78471
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                                                                                                                                           Best Local Similarity
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Query Match Matches

g à

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

4, 2001, 16:12:14; Search time 80.15 Seconds September Run on:

(without alignments)
38.966 Million cell updates/sec

US-09-512-363-2\_COPY\_114\_154
246
1 DCASGTFSGGHEGHCKPWTD......TQFGFLTVFPGNKTHNAVCV Perfect score: Title:

Sequence:

41

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

219241

length: 0 length: 2000000000 sed 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

SUMMARIES	ID Description	37552 OX40 homolog - hum	ox40 prote	Ivmph		T-cel		ι,	38634 tumor necrosis fac	æ	l B1 protein -		agkisacutaci		JC4329 coagulation factor													50983 probable pleiotrop	
	DB I	1		2 I	O)	ш				-			Ī																C
	ngth	277	272	255	271	256	459	461	474	416	866	866	152	880	129	146	123	231	350	425	435	612	616	152	327	305	420	504	70
di	Query		38.6	37.8	34.1	28.7	24.8	24.8	24.8	24.6	24.0	24.0	23.4	22.8	22.6	22.6	22.2	22.2	22.2	22.2	22.0	22.0	22.0	21.7	21.7	21.5	21.5	21.5	5
	Score	96	95	93	84	70.5	61	61	61	60.5	59	S	57.5	26	δ.	ς.	4.	٠	4.	4.	54	24	54		53.5			23	
	Result No.	7	7	e	4	ß	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	ď

disintegrin-like m hypothetical prote	laminin beta-1 cha	conserved hypothet	competence factor	exodeoxyr1.bonuclea	mucin MUC5B, trach	laminin beta-1 cha	molybdenum cofacto	cytochrome c-type	metallothionein-11	guanine nucleotide	hypothetical prote	hypothetical prote	B-cell activation	hypothetical prote
165967 T14764	MMMSB1.	G69267	T09049	B82619	JE0352	MMHUB1	A84169	S35237	T03787	S48839	S76085	A96690	A60771	T24307
7 7	٦	~	7	7	~	-	~	7	7	7	~	~	~	~
670 898	1786	469	1208	264	1321	1786	278	579	84	327	538	700	277	415
21.5	21.5	21.3	21.3	21.1	21.1	21.1	20.9	20.9	20.7	20.5	20.5	20.5	20.3	20.3
53	53	52.5	52.5	52	52	25	51.5	51.5	51	50.5	50.5	50.5	20	20

## ALIGNMENTS

```
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 29-May.1998 #sequence_revision 29-May.1998 #text_change 11-Jan-2000
C; Date: 29-May.1998 #sequence_revision 29-May.1998 #text_change 11-Jan-2000
E; Accession: 137552
Eur. J. Immunol. 24, 677-683, 1994
A; Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen A; Reference number: 137552; MUID:94170844
A; Accession: 137552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958 C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-277 <RES>
OX40 homolog - human
```

Gaps ö Length 277; Indels 39.0%; Score 96; DB 2; Le 43.6%; Pred. No. 0.00014; tive 6; Mismatches 16; Query Match 39.0 Best Local Similarity 43.6 Matches 17; Conservative

ö

128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAIC 166 2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40 à q

gene ox40 protein - mouse

N'Alternate names: OX10 antigen C;Species: Mus musculus (house mouse) C;Date: O2-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000 C;Accession: I48700; I48334; S34377 R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J J. Immunol. 151, 5561-5271, 1993 A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell

A; Accession: I48700

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-272 <RES>

A; Cross-references: EMBL:221674; NID:9312827; PIDN:CAA79772.1; PID:9312828
R; Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 936-930, 1995
A; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX A; Reference number: I48334; MUID:95255413

A;Residues: 1-14,'G',16-272 <RE2> A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819 A,Accession: I48334
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-14, 'G', 16-272 <RE2>

Genetics

g à

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the T-Cell Antigen 4-1B
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A;Residues: 1-459 <RES>
A;Cross-references: BMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
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R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: B32393; I48879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rossidues: 1-256 <RES>
A,Cross-references: EMBL:U02567; NID:91117783; PIDN:AAA93113.1; PID:9409178
C,Genetics:
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122 K;Won, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T. J. Immunol. 152, 2256-2262, 1994 A;Title: Genomic Organization and Chromosomal Localization of the T-Cell
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                                                                                                                                                                                                                                Length 271;
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C; Superfamily: CD27 antigen; NGF receptor repeat homology C (Keywords: growth factor receptor; transmembrane protein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-271/Froduct: OX40 antigen #status predicted <AMI>F;211-235/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Introns: 35/1, 69/1, 115/1, 138/2, 156/3, 181/1, 225/1 Superfamily: CD27 antigen; NGF receptor repeat homology
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>
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Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A; Title: cDNA sequence of two inducible T-cell genes.
A; Reference number: A32393; MUID:89184547
                                                                                                                                                                                                                             Score 84; DB 2;
Pred. No. 0.0042;
4; Mismatches 1
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A; Accession: I48879
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35.0%;
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ilarity 41.0%;
Conservative
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Best Local Similarity 35.0°
Matches 14; Conservative
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Best Local Similarity
Matches 16; Conserv
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A; Residues: 1-256 < KWO>
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C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro C:Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix C:Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix C:Superfamily: CD27 antigen; NGF receptor receptor it ransmembrane protein C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein F:118-125/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT> F:187-213/Domain: transmembrane #status predicted <TWM>
F:188-149/Binding site: carbohydrate (Asn) (covalent) (by casein kinase II) #status predict F:234,235/Binding site: phosphate (Thr) (covalent) (by protein kinase II) #status predicted
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A;Reference number: JT0752; MUID:94085794
A;Accession: JT0752
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C;Accession: I38426, JV075.
Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molecular and blological characterization of human 4-1BB and its ligand.
A;Reference number: I38426; MUID:94374434
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Ox40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
E;Rallett, S; Fossum, S; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                      Length 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocyte activation-induced receptor ILA precursor - human
                                                                  A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                        DB 2; I
0.00018;
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A;Molecule type: mRNA
A;Residues: 1-255 <RES>
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Pred. No. 0.000
5; Mismatches
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46.2%;
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Best Local Similarity 46.2'
Matches 18; Conservative
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Matches 16; Conserv
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Matcaraki K., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T.;
"EDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
protein from snake venom.";
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                                                                                                                                                                             BY SIMILARITY.
COMMENCE (GLONAC...) (POTENTIAL).
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
NCBL_raxID-88087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atoda H., Hyuga M., Morita T.;
"The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.";
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P23806; Q91246;
D1-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN A CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                           LINKED (GLCNAC. . .) (POTENTIAL) 624626E6022F656F CRC64;
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                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 435;
Pred. No. 9.6;
5; Mismatches 23; Indels
                           InterPro; IPR001368; -.
Pfam: PE00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50065; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                        LYMPHOTOXIN-BETA RECEPTOR
                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                    CYTOPLASMIC (POTENTIAL)
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TNFR-CYS 3.
TNFR-CYS 4.
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MEDLINE=91332000; PubMed=1831197;
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                                                                                                                                                                                                                                                                                                                                Query Match 22.0%;
Best Local Similarity 26.8%;
Matches 11; Conservative
 L04270; AAA36757.1;
P25942; 1CDF.
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124
168
211
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                     MIM; 600979;
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DOMAIN
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HSSP;
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                                              *ATA CRYSTALLOGRAPHY (2.5 ANGSTROMS).

**BEDLINE=97331317; PubMed=9187649;

Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;

**Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;

**Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains.";

Nat. Struct. Biol. 4:438-441(1997).

-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.

-!- FUNCTION: AT HETERODIMER OF CALCIUM FOR EIGEND BINDING.

-!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.

-!- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COAGULATION FACTOR IX/FACTOR X-BINDING
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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SEQUENCE FROM N.A.
MEDLINE-92105763; Pubmed-1370315;
Torres R.M., CLE.A.;
"Differential increase of an alternatively polyadenylated mRNA
"Define of murine CD40 upon B lymphocyte activation.";
"Tmmunol, 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH C-98 OF B CHAIN) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
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C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FB3DDD2369009263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53.5; DB 1;
Pred. No. 4.4;
2; Mismatches 5;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A39332. A39332.
PDB; IIXX; 06-MAY 9B.
InterPro; IPR001304; -.
Pfam; PF00059; lectin_c; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D83331; BAA11887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 21.7%;
Best Local Similarity 41.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17213
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P27512;
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                                    TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS0050; TNFR_NGFR_2; 4.
PROSITE; PSc0050; TNFR_NGFR_2; 4.
SHECEPLOT; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.5%; Score 53; DB 1; Length 289; 29.3%; Pred. No. 9; Live 2; Mismatches 25; Indels
Torres R.M.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD40L RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X TWER-CYS.
TWER-CYS 1.
TWER-CYS 2.
                                                                                                                                                                                                                                                                                                     EMBL; M94126; AAA37404.1; --
EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 29.3
Matches 12; Conservative
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HSSP; P25942; 1CDF.
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DOMAIN
DOMAIN
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Search completed: September 4, 2001, 16:15:26 Job time: 1138 sec

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        InterPro; IPR000812; -.
Pfam; PF00096; zf-C2H2; 7.
PRINTS; PR00048; ZINCFINGER.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
PROSITE; PS5015; ZINC_FINGER_C2H2_2; 5.
Transcription regulation; Nuclear protein; Zinc-finger; Metal-binding; DNA_binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park S.H., Hwang H.J., Kang H.S.; "MSS1 gene, encoding a zinc-finger motif, is involved in glucose repression and STA10 repression of glucoamylase gene in Saccharomyces
                                                                                                                                                                                                                                      18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR INVOLVED IN REGULATION OF GLUCOSE REPRESSION. BINDS TO UAS-1 IN THE STA1 PROMOTER.
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: STRONG, TO NRG2.
                                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
11-OCT-2000 (Rel. 40, Last annotation update)
17RANSCRIPTIONAL REGULATOR NRG1 (ZINC FINGER PROTEIN MSS1).
18RG1 OR MSS1 OR YDS12.01C.
18ACCharcmyces cerevistae (Baker's yeast).
18 Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
18ACCharomycetales; Saccharomycetaceae; Saccharomycetes;
                                                                                                                                                                                                                                                             -----LTVFPGNKTHNA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oliver K., Harris D., Barrell B., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             Score 56; DB 1; Length 880;
Pred. No. 10;
                                                                                                                                                                                                                                    15; Indels
                                                                                        C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
A; 4B0C2E818FAFE7F6 CRC64;
                                                                                                                                                                                                                                                                                                                                              231 AA
                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                            DCASGTFSGG--HE-----GHCKPWTDCTQFGF
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Pfam; PF00096; zf-C2H2; 2.
PRIMS; PR00048; zINCFINGER.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                             22.8%;
28.6%;
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Best Local Similarity 28.6'
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                730
762
790
818
846
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738
768
796
824
880 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae."
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Q03125;
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SEQUENCE
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ZN_FING
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ZN_FING
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Repressor;
Transcription regulation; Repeat.
ZN_FING 174 196 C2H2-TYPE.
ZN_FING 202 226 C2H2-TYPE.
                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukuda H., Ogawa T., Ishihara K., Fujii T., Nagahama K., Omata T., Inoue Y., Tanase S.; Morino Y.;

Inoue Y., Tanase S.; Morino Y.;

Molecular cloning in Escherichia coli, expression, and nucleotide sequence of the gene for the ethylene-forming enzyme of Pseudomonas syringae pv. phaseolicola PK2.";

Bloching Blochem. Blophys. Res. Commun. 188:826-832(1992).

-I. CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXXLATE + 02 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETHYLENE + HCN + CO(2) + 2 H(2)0.
--- COFACTOR: IRON AND ASCORBATE.
--- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE.
--- SIMILARIY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00671; Fe_Asc_oxidored; 1.
Ethylene blosynthesis; Oxidoreductase; Iron; Vitamin C; Plasmid.
SEQUENCE 350 AA; 39444 MW; 5FD86F07EFCD392B CRC64;
                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                  DB 1; Length 231;
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Pred. No. 6.9;
                                                                                                                                                                                                                                                                     8; Indels
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                                                                            C2H2-TYPE.
C2H2-TYPE.
50F7E7ED4690D109 CRC64;
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                                                                                                                                                                                                                  Score 54.5; E
Pred. No. 4.8;
                                                                                                                                                                                                                                                                   3; Mismatches
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                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv. phaseolicola).
                                                                                                                                                                                                                                                                                                                      2 CASGTFSGGH------EGHCKPWTDCTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ETHYLENE-FORMING ENZYME) (EFE).
                                                                                                                                     26743 MW;
                                                                                                                                                                                                                  22.2%;
33.3%;
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46.7%;
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Best Local Similarity 46.7
Matches 14, Conservative
                                                                                                                                                                                                                                                                   11; Conservative
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                                                                                                                                     231 AA;
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Best Local Similarity
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P32021;
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SEQUENCE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                   Liepinsh E., Ilag L.L., otting G., Ibanez C.F., "NMR structure of the death domain of the p75 neurotrophin receptor."; EMBO J. 16:4999-5005(1997).
-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
                                                                                                                                                                                                                                                                           TISSUE-Liver;
MEDLINE-93077038; PubMed-1446821;
MEDLINE-93077038; PubMed-1446821;
METSIS M., Timmusk T., Allikmets R., Saarma M., Persson H.;
"Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter.";
Gene 121:247-254(1992).
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                               SEGUENCE FROM N.A.
MEDILINE-87115859; PubMed-3027580;
RAGORGE M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
"Gene transfer and molecular cloning of the rat nerve growth factor
                                                          01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: N-AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
SIMILARITY: COWTAINS A LA-NGFR,TWFF TYPE CYSTEINE-RICH REGION
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
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InterPro; IPR001488; -.
InterPro; IPR001368; -.
InterPro; IPR001368; -.
PF00020; Tart. -.
Pfam; PF00050; Tart. -.
PROSTIE; PS00652; TNFR_NGFR_1; 3.
PROSTIE; PS50050; TNFR_NGFR_2; 4.
PROSTIE; PS50017; DEATH_DOWAIN.
PROSTIE; PS50017; DEATH_DOWAIN:
PROSPICE; Naurogenesis; Transmembrane; Glycoprotein; Repeat; Phosphorylation; Signal; 3D-structure.
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4 X TNFR-CYS.
TNFR-CYS 1.
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                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97449145; PubMed-9305641;
                                               07, Created)
                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 334-418
                                                                                                                                                                                                                                                                  SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X05137; CAA28783.1;
                        STANDARD;
                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                          Nature 325:593-597(1987)
                                                                                              (GP80-LNGFR) (P75 ICD).
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425
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425
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                                                (Rel.
                                                                                                                                                        NCBI_TaxID=10116,
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                                                01-APR-1988
                       NGFR_RAT
P07174:
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RESULT 12
            NGFR_RAT
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
LYMPHOTOXIN-BETA PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR
LIBR OR INFCR OR INFRSF3.
                                                                                                SERYTHR-RICH.

DEATH DOMAIN.

BY SIMILARITY.

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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C. Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; "A lymphotoxin-beta-specific receptor.";
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                                  TNFR-CYS
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Best Local Simi
Matches 13;
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P36941;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Last sequence update) Last annotation update) RECEPTOR 2 PRECURSOR (TNF-R2) (P75).

P25119; P97893; 01-MAY-1992 (Rel. 22, Created) 01-MAY-1999 (Rel. 22, Last seq 15-JUL-1999 (Rel. 38, Last seq TUMOR NECROSIS FACTOR RECEPTOR

TNFRSF1B OR TNFR2 OR TNFR-2

Mus musculus (Mouse).

NCBI\_TaxID=10090;

474 AA

STANDARD;

TNR2\_MOUSE

SEQUENCE FROM N.A.

MEDLINES-91187885; PubMed-1849278;

Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,

Wong G.H., Chen E.Y., Goeddel D.V.;

"Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is species
specific.";

Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)

MEDLINE-91246168; PubMed-1645445;

SEQUENCE FROM N.A.

Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; "Molecular cloning and expression of the type I and type 2 murine receptors for tumor necrosis factor.";

Cell. Biol. 11:3020-3026(1991)

SEQUENCE OF 1-26 FROM N.A.

STRAIN=NOD; Jacob C.O., Liu J.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.

SEQUENCE OF 1-22 FROM N.A.

TISSUE-Liver;

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TURR-CYS 1.

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TURR-CYS 4.

BY SIMILARITY.

BY SIMILARI
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Pfam; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
SIGNAL.
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603B580ECD67636F CRC64;
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EMBL, U52165, AAC50622.1;
EMBL, U52156, AAC50622.1;
EMBL, U52158, AAC50622.1;
U52159, AAC50622.1;
U52159, AAC50622.1;
U52159, AAC50622.1;
U52159, AAC50622.1;
U52161, U52161, AAC50622.1;
U52161, U52162, AAC50622.1;
U52161, U52162, AAC50622.1;
U52161, U52162, AAC50622.1;
U52162, AAC50622.1;
U52164, AAC50622.1;
U518594, AAA3675.1;
U518594, AAA3675.1;
U518594, AAA3675.1;
U518594, AAA3665.1;
U518594, A
                                                                                                                                                                            EMBL; M32315; AAA59929.1; --
EMBL; M38857; AAA63362.1; --
EMBL; U52165; AAC50622.1; --
EMBL; U52156; AAC50622.1; JOINE
EMBL; U52157; AAC50622.1; JOINE
EMBL; U52159; AAC50622.1; JOINE
EMBL; U52159; AAC50622.1; JOINE
EMBL; U52160; AAC50622.1; JOINE
EMBL; U52161; AAC50622.1; JOINE
EMBL; U52161; AAC50622.1; JOINE
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Matches 15; Conservative
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TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1314883; Tnfrsflb.
InterPro; IPR001368; -
InterPro; PR00020; TNFR_c6; 4.
PROSITE: PS00052; TNFR_NGFR_1; 2.
PROSITE: PS50050; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Slgnal.
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A TURE-CYS.
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TURE-CYS 3.
TURE-CYS 4.
BY SIMILARITY.
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ò g RESULT 7
TNR2\_MOUSE

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NCBI_TaxID-4932;
                                                       ZAPL_YEAST
ID ZAPL_YEAST
AC P47043;
)T 01----
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TRANSMEM
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                                                                                                                          REPEAT
REPEAT
REPEAT
                                                                                                            DOMAIN
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        SIGNAL
                                                                                            DOMAIN
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                          CHAIN
          Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 21-416 FROM N.A.

MEDLINE-90152140; Pubmed-2154393;
Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
"Structure and developmental expression of the chicken NGF receptor.";
Dev. Biol. 137:287-304(1990).

-1-FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.

-1-SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoťa; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
BY SIMILARITY.
CHARGE (GLONAC. . .) (POTENTIAL).
CHARGE (GLONAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P., Shooter E.M., Reichardt L.F.; Shooter E.M., Reichardt L.F.; Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system."; Neuron 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOND FORMATION.

-!- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- FTW: N- AND O'GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
-!- SIMILARITY: CONTAINS 1 LA-NGFR/THER-TYPE CYSTEINE-RICH REGION.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
PIR; JN0006; JN0006.
PIR; JN0006; JN0006.
PIR; AG0504.
HSSP: P07174; INGR.
InterPro; IPR001488; -.
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Pfam: PF00531; death; 1.
PROSITE: PS00652; TNFR_NGFR_1; 3.
PROSITE: PS50050; TNFR_NGFR_2; 3.
PROSITE: PS5017; DEATH_DOMAIN; 1.
Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat; Phosphorylation; Signal.
                                                                                                                                                                                                                                             Score 61; DB 1; Length 474; Pred. No. 1.4;
                                                                                                                                                                                                                                                                               15; Indels
                                                                                                                                                                                  LINKED (GLCNAC. . .) (P
462EAE398C4D6563 CRC64;
                                                                                                                                                                                                                                                                                                                                 166 CAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVC 202
                                                                                                                                                                                                                                                                                                              2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                416 AA
                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=90166579; PubMed=2560385;
                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                             24.8%;
                                                                                                                                                                                           50319
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.6
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GP80-LNGFR) (P75 ICD).
                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                               RESULT B
NOFR_CHICK
NOFR_CHICK
AC P18519;
DT 01-NOV-1990
DT 01-NOT-100
CG dallus gallu
CC Gallus
CG Gallus
CC G
                                                                                     DISULFID
                   DISULFID
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     SPETTELLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pohl T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN ZINC ION HOMEOSTASIS BY ZINC-RESPONSIVE
TRANSCRIPTIONAL REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL)
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LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 CAYGYFQDELSGSCKECSIC-EVGFGLMFPCRDSQDTVC 138
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6BCEAAB54F4D2D56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB'1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ZINC-RESPONSTVE TRANSCRIPTIONAL REGULATOR ZAPI. OR XJL056C OR J1145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                                                               DEATH DOMAIN.
BY SIMILARITY.
NY SIMILARITY.
NY SIMILARITY.
NY SIMILARITY.
NY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                               4 X TNFR-CYS.
                                                                                                                                                                                                                                                            SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60.5;
Pred. No. 1.
                                                                                                                                                    TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                               POTENTIAL.
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35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44654
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Best Local Similarity 35.99
Matches 14; Conservative
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Science 248:1019-1023(1990).
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01-GCT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR ECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
THERSFIB OR INFR2 OR INFBR.
                                                                                                                                                                 ACTIVATED T-CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE-90260639; PubMed-2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy F.
Smith C.A., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
                                                ACTIVE DURING T CELL ACTIVATION.
SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER
                                                                                                                                                                                                                   -! SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POINTED (GLCNAC. . . ) (POINTED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00020; TNFR_C6; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                     ASSOCIATES WITH P56-LCK.

-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
--- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF
--- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-1BB LIGAND RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CASGIFSGGH-EGHCKPWIDCIQFGFLIVFPGNKTHNAVC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70.5; DB Pred. No. 0.049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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01-AUG-1991 (Rel. 19, Last seq
01-OCT-2000 (Rel. 40, Last ann
Immunol. 150:771-781(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27598 MW;
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35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J04492; AAA40167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : U02567; AAA93113.1; -. B32393; B32393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1101059; Infrsf9.
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256
187
208
208
256
159
45
85
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P20333;
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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TREALHUMAN
1D TRIRE, H
AC P20333
DT 01-070
DT 01-070
DE TUMOR
DE TUMOR
DE HINDIN
GN HOMO S
OC EUKARY
OC EUKARY
OC MENMAN
OC NCBLT
RR SEQUEN
RX SEQUEN
RX SEGUEN
RX SEG
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NATURE 398:533-538(1999).

-! FUNCTION: RECEPTOR FOR TNF-ALPHA, HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-! PIM: PHOSPHORYLATED: MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES THE NAME ENBREL (IMMUNEX AND WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITS (RA). BUBREL CHAIN FOR ENGLOBULIN FOR THE EXTRACELLULAR LIGAND-BINDING PORTION OF THERE LINKED TO AN IMMUGLOBULIN FOR CHAIN. IT BINDS TO THE ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 47.31.

MEDLINE=90110215; bubMed=2153136;

MEDLINE=90110215; bubMed=2153136;

MEDLINE=90110215; bubMed=2153136;

"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface urine. Evidence for immunological cross-reactivity with cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.; "Blochemical properties of the 75-kba tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91056048; Pubmed-2173696; Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Complementary DNA cloning of a receptor for tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; "Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

BELLINE-26299745; PubMed-8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
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SEQUENCE FROM N.A.
MEDLINE=91045991; PubMed=2172983;
Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
"A second tumor necrosis factor receptor gene product can shed
naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
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MEDLINE-90349572; PubMed-2166946;
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
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MEDLINE-93016040; PubMed-1328224;
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There are no restrictions on

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European Bioinformatics Institute.
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P20334;
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MEDLINE-90214614; PubMed-2157591;
Mallett S., Fossum S., Barclay A.N.;
Mallett S., Fossum S., Barclay A.N.;
Mallett S., Fossum C., Barclay A.N.;
Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFRSF4 OR TXGP1L OR OX40.

Rattus norvegicus (Rat).

Elwaryota; Metaria; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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            A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                     TUFR-CYS 2.
TUFR-CYS 3.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
F3A563FE5EF00460 CRC64;
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          SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RIC
DATABASE: NAME-PROW; NOTE-CD guide CDw137 entry;
WWW-"http://www.ncb1.nlm.nih.gov/prow/cd/cdw137.htm".
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                  Pfam; PF00020; TNFR_C6; 2.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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1-APR-1990 (Rel. 14, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC 0X40).
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TNFR-CYS 1.
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149
255 AA;
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MIM; 602250;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-94179805; PubMed-8133039;
Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
"Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (POTENTIAL). C06465136B16E821 CRC64;
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PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
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15-JUL-1999 (Rel. 38, Last annotation update)
4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).
TNFRSF9 OR LIA OR LYG3 OR CD137 OR CD157.
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TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
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Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
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MEDLINE-93139510; PubMed-7678621;
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MEDLINE-89184547; PubMed-2784565;
Kwon B.S., Weissman S.M.;
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41.08;
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GenCore version 4.5
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OM protein - protein search, using sw model

September 4, 2001, 16:15:26 : Search time 43.78 Seconds (without alignments) 32.080 Million cell updates/sec. Run on:

US-09-512-363-2\_COPY\_114\_154
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1 DCASGTFSGGHEGHCKPWTD......TOFGFLTVFPGNKTHNAVCV 41

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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SUMMARIES	DI	OX40_HUMAN	OX40_MOUSE	41BB_HUMAN	OX40_RAT	41BB_MOUSE	TNR2_HUMAN	TNR2_MOUSE	NGFR_CHICK	ZAP1_YEAST	NRG1_YEAST	ACCO_PSESH	NGFR_RAT	TNRC_HUMAN	IXA_TRIFL	CD40_MOUSE	LMB1_MOUSE	TNRC_MOUSE	LMB1_HUMAN	CCBS_OENBE	CCBS_DAUCA	ITA5_XENLA	MT22_ORYSA	ATS7_HUMAN	GBLP_ARATH	GBLP_BRANA	CD40_BOVIN .	CD40_HUMAN	LMB1_DROME	IXB_TRIFL		-1	CKI3_SCHPO	CPC2_RABIT
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### ALIGNMENTS

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                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/C;
MEDLINE=94044750; PubMed=8228223;
Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Gene structure and chromosomal localization of the mouse homologue
                                                       4 X TNFR-CYS:
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
TNFR-CYS 4.
TNFR-CYS 4.
TNFR-CYS 6.
TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Immunol. 25:926-930(1995).

-i- FUNCTION: RECEPPOR FOR THE OX40L/GP34 CYTOKINE.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SIMILARITY: CONPAINS A LA-NGFR/TWPE-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCEPTIO, INTOLISES; ...
Pfam; PC000060; TNFR_G.; 3.
PROSITE; PS00062; TNRR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                   39.0%; Score 96; DB 1; Length 277 43.6%; Pred. No. 3.1e-05; Live 6; Mismatches 16; Indels
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                             49F15525941550BF CRC64;
                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      2 CASGTFSGGHEGHCKPWIDCTQFGFLTVFPGNKTHNAVC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-95255413; PubMed=7737295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s cell interactions.";
Immunol. 151:5261-5271(1993).
                                                                                                                                                                                               29340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 221674; CAA79772.1; -. EMBL; X85214; CAA59476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:104512; Infrsf4.
InterPro; IPR001368; -.
                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
214
235
277
277
169
65
107
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of rat OX40 protein
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                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barclay A.N.;
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CARBOHYD
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwarz H., Tuckwell J., Lotz M.; "A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
-!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVE DURING T CELL ACTIVATION.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
4-IBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-IBB HOMOLOG)
(T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Blood;
MEDINE-95347766; PubMed-7622190;
Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
Kwon B.S.,
                                                                                                                                                                                                                                                                                                                       Length 272;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                             TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                       Score 95; DB 1; 1
Pred. No. 4.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                            2 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 40
                   OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 AA
                                                                                                     4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Immunol. 24:2219-2227(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Blood;
MEDLINE-94085794; PubMed-8262389;
                                                                                                                                                                                                                                                              ž
                                                                                                                                                                                                                                                                                                                     Query Match 38.6%;
Best Local Similarity 46.2%;
Matches 18; Conservative
                                                                                                                                                                                                                                                       30153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
19
272
272
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1165
1165
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                                                                                                                                                                                                                                   15
272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFRSF9 OR ILA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwarz H.;
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Q07011;
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3. Heynick, K. et al. Molecular Cell Biology Res. Communications (2001) 4(5): 259-265

Handel, M.L. et al. Clinical and Experimental Pharmacology and Physiology (2000) 27(3): 139-144 (4.

5. Jue, D.-M. et al. J. Korean Med. Sci. (1999) 14(3): 231-238

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